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Copyright (c) 1993 - 2003 Compugen Ltd.
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score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result   Cuts  |  | •                            |
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| Description  ARALO265  ARACOCCA  BRIGGS  ARACOCCA  ARACOCCA  ARACOCCA  BRIGGS  ARACOCCA  A |  | 66 DB                        |
| cription  10265 Sequence  103274 Streptoco  103274 Streptoco  103274 Streptoco  103274 Sequence  103274 Sequence  103274 Sequence  103274 Sequence  103275 Sequence  103275 Sequence  103276 Sequence  103277 Sequence  103277 Sequence  103277 Sequence  103277 Sequence  103278 Sequence  103279 Streptoco  103279 Streptoco  103279 Streptoco  103279 Streptoco  103279 Sequence  103278 Sequence  103279 Sequence  103279 Sequence  103279 Sequence  103279 Sequence  103279 Sequence   | 916139<br>916139<br>91714613<br>91714613<br>91714613<br>91714613<br>91714613<br>91714613<br>91714613<br>91714613<br>91714613<br>91714613<br>91714613<br>91714613<br>91714613<br>91714613<br>91714613<br>91714613<br>91714613<br>91714613<br>91714613<br>91714613<br>91714613<br>91714613<br>91714613<br>91714613<br>91714613<br>91714613<br>91714613<br>91714613<br>91714613<br>91714613<br>91714613<br>91714613<br>91714613<br>91714613<br>91714613<br>91714613<br>91714613<br>91714613<br>91714613<br>91714613<br>91714613<br>91714613<br>91714613<br>91714613<br>91714613<br>91714613<br>91714613<br>91714613<br>91714613<br>91714613<br>91714613<br>91714613<br>91714613<br>91714613<br>91714613<br>91714613<br>91714613<br>91714613<br>91714613<br>91714613<br>91714613<br>91714613<br>91714613<br>91714613<br>91714613<br>91714613<br>91714613<br>91714613<br>91714613<br>91714613<br>91714613<br>91714613<br>91714613<br>91714613<br>91714613<br>91714613<br>91714613<br>91714613<br>91714613<br>91714613<br>91714613<br>91714613<br>91714613<br>91714613<br>91714613<br>91714613<br>91714613<br>91714613<br>91714613<br>91714613<br>91714613<br>91714613<br>91714613<br>91714613<br>91714613<br>91714613<br>91714613<br>91714613<br>91714613<br>91714613<br>91714613<br>91714613<br>91714613<br>91714613<br>91714613<br>91714613<br>91714613<br>91714613<br>91714613<br>91714613<br>91714613<br>91714613<br>91714613<br>91714613<br>91714613<br>91714613<br>91714613<br>91714613<br>91714613<br>91714613<br>91714613<br>91714613<br>91714613<br>91714613<br>91714613<br>91714613<br>91714613<br>91714613<br>91714613<br>91714613<br>91714613<br>91714613<br>91714613<br>91714613<br>91714613<br>91714613<br>91714613<br>91714613<br>91714613<br>91714613<br>91714613<br>91714613<br>91714613<br>91714613<br>91714613<br>91714613<br>91714613<br>91714613<br>91714613<br>91714613<br>91714613<br>91714613<br>91714613<br>91714613<br>91714613<br>91714613<br>91714613<br>91714613<br>91714613<br>91714613<br>91714613<br>91714613<br>91714613<br>91714613<br>91714613<br>91714613<br>91714613<br>91714613<br>91714613<br>91714613<br>91714613<br>91714613<br>91714613<br>91714613<br>91714613<br>91714613<br>91714613<br>91714613<br>91714613<br>91714613<br>91714613<br>91714613<br>91714613<br>91714613<br>91714613<br>91714613<br>91714613<br>91714613<br>91714613<br>91714613<br>91714613<br>91714613<br>91714613<br>91714613<br>91714613<br>91714613<br>91714613<br>91714613<br>91714613<br>91714613<br>91714613<br>91714613<br>91714613 | 2026                         |
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| Query Match Best Local Similarity 100.0%; Score 2388; DB 6; Length 2389; Best Local Similarity 100.0%; Pred. No. 0; Matches 2389; Conservative 0; Mismatches 0; Indels 0; Gaps  Qy 1 TTCTTACGAGTTGGGACTGTATCAAGCTAGAACGGTTAAGGAAAATAATCGTGTTTCCTA Db 1 TTCTTACGAGTTGGGACTGTATCAAGCTAGAACGGTTAAGGAAAATAATCGTGTTTCCTA  Qy 61 TATAGATGGAAAACAAGCGACGCAAAAAACGGAGAATTTGACTCCTGATGAGGTTAGCAA  Qy 61 TATAGATGGAAAACAAGCGACGCAAAAAACGGAGAATTTGACTCCTGATGAGGTTAGCAA  Ob 61 TATAGATGGAAAACAAGCGACGCAAAAAACGGAGAATTTGACTCCTGATGAGGTTAGCAA  Ob 61 TATAGATGGAAAACAAGCGACGCAAAAAACGGAGAATTTGACTCCTGATGAGGTTAGCAA | ORGANISM Unknown.  REFERENCE 1 (bases 1 to 2389) AUTHORS Choi,G.H., Kunsch,C.A., Barash,S.C., Dillon,P.J. Fannon,M.R. and Rosen,C.A. TITLE Streptococcus pneumoniae antigens and vaccines JOURNAL Patent: US 6159469-A 55 12-DEC-2000; FEATURES Location/Qualifiers source /organism="unknown"  BASE COUNT 830 a 461 c 486 g 611 t 1 othe  | RESULT 1 AR120765 LOCUS DEFINITION Sequence 55 from patent US 6159469. VERSION AR120265 VERSION AR120265 VERSION AR120265 GI:14103841 KEYWORDS SOURCE Unknown. | 58.2 2.4 253394 3 AB014833<br>58 2.4 94434 5 AL929250<br>57.8 2.4 249995 3 AB014840<br>57.8 2.4 253305 3 PFMAL3P7<br>57.2 2.4 110000 2 PFMALBP1 02<br>57.2 2.4 114226 2 AC004710<br>57.2 2.4 126429 2 AC004710<br>57.2 2.4 126429 2 AC005507<br>57.2 2.4 250421 3 AB014849<br>57 2.4 250421 3 AB014849<br>57 2.4 250421 3 AB014849<br>57 2.4 250421 3 AB014869<br>57 2.4 2618 5 AL591365<br>56 2.4 203138 2 BX530070<br>56.4 2.4 151343 5 AL929536 | 78 61.4 2.6 250195 3 AE014831 79 60.6 2.5 96249 9 AC116612 80 60.6 2.5 225581 2 BX537105 81 60.4 2.5 110000 2 PFMAL7P1 06 82 60.4 2.5 253924 3 AE014822 83 60.2 2.5 513939 9 AC099341 84 60.2 2.5 513939 9 AC099341 85 60 2.5 61052 2 AC123513 86 60 2.5 136240 3 AC117070 87 59.4 2.5 250029 3 AE014820 88 58.6 2.5 272545 2 AC090533 | 2.6 4.3 1239 6 AX608408 5.6 3.2 110000 2 BX005010 3 5.6 3.2 198550 2 BX004991 5.4 3.2 110000 2 PFWALI3 07 0.6 3.0 115758 9 AC104634 70 2.9 250029 3 AE014839 9.4 2.9 110000 2 PFWALI3 24 6.6 2.8 145265 2 AL935272 6.4 2.7 164347 9 AC104805 3.6 2.7 215333 9 AP002387 2.8 2.6 2000 6 AX855393 |
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| gth 2389; els 0; Gaps 0; ATAATCGTGTTTCCTA 60 ATAATCGTGTTTCCTA 60 ATAATCGTGTTTCCTA 60 OD ATAATCGTGTTAGCAA 120 CTGATGAGGTTAGCAA 120 CTGATGAGGTTAGCAA 120 CTGATGAGGTTAGCAA 120 Oy  | ., Dougherty,B.,   | Qy Db Qy Qy Qy Db Qy Db  | ABO14833 Plasmodiu AL929250 Zebrafish AEO14840 Plasmodiu AL034559 Plasmodiu Db 166494 Sequence 14 Continuation (3 of ACO04710 Plasmodiu ACO05507 Plasmodiu ABO14849 Plasmodiu AL591365 Zebrafish BX530070 Danio rer AL929536 Zebrafish Db  | AB014831 Plasmodiu Qy AC116612 Homo sapi BX537105 Danio rer Continuation (7 of AB014822 Plasmodiu AC099341 Homo sapi BX510939 Danio rer AC123513 Dictyoste AC17070 Dictyoste AB014820 Plasmodiu AC090533 Mus muscu Db  | AX608408 Sequence Continuation (4 of BX004991 Danio rer Continuation (8 of AC104634 Homo sapi AE014839 Plasmodiu Continuation (25 o AL935272 Danio rer AC104805 Homo sapi AP002387 Homo sapi AP002387 Homo sapi AP002387 Homo sapi Db Db   |
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|   | 1 TAAGAACTTCAAAGCGGATGAAGAGCCAGTAGAGGAAACACCTGCTGAGCCAGAAGTCCC 21          |
|   | TGGATGGGG<br>        <br>TGGATGGGG   |
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|   | 1681 CCTTTCTGATAAGGAAAAAGTTGCAGCTCAAGCCTATACTAAAGAAAAAGGTATCCTACC 1740<br> |
|   | TGAAGGAGATGCATATGTAACGCCTCATATGGGCCATAGTCACTGGATTGGAAAAGATAG 16            |
|   | 1561 AGCTGATAAGTATACAACGTCAGATGGTTACATTTTTGATGAACATGATATAATCAGTGA 1620<br> |
|   | 1501 ACTTGGCAAACCAAATTCTCAAATTGAGTATACTGAAGACGAAGTTCGTATTGCTCAATT 1560<br> |
|   | 1441 TAAAGAAAAATTGGTAGATGATTATTGGCATTCCTAGCACCAATTACCCATCCAGAGCG 1500<br>  |
|   | 1381 TAATTCTGATTTCCAAGCCTTAGACAAATTATTAGAACGCTTGAATGATGAATCGACTAA 1440<br> |
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Kunsch,C.A., Choi,G.H., Johnson,S.L. and Hromockyj,A.
Streptococcus pneumoniae antigens and vaccines
Patent: JP 2001505415-A, 28 24-APR-2001;
HUMAN GENOME SCIENCES INC
PN JP 2001505415-A/28
PD 24-APR-2001
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R 31-OCT-1996 US 60/029960

I CHARLES A KUNSCH,GIL H CHOI,SYDNOR L JOHNSON,ALEX HROMOCKYJ PC
C12N15/31,C12N5/18,C12N1/21,C07K14/315,C12Q1/68,A61K39/09, PC
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/mol type="genomic DNA"
/db_xref="taxon:32644"
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| 1501 ACTTGGCAAACCAAATTCTCAAATTGAGTATACTGAAGACGAAGTTCGTATTGCTCAATT 1560 | 1441 TAAAGAAAATTGGTAGATGATTATTGGCATTCCTAGCACCAATTACCCATCCAGAGCG 1500<br>                               | 1381 TAATTCTGATTTCCAAGCCTTAGACAAATTATTAGAACGCTTGAATGATGAATCGACTAA 1440                             | 1321 TGATAAAGCATATAATCTGTTAACTGAGGCTCATAAAGCCTTGTTTGNAAATAAGGGTCG 1380 | 1261 TGTTTCACACACTTTAACTGCTAAAAAAGAAAATGTTGCTCCTCGTGACCAAGAATTTTA 1320 · | 1201 GAAAGATTTACCATCTGAAACTGTTAAAAATCTTGAAAGCAAGTTATCAAAACAAGAGAG 1260<br> | 1141 ACGAAAAGTTGGGGAAGGATATGTATTCGAAGAAAAGGGCATCTCTCGTTATGTCTTTGC 1200 | 1081 CCCGCAACCTGCACCAAATCTTAAAATAGACTCAAATTCTTCTTTGGTTAGTCAGCTGGT 1140 | 1021 GGTACCAGATTCAAGGCCAGAACAACCAAGTCCACAACCGGACTCCGGAACCTAGTCCAGG 1080 | 961 GTCTGAATTGGAAGAACGAATCGCTCGTATTATTCCCCTTCGTTATCGTTCAAACCATTG 1020<br> | 901 AGCTAGAGGTGTTGCAGTGCCACACGGAGATCATTACCACTTCATCCCTTACTCTCAAAT 960 | 841 TCAACGACATGTAGAATCTGATGGCCTTGTCTTTGATCCAGCACAAATCACAAGTCGAAC 900 | 781 AGCAAGTCAAAGTAATGACATTGATAGTCTCTTGAAACAGCTCTACAAACTGCCTTTGAG 840 | 721 TGTAAGCAATCCAGGAACTACAAATACTAACACAAGCAACAACAGCAACACACAC | 661 TTCAAGAACCTATCGCCGACAAATAGCGATAACACTTCAAGAACAAACTGGGTACCTTC 720 | 601 ATCAGCTAGCGAGTTGGCTGCAGAAGCCTTCCTATCTGGTCGAGGAAATCTGTCAAA 660 | 541 TGGTGATGCTTATATCGTTCCTCATGGAGATCATTACCATTACATTCCTAAGAATGAGTT 600 | 481 AGGACGCTATACTACAGATGATGGTTATATCTTTAATGCTTCTGATATCATAGAGGATAC 540 | 421 TCAACATCGTGAAGGTGGAACTCCAAGAAACGATGGTGCTGTTGCCTTGGCACGTTCGCA 480 |
| AUTHORS  | ORGANISM Streptococcus preumoniae organism Streptococcus; Lac Bacteria; Firmicutes; Lac Streptococcus. | ACCESSION AX569139  ACCESSION AX569139.1 GI:26002636  KEYWORDS  SOURCE Street Concerns presumoniae |  | 2341   | 2281 T   | 2221   | 2161 T   | 2101 7  | 101 1   | у <b>н</b> ,   | 1921 T   | ,  | 1801  | ا دسو دس  | 4 6 6   | 1621   | 1561   | Db 1501 ACTTGGCAAACCAAATTCTCAAA                                      |

s pneumoniae s pneumoniae micutes; Lactobacillales; Streptococcaceae;

2406 bp DNA from Patent WO02077021.

linear PAT 29-NOV-2002

유양

Tettelin, H. and Fraser, C.

| Оу  | Qy<br>db   | Db Qy  | Qy<br>Db   | Qy<br>Db  | Qy<br>dd   | Qy<br>Db   | Qy<br>Db   | Qy<br>Db  | Qy<br>Db   | Qу   | Qу   | Оу   | Qy<br>Db  | Qy<br>Db  | Query<br>Best L<br>Matche   | BASE COUNT<br>ORIGIN  | FEATURES<br>sou   | TITLE<br>JOURNAL   |
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| 841 TCAACGACATGTAGAATCTGATGGCCTTGTCTTTGATCCAGCACAAATCACAAGTCGAAC 900      | 781 AGCAAGTCAAAGTAATGACATTGATAGTCTCTTGAAACAGCTCTACAAACTGCCTTTGAG 840   | 721 TGTAAGCAATCCAGGAACTACAAATACTAACACAAGCAACAACAGCAACACCTAACAGTCA 780<br>  | 661 TTCAAGAACCTATCGCCGACAAAATAGCGATAACACTTCAAGAACAAACTGGGTACCTTC 720 | 601 ATCAGCTAGCGAGTTGGCTGCAGAAGCCTTCCTATCTGGTCGAGGAAATCTGTCAAA 660 | 541 TGGTGATGCTTATATCGTTCCTCATGGAGATCATTACCATTACATTCCTAAGAATGAGTT 600 [ | 481 AGGACGCTATACTACAGATGATGGTTATATCTTTAATGCTTCTGATATCATAGAGGATAC 540     | 421 TCAACATCGTGAAGGTGGAACTCCAAGAAACGATGGTGCTGTTGGCTTCGCACGTTCGCA 480 | 361 TGCCCACGCGGATAACGTCCGTACAAAAGAGGAAATCAATC                     | 301 GGTCAAGGGTGGATATGTTATCAAGGTAGATGGAAAATACTATGTTTACCTTAAGGATGC 360<br> | 241 TGAAGAATTACTCATGAAAGATCCAAACTATAAGCTAAAAGATGAGGATATTGTTAATGA 300   | 181 TTCACATGGCGACCACTATCATTATTACAATGGTAAGGTTCCTTATGACGCTATCATCAG 240 | 121 GCGTGAAGGAATCAATGCTGAGCAAATCGTCATCAAGATAACAGACCAAGGCTATGTCAC 180<br> | 61 TATAGATGGAAAACAAGCGACGCAAAAAACGGAGAATTTGACTCCTGATGAGGTTAGCAA 120<br> | 1 TTCTTACGAGTTGGGACTGTATCAAGCTAGAACGGTTAAGGAAAATAATCGTGTTTCCTA 60 | Query Match 100.0%; Score 2388; DB 6; Length 2406; Best Local Similarity 100.0%; Pred. No. 0; Matches 2388; Conservative 0; Mismatches 1; Indels 0; Gaps 0; | /mol_type="genomic DNA"<br>/db_xref="taxon:1313"<br>834 a 461 c 490 g 621 | Chiron Sp   |  |
| D 64  | D B  | ) B &  | S B &  | o da Qy   | A A  | ) DD QY  | ρb   | - 8g - 82   | B &  | D &  | D QQ   | D CY   | D Dy  | Ωy  | Qγ  | Qy<br>db  | Db Qy   | ממ   |
| 1921 TAMATITIGETINGTITIGATIGATCACACATACAAAGCTCCAAATGGCTATACCTTGGAAGA 1997 | 61 TACAGTIGAGGITAAAAACGGITAATITUGATTATICCTCATAAGGATCATTACCATAATAT 19 [ | 1 CAATCGTGTGAAAGGGGAAAAACGAATTCCACTCGTTCGACTTCCATATATGGTTGAGCA 1 18 CAATCGTGTGAAAGGGGAAAAACGAATTCCACTCGTTCGACTTCCATATATGGTTGAGCA 1 | 41 TCCATCTCCAGACGCAGATGTTAAAGCAAATCCAACTGGAGATAGTGCAGCAGCTATTTA 180  | CCTTTCTGATAAGGAAAAGTTGCAGCTCAAGCCTATACTAAAGAAAAAGGTATCCTACC 17    | 1 TGAAGGAGATGCATATGTAACGCCTCATATGGGCCATAGTCACTGGATTGGAAAAGATAG 1 -     | 61 AGCTGATAAGTATACAACGTCAGATGGTTACATTTTTGATGAACATGATATAATCAGTGA 162   11 | 18   | 41 TAAAGAAAATTGGTAGATGATTTATTGGCATTCCTAGCACCAATTACCCCATCCAGGCG 15 | AITICIGATITICCAAGCCTTAGACAAATTATTAGAACGCTTGAATGATGATGAATCACTAA           | TGATAAAGCATATAATCTGTTAACTGAGGCTCATAAAGCCTTGTTTGAAAATAAGGGTCG TGATAAAGCATATAATCTGTTAACTGAGGGTCATAAAGCCTTGTTTGAAAATAAGGGTCG TGATAAAGCATATAATCTGTTAACTGAGGGTCATAAAGCCTTGTTTGAAAATAAGGGTCG | TGTTTCACACACTTTAACTGCTAAAAAAGAAATGTTGCTCCTGGTGACCAAGAATTTTA          | GAMAGATTIACCATCIGAAACIGTTAAAAATCTIGAAAGCAAGTTATCAAAACAAGAGAG             | A CGAAAAGTTGGGGAAGGATATGTATTGAAGAAAAGGGCATCTCTGTTATGTCTTTGC             | CCCGCAACCTGCACCAAATCTTAAAATAGACTCAAATTCTTCTTTGGTTAGTCAACTGGT      | GTACCAGATTCAAGGCCAGAACAACCAAGTCCACAACCGACTCCGGAACCTAGTCCAGG<br>   | 61<br>78  | 901 AGCTAGAGGTGTTGCAGTGCCACACGGAGATCATTACCACTTCATCCCCTTACTCTCAAAT 960<br> | 858 TCAACGACATGTAGAATCTGATGGCCTTGTCTTTGATCCAGCACAAATCACAAGTCGAAC 917 |

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AF291695
AF291695.1 GI:13345012
                                                                                                                                                                                                                                                                  Wizemann, T.M., Heinrichs, J.H., Adamou, J.E., Erwin, A.L., Kunsch, C., Choi, G.H., Barash, S.C., Rosen, C.A., Masure, H.R., Tuomanen, E., Gayle, A., Brewah, Y.A., Walsh, W., Barren, P., Lathigra, R., Hanson, M., Langermann, S., Johnson, S. and Koenig, S.
Use of a whole genome approach to identify vaccine molecules affording protection against Streptococcus pneumoniae infection Infect. Immun. 69 (3), 1593-1598 (2001)
                                                                                                                                                                         Submitted (01-AUG-2000) Molecular Biology, Human Garden, 9410 Key West Ave., Rockville, MD 20850, USA Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                      Streptococcus pneumoniae Streptococcus pneumoniae
                                                                                                                                                                                                             Direct Submission
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88 a 476 c 516 9 660 t 1 others

Query Match Best Local Similarity 1 TTCTTACGAGTTGGGACTGTATCAAGCTAGAACGGTTAAGGAAAATAATCGTGTTTTCCTA GCGTGAAGGAATCAATGCTGAGCAAATCGTCATCAAGATAACAGACCAAGGCTATGTCAC 180 ATCAGCTAGCGAGATTGGCTGCTGCAGAAGCCTTCCTATCTGGTCGAGGAAATCTGTCAAA AGGACGCTATACTACAGATGATGGTTATATCTTTAATGCTTCTGATATCATAGAGGATAC GGTCAAGGGTGGATATGTTATCAAGGTAGATGGAAAATACTATGTTTACCTTAAGGATGC TTCACATGGCGACCACTATCATTACTACAATGGTAAGGTTCCTTATGACGCTATCATCAG TATAGATGGAAAACAAGCGACGCAAAAAAACGGAGAATTTGACTCCTGATGAGGTTAGCAA 120 TGTAAGCAATCCAGGAACTACAAATACTAACACAAGCAACAACAGCAACACTAACAGTCA TTCAAGAACCTATCGCCGACAAAATAGCGATAACACTTCAAGAACAAACTGGGTACCTTC TGGTGATGCTTATATATCGTTCCTCATGGAGATCATTACCATTACCATTACCATTACCATAGAATGAGTT TCAACATCGTGAAGGTGGAACTCCAAGAAACGATGGTGCTGTTGCCTTTGGCACGTTCGCA GGTCAAGGGTGGATATGTTATCAAGGTAGATGGAAAAATACTATGTTTACCTTAAGGATGC TGAAGAATTACTCATGAAAGATCCAAACTATAAGCTAAAAGATGAGGATATTGTTAATGA TTCACATGGCGACCACTATCATTATTACAATGGTAAGGTTCCTTATGACGCTATCATCAG TATAGATGGAAAACAAGCGACGCAAAAAAACGGAGAATTTGACTCCTGATGAGGTTAGCAA TTCTTACGAGTTGGGACTGTATCAAGCTAGAACGGTTAAGGAAAATAATCGTGTTTCCTA TTCAAGAACCTATCGCCGACAAAATAGCGATAACACTTCAAGAACAAACTGGGTACCTTC AGGACGCTATACTACAGATGATGGTTATATCTTTAATGCTTCTGATATCATAGAGGATAC TCAACATCGTGAAGGTGGAACTCCAAGAAACGATGGTGCTGTTGCCTTGGCACGTTCGCA TGAAGAATTACTCATGAAAGATCCAAACTATAAGCTAAAAGATGAGGATATTGTTAATGA GCGTGAAGGAATCAATGCTGAGCAAATCGTCATCAAGATAACAGACCAAGGCTATGTCAC Conservative 100.0%; <u>.</u> Score 2388; Pred. No. 0; Mismatches DΒ 1; <u>,</u> Indels Length 0 Gaps 600 540 480 420 449 300 209 60 929 780 869 720 809 660 749 689 629 569 509 389 240 329 0

| 1860<br>2009 | ATATGGTTGAGCA<br>         <br>ATATGGTTGAGCA                         |  |
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| 1740<br>1889 | 681 CCTTTCTGATAAGGAAAAGTTGCAGCTCAAGCCTATACTAAAGAAAAAGGTATCCTACC     |  |
| 1680<br>1829 | GCCTCATATGGGCCATAGTCACTGGATTGGAAAAGATAG<br>                         |  |
| 1620<br>1769 | 1561 AGCTGATAAGTATACAACGTCAGATGGTTACATTTTTGATGAACATGATATAATCAGTGA   |  |
| 1560<br>1709 | 501 ACTTGGCAAACCAAATTCTCAAATTGAGTÁTACTGAAGACGAAGTTCGTATTGCTCAATT    |  |
| 1500<br>1649 | 441 TAAAGAAAAATTGGTAGATGATTTATTGGCATTCCTAGCACCAATTACCCATCCAGAGCG    |  |
|              | 81 TAATTCTGATTTCCAAGCCTTAGACAAATTATTAGAACGCTTGAATGATGAATCGACTAA<br> |  |
| 1380<br>1529 | 321 TGATAAAGCATATAATCTGTTAACTGAGGCTCATAAAGCCTTGTTTGNAAATAAGGGTCG    |  |
| 1320<br>1469 | 261 TGTTTCACACACTTTAACTGCTAAAAAAGAAATGTTGCTCCTCGTGACCAAGAATTTTA     |  |
| 1260<br>1409 | 01 GAAAGATTTACCATCTGAAACTGTTAAAAATCTTGAAAGCAAGTTATCAAAACAAGAGAG<br> |  |
| 1200<br>1349 | 141 ACGAAAAGTTGGGGAAGGATATGTATTCGAAGAAAAGGGCATCTCTCGTTATGTCTTTGC    |  |
| 1140<br>1289 | 081 CCCGCAACCTGCACCAAATCTTAAAATAGACTCAAATTCTTCTTTGGTTAGTCAGCTGGT    |  |
| 1080         | .021 GGTACCAGATTCAAGGCCAGAACAACCAAGTCCACAACCGACTCCGGGAACCTAGTCCAGG  |  |
| 1020<br>1169 | 961 GTCTGAATTGGAAGAACGAATCGCTCGTATTATTCCCCTTCGTTATCGTTCAAACCATTG    |  |
| 960          | 01 AGCTAGAGGTGTTGCAGTGCCACACGGAGATCATTACCACTTCATCCCTTACTCTCAAAT     |  |
| 900          | 1 TCAACGACATGTAGAATCTGATGGCCTTGTCTTTGATCCAGCACAAATCACAAGTCGAAC      |  |
| 840<br>989   | 81 AGCAAGTCAAAGTAATGACATTGATAGTCTCTTGAAACAGCTCTACAAACTGCCTTTGAG     |  |

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| 0   | O C K                     | SOURCE ORGANISM REFERENCE AUTHORS TITLE JOURNAL FEATURES FEATURES SOURCE BASE COUNT ORIGIN  | RESULT 5 AR218862 LOCUS DEFINITION ACCESSION VERSION VERSION                                 | 유<br>장,   | 8 8  | 4d.   | dy<br>VQ   | Db<br>Qy   | D Q  | 4<br>8  | B &   | B Q   |
|---|---------------------------|---|--|---|--|---|--|--|--|---|---|---|
| 1 TTCTTACGACTTGGGACTGTATCAAGCTAGAACGGTTAAGGAAATAATCGTGTTTCCTA | Match<br>ocal S<br>s 2388 | Unknown.  Unknown.  Unclassified.  1 (bases 1 to 8195)  1 (bases 1 to 8195)  Kunsch,C.A., Choi,G.H., Dillon,P.S., Rosen,C.A., Baras Fannon,M.R. and Dougherty,B.A.  Streptcocccus pneumoniae polynucleotides and sequences of the patent: US 6420115-A 94 16-JUL-2002;  Legation/Qualifiers  1. 8195  /organism="unknown"  2688 a 1622 c 1777 g 2105 t 3 others | AR218862 8195 bp DNA linear P<br>Sequence 94 from patent US 6420135.<br>AR218862 GI:23319796 | 2341 GTTGTTADAAGGAAGTAATCCTTCATCTGTAAGTAAGGAAAAAATAAAC 23<br> | 2281 TTTGACTCTTCAAATTATGGATAACAATAGTATCATGGCAGAAGCAGAAAAATTACTTG | 2221 AGTAACGGATTCTAGTCTGAAAGCCAATGCAACAGAAACTCTAGCTGGTTTACGAAATAA | 2161 TCAAGTAGAGACTGAAAAAGTAGAAGCCCAACTCAAAGAAGCAGAAGTTTTGCTTGC | 2101 TAAGAACTTCAAAGCGGATGAAGAGCCAGTAGAGGAAACACCTGCTGAGCCAGAAGTCC | 2041 TGGATGGGGCAATGCCAGTGAGCATGTGTTTAGGCAAGAAAGA | 1981 TTTGTTTGCGACGATTAAGTACTACGTAGAACACCCTGACGAACGTCCACATTCTAATGA | 1921 TAAATTIGCTIGGITTGAIGATCACACATACAAAGCTCCAAATGGCTATACCTIGGAAGA | 1861 TACAGTTGAGGTTAÀAAACGGTAATTTGATTATTCCTCATAAGGATCATTACCATAATAT<br> |
| GTTTCCTA         GTTTCCTA GTTTAGCAA          GTTAGCAA         | Gaps                      | h,s.c.,   | AT 25-SEP  | 38  | TTACTTGC   | CGAAATAA<br>        <br> CGAAATAA                                 | CTTGCGAA   | GAAGTCCC   | GATCCAAA<br>       <br>GATCCAAA                  | TCTAATGA  | TTGGAAGA  | CATAATAT<br>        <br> CATAATAT                                     |
| 3112<br>120<br>120<br>3172<br>180<br>3232                     | 0                         |   | -2002  |   | 2340<br>2489   | 2280<br>2429  | 2220<br>2369   | 2160<br>2309   | 2100<br>2249                                     | 2040<br>2189  | 1980<br>2129  | 1920<br>2069  |

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|---|--|--|--|---|--|--|---|--|---|---|--|--|---|---|--|--|---|
| 1201 GAAAGATTTACCATCTGAAACTGTTAAAAATCTTGAAAGCAAGTTATCAAAACAAGAGAG 1260<br>    | ACGAAAAGTTGGGGAAGGATATGTATTCGAAGAAAAGGGCATCTCTCGTTATGTCTTTGC 1 | CCCGCAACCTGCACCAAATCTTAAAATAGACTCAAATTCTTCTTTGGTTAGTCAGCTGGT 114 | 1021 GGTACCAGATTCAAGGCCAGAACAACCAAGTCCACAACCGACTCCGGAACCTAGTCCAGG 1080 | 961 GTCTGAATTGGAAGAACGAATCGCTCGTATTATTCCCCTTCGTTATCGTTCAAACCATTG 1020 | 901 AGCTAGAGGTGTTGCAGTGCCACACGGAGATCATTACCACTTCATCCCTTACTCTCAAAT 960<br> | 841 TCAACGACATGTAGAATCTGATGGCCTTGTCTTTGATCCAGCACAAATCACAAGTCGAAC 900 | 781 AGCAAGTCAAAGTAATGACATTGATAGCTCTTGAAACAGCTCTACAAACTGCCTTTGAG 840 | 721 TGTAAGCAATCCAGGAACTACAAATACTAACACAAGCAACAACAGCAACACTAACAGTCA 780 |   | 01 ATCAG<br>     <br>53 ATCAG                                     | GTTCCTCATGGAGATCATTACCATTACATTCCTAAGAI                       | CTATACTACAGATGATGGTTATAT<br>              <br>CTATACTACAGATGATGGTTATAT | 421 TCAACATCGTGAAGGTGGAACTCCAAGAAACGATGGTGCTGTTGCCTTTGGCACGTTCGCA 480 | TGCCCACGCGGATAACGTCCGTACAAAAGAGGAAATCAATC                         | 301 GGTCAAGGGTGGATATGTTATCAAGGTAGATGGAAAATACTATGTTTACCTTAAGGATGC 36        | 241 TGAAGAATTACTCATGAAAGATCCAAACTATAAGCTAAAAGATGAGGATATTGTTAATGA 3         | 181 TTCACÀTGGCGACCACTATCATTATTACAATGGTAAGGTTCCTTATGACGCTATCATCAG 240        |
| 8 B 8   | ) B &  | D 99   | 문왕   | B 8   | 당 왕  | g 49   | γ d,  | y da y   | g<br>S  | g Qy  | g S  | β Q  | B &   | B 8   | dg<br>VQ   | g Q  | dg<br>Qy  |
| 2281 TITGACTCITCAMATTA ISGA PACAMINGTA TA INGENIA CAMBANG ANA ANA TACE 2340 [ | 221 AGTAACGGATTCTAGTCTGAAAGCCAATGCAACAGCAACACTTAGCTAGC         | 61 TCAAGTAGAGACTGAAAAAGTAGAAGCCCAACTCAAAGAAGCAGAAGTTTTGCTTGC     | 2101 TAAGAACTTCAAAGCGGATGAAGAGCCAGTAGAGGAAACACCTGCTGAGCCAGAAGTCCC 2160 | 41 TGGATGGGCAATGCCAGTGACATGTGTTAGGCAAGAAGACCACAGTGAAGATCCAAA          | 1981 TTTGTTTGCGACGATTAAGTACTACGTAGAACACCCTGACGAACGTCCACATTCTAATGA 2040 [ | TAAATTTGCTTGGTTTGATGATCACCACATACAAAGCTCCAAATGGCTATACCTTGGAAGA        | TACAGTTICAGGTTAAAAACGGTAATTTCGATTATTCCTCATAAGGATCATTACCATAATAT<br>  | 01 CAATCGTGTGAAAGGGAAAAACGAATTCCACTGGTTCCATTTCATATATGGTTGAGCA        | TCCATCTCCAGACGCAGATGTTAAAGCAAATCCAACTGGAGATACTGCAGCCAGC | 1 CCTTTCTGATAAGGAAAAGTTGCAGCTCAAGCCTATACTAAAGAAAAAGGTATCCTACC<br> | TGAAGGACATGCATATGTAACGCCTCATATGGGCCATAGTCACTGGATTGGAAAAGATAG | ACCTGATAAGTATACAACGTCACATGGTTACATTTTTGATGAACATGATATAATCAGTGA           | 01 ACTIGGCAAACCAAATICTCAAATTGAGTATACTGAAGACGAAGTTCGTATTGCTCAATT<br>   | 41 TAAAGAAAATTGGTAGATGATTTATTGGCATTCCTAGCACCAATTACCCATCCAGAGCG 15 | 1381 TAATTCTGATTTCCAAGCCTTAGACAAATTATTAGAACGCTTGAATGATGAATCGACTAA 1440<br> | 1321 TGATAAAGCATATAATCTGTTAACTGAGGCTCATAAAGCCTTGTTTGNAAATAAGGGTCG 1380<br> | 1261 TGTTTGACACACTTTAACTGCTAAAAAAAGAAAATGTTGCTCCTCGTGACCAAGAATTTTA 1320<br> |

| 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0   | 0  | Query Ma<br>Best Loc<br>Matches<br>Qy<br>Db 3   | FEATURES source BASE COUNT ORIGIN   |  | COMMENT   | REFERENCE<br>AUTHORS.<br>TITLE<br>JOURNAL   | LOCUS DEFINITION ACCESSION VERSION KEYWORDS SOURCE ORGANISM  | Db 5 RESULT 6 BD003774                        |
|---|--|---|---|--|---|---|--|---|
| 181 TTCACATGGCGACCACTATCATTATTACAATGGTAAGGTTCCTTATGACGCTATCATCAG 240  | 61 TATAGATGGAAAACAAGCGACGCAAAAAACGGAGAATTTGACTCCTGATGAGGTTAGCAA 120  | Match 100.0%; Score 2388; DB 6; Length 8195; Local Similarity 100.0%; Pred. No. 0; Les 2388; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  1 TTCTTACGACTTGGGACTGTATCAAGCTAGAACGGTTAAGGAAAATAATCGTGTTTCCTA 60 | FT Location/Qualif<br>e 18195<br>/organism="unid<br>/mol_type="geno<br>/db_xref="taxon<br>2688 a 1622 c 177 | PC C12N15/09,A01K67/027,C07K14/315,C07K16/12,C12N1/15,C12N1/19, PC C12N1/21, PC C12N15/10,C12P21/02,C12Q1/68,G06F17/30,C12N15/00,C12N5/00, PC G06F15/40 CC Strandedness: Double; CC Topology: Linear; CC Topology: Linear; FH Key Location/Qualifiers FT source 1.8195 | OS Unidentified PN JP 2001501833-A/94 PN JP 2001501833-A/94 PD 13-FEB-2001 PF 30-OCT-1997 JP 1998520718 PF 31-OCT-1996 US 60/029960 PI CHARLES A KUNSCH,GIL H CHOI, PATRICK J DILLON, CRAIG A ROSEN, PI STEVEN C BARASH, PI MICHAEL FANNON, BRIAN A DOUGHERTY | 1 (bases 1 to 8195)  1 (bases 1 to 8195)  Kunsch,C.A., Choi,G.H., Dillon,P.J., Rosen,C.A., Bara,S.C.,  Fannon,M. and Dougherty,B.A.  Polynucleotide of Streptococcus pneumoniae and sequence Patent: UP 2001501833-A 94 13-FEB-2001;  HUMAN GENOME SCIENCES INC | BD003774  8195 bp DNA linear PAT 31-JAN-2002 Polynucleotide of Streptococcus pneumoniae and sequence. BD003774 BD003774.1 GI:18631735 JP 2001501833-A/94. unidentified unidentified unidentified |   |
| Q   | S B S B S  | אם א  | 0 Qy Qy   | D Q D Q  | D Q D Q   | рь<br>рь  | Q D Db   | ОУ<br>ОУ                                      |
| 4313 TGTTTCACACACTTTAACTGCTAAAAAAAGAAAATGTTGCTCCTCGTGACCAAGAATTTTA  1321 TGATAAAGCATATAATCTGTTAACTGGAGGCCCATAAAGCCTTGTTTGNAAATAAGGGTCG  1321 TGATAAAGCATATAATCTGTTAACTGAGGCTCATAAAGCCTTGTTTGNAAATAAGGGTCG  1373 TGATAAAGCATATAATCTGTTAACTGAAGCTTCATAAAGCCTTGTTTGAAAATAAGGGTCG  1381 TAATTCTGATTTCCAAGCCTTAGACAAATTATTAGAACGCTTGAATGAA | 1141 ACGARAGYTYGGGGAAGGATATYGTATYCGAAGAAAGGGCATCTCTCTGTTATGTCTTTTGC 1141 ACGARAGYTYGGGGAAGGATATYGTATYCGAAGAAAGGGCATCTCTCTCTTTGTCTTTTGC 1193 ACGARAAGTTGGGAAGGATATGTATTCGAAGAAAAGGGCATCTCTCTGTTATGTCTTTTGC 1201 GAAAGATTTACCATCTGAAACTGTTAAAAATCTTGAAAAGCAAGTTATCAAAACAAGAGAG 1201 GAAAGATTTACCATCTGAAACTGTTAAAAATCTTGAAAGCAAGTTATCAAAACAAGAGAG 4253 GAAAGATTTACCATCTGAAACTGTTAAAAATGTTGCTCCTCGTGACCAAGAATTTTA 1261 TGTTTCACCACCACTTTAACTGCTAAAAAAAGGAAAATGTTGCTCCTCGTGACCAAGAAATTTTA |   | 01<br>53<br>53<br>13  | 781 AGCAAGTCAAAGTAATGACATTGATAGTCTCTTGAAACAGCTCTACAAACTGCCTTTGAG   | 661 TTCAAGAACCTATCGCCGACAAATAGCGATAACACTTCAAGAACAAACTGGGTACCTTC   | 3593 TGGTGATGCTTATATCGTTCCTCATGGAGATCATTACCATTACCATTCCTAAGAATGAGTT  601 ATCAGCTAGCGAGTTGGCTGCTGCAGAAGCCTTCCTATCTGGTCGAGGAAATCTGTCAAA  | 3473 TCAACATCGTGAAGGTGGAACTCCAAGAAACGATGGTGCTTTGCCTTTGGCACGTTCGCA 481 AGGACGCTATACTACAGAGATGATGGTTATATCTTAATGGTTCTGATATCATAGAGGATAC  | 361 TGCCCACGCGGATAACGTCCGTACAAAAGAGGAAATCAATC |

| RESULT 7 ABO07418/c LOCUS LOCUS DEFINITION Streptococcus pneumoniae TIGR4 section 101 of 194 of the | Qy 2281 TTTGACTCTTCAAATTATGATAACAATAGTATCATGGCAGAAGCAGAAAAATTACTTGC  | Qy 2161 TCAAGTAGAGACTGAAAAAGTAGAAGCCCAACTCAAAGAAGCAGAAGTTTTTGCTTGC  | Db 5093 TGGATGGGGCAATGCCAGTAAAGGCCAGTAAGAGAACACCTGCTGAGCCAGAAAGTCCAAA  Oy 2101 TAAGAACTTCAAAGCGGATGAAGAGCCAGTAGAGGAAACACCTGCTGAGCCAGAAGTCCC  Db 5153 TAAGAACTTCAAAGCGGATGAAGAGCCAGTAGAGGAAACACCTGCTGAGCCAGAAGTCCC                 | 1981   | Db 4913 TACAGTTGAGGTTAAAAACGGTAATTTGATTATTCCTCATAAGGATCATTACCATAATAT  Qy 1921 TAAATTTGCTTGGTTTGATGATCACACATACAAAGCTCCAAATGGCTATACCTTGGAAGA                 | Qy 1801 CAATCGTGTGAAAGGGGAAAAACGAATTCCACTCGTTCGACTTCCATATATGGTTGAGCA                  | OY 1681 CCTTTCTGATAAGGAAAAGTTGCAGCTCAAGCCTATACTAAAGAAAAAGGTATCCTACC  | QY 1561 AGCTGATAAGTATACAACGTCAGATGGTTACATTTTTGATGACATGATATAATCAGTGA   |  |
|---|--|---|---|--|--|---|--|---|--|
| 1-AUG-2001 gene<br>complete CDS   | TTGC 2340<br>    <br>TTGC 5392   | GAA 2220<br>    <br> GAA 5272 gene<br>    <br>     CDS  | CAAA 5152<br>CAAA 5152<br>    <br>    <br>  |  | 4972 FEATURES 1980 Source 5032   | 1860<br>4912<br>1920 TITLE  | 1740 JOURNAL MEDLINE PUBNED REFERENCE AUTHORS  | GA 1620<br>   | ORGANISM 1560 REFERENCE AUTHORS  |
| GAHDLDSLIERDYNLYAATWGITAIQTGRLAQSGLAPYENQVFISEQLQTQKPDALF YEKIGQQLAGFSKEKTLMIGDSLTADIQGGNNAGIDTIWYNPHHLENHTQAQPTYEVY SYQDLDCLDKNILEKITF" complement(17241843) /gene="SP1172" complement(17241843) /gene="SP1172" /note="identified by Glimmer2; putative" /rodon_start=1 /transI_table=11   | PF00702"  (codon start=1)  /transI_table=11  /product="hydrolase, haloacid dehalogenase-like family"  /protein_id="AAK75280.1"  /db_xref="GI:14972651"  /translation="MFYKFLLFDLDHTLLDFDAAEDVALTQLLKEEGVADIQAYKDYY  /bwakatwkrlfikktiskort.Nymprski.pahfcoekdosffladbyoffladogoTis | TWKSPSLVKEGDYIGRRDSQVDNLRVIGNIFPNÝLTNRKYSLNMNRNGCMGDFPHDFF<br>DIYLDHVAKYAYBOKVNNIKEYYPLKRAILHQENALYFRFSNFDDFLEKNYLKTIWQ<br>VSKETPFSEMDFNMFKNISEKIIFERGSKMLNDLKSNYKK"<br>complement (7601473)<br>/gene="SP1171"<br>/gene="SP1171"<br>/gene="SP1171"<br>/gene="SP1171"<br>/note="identified by match to PFAM protein family HMM | /gene identified by Glimmer2; putative" /codon start=1 /codon_start=1 /transT_table=11 /product="hypothetical protein" /protein_id="AAK75279.1" /db xref="GI:14972650" /trans1ation="MSEVJENHANNYEFTSDTCOLANSIVOSLFKFFDKKNESGDLIF | /db xref="taxon:170187" /db xref="taxon:170187" complement(100702) /gene="Sp1170" complement(100702) | Medical Center Dr, Rockville, MD 20850, USA Location/Qualifiers 110256 /organism="Streptococcus pneumoniae TIGR4" /mol_type="genomic DNA" /strain=""TIGR4" | aneen,C.L., McDonald, , Hickey,B.K., Holt,I ,H.O., Venter,J.C., head,S.K. and Fraser, | Science 293 (5529), 498-506 (2001) Science 293 (5529), 498-506 (2001) 21357209 21357209 2 (bases I to 10256) 2 (bases I to 10256) Tettelin, H., Nelson, K.E., Paulsen, I.T., Eisen, J.A., Read, T.D., Peterson, S., Heidelberg, J., DeBoy, R.T., Haft, D.H., Dodson, R.J., Peterson, S., Gwinn, M., Kolonay, J.F., Nelson, W.C., Peterson, J.D., Umayam, L.B., White O. Levie M.B., Padino D. Holtzanle F. Umayam, L.B., White O. Levie M.B., Padino D. Holtzanle F. | Umayam, L.A., White,O., Salzberg,S.L., Lewis,M.R., Radune,D., Holtzapple,E., Khouri,H., Wolf,A.M., Utterback,T.R., Hansen,C.L., McDonald,L.A., Feldblyum,T.V., Angiuoli,S., Dickinson,T., Hickey,E.K., Holt,I.E., Loftus,B.J., Yang,F., Smith,H.O., Venter,J.C., Dougherty,B.A., Morrison,D.A., Hollingshead,S.K. and Fraser,C.M.  Complete genome sequence of a virulent isolate of Streptococcus preumoniae | Streptococcus pneumoniae TIGR4 Bacteria; Firmicutes; Lactobacillales; Streptococcaceae; Streptococcus. 1 (bases 1 to 10256) 1 (bases 1 to 10256) Tettelin,H., Nelson,K.E., Paulsen,I.T., Eisen,J.A., Read,T.D., Peterson,S., Heidelberg,J., DeBoy,R.T., Haft,D.H., Dodson,R.J., Durkin,A.S., Gwinn,M., Kolonay,J.F., Nelson,W.C., Peterson,J.D., |

gene

CDS

Sg gene

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QDNNTIMAEAEKLLALLKESK"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               complement (1933. .2307)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        hote="similar to GP:4249624; identified by sequence"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /gene="SP1174"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /product="conserved hypothetical protein"
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/db_xref="GI:14972652"
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Matches 2388
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  TGGTGATGCTTATATCGTTCCTCATGGAGATCATTACCATTACATTCCTAAGAATGAGTT
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Local Similarity
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                                                                                                                                                                                                                        TCAACATCGTGAAGGTGGAACTCCAAGAAACGATGGTGCTGTTGCCCTTGGCACGTTCGCA
                                                                                                                                                                                                                                                                                                                                        GGTCAAGGGTGGATATGTTATCAAGGTAGATGGAAAATACTATGTTTACCTTAAGGATGC
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TGGTGATGCTTATATCGTTCCTCATGGAGATCATTACCATTACATTCCTAAGAATGAGTT
                                                                                                                               AGGACGCTATACTACAGATGATGGTTATATCTTTAATGCTTCTGATATCATAGAGGATAC
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complement (9788. .10051)
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MAGDQQAVPLLVGMGLDEFSMSATSVLRTRSLMKKLDTAKMEEYANRALTECSTMEEV
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TMDIGGDKELPYFMPHEMNPFLGFRALRISISETGDAMFRTQIRALLRASVHGQLRI
MFPMVALLKEFRAAKAVFDEEKANLLAEGVAVADNIQVGIMIEIPAAAMLADQFAKEV
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AGLKEVTDMFITIFEGMEDNPYMQERAADIRDVTKRVLANLLGKKLPNPASINEEVIV
IAHDLTPSDTAQLDKNFVKAFVTNIGGRTSHSAIMARTLEIAAVLGTNNITEIVKDGD
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/producf="phosphoenolpyruvate-protein phosphotransferase"
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/db_xrff="GI:14972656"
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transl_table=11
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|                            | 1621 TGAAGGAGATGCATATGTAACGCCTCATATGGGCCATAGTCACTGGATTGGAAAAGATAG 1680      |
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| FEATURES                   | 1561 AGCTGATAAGTATACAACGTCAGATGGTTACATTTTTGATGAACATGATATAATCAGTGA 1620<br>  |
| AUTHOI<br>TITLE<br>JOURN   | 1501 ACTTGGCAAACCAAATTCTCAAATTGAGTATACTGAAGACGAAGTTCGTATTGCTCAATT 1560<br>  |
| ORGAN                      | 1441 TAAAGAAAAATTGGTAGATGATTTATTGGCATTCCTAGCACCAATTACCCATCCAGAGCG 1500      |
| ACCESSION VERSION KEYWORDS | 1381 TAATTCTGATTTCCAAGCCTTAGACAAATTATTAGAACGCTTGAATGATGAATCGACTAA 1440<br>  |
| RESULT ( AX57176: LOCUS    | 1321 TGATAAAGCATATAATCTGTTAACTGAGGCTCATAAAGCCTTGTTTGNAAATAAGGGTCG 1380<br>  |
| Db .                       | 1261 TGTTTCACACACTTTAACTGCTAAAAAAGAAATGTTGCTCCTCGTGACCAAGAATTTTA 1320<br>   |
| S B &                      | TGTTAAAAATCTTGAAA<br>   |
| Q B 4                      | 1141 ACGAAAAGTTGGGGAAGAATATGTATTCGAAGAAAAAGGGCATCTCTCGTTATGTCTTTGC 1200     |
| O B &                      | 1081 CCCGCAACCTGCACCAAATCTTAAAATAGÀCTCAAATTCTTTCTTTGGTTAGTCAGCTGGT 1140<br> |
| S B &                      | 1021 GGTACCAGATTCAAGGCCAGAACAACCAAGTCCACAACCGACTCCGGAACCTAGTCCAGG 1080<br>  |
| S B 4                      | 961 GTCTGAATTGGAAGAACGAATCGCTCGTATTATTCCCCTTCGTTATCGTTCAAACCATTG 1020<br>   |
| S B &                      | 901 AGCTAGAGGTGTTGCAGTGCCACACGGAGATCATTACCACTTCATCCCCTTACTCTCAAAT 960<br>   |
| S B 4                      | 841 TCAACGACATGTAGAATCTGATGGCCTTGTCTTTGATCCAGCACAAATCACAAGTCGAAC 900        |
| Q B 1                      | 781 AGCAAGTCAAAGTAATGACATTGATAGTCTCTTGAAACAGCTCTACAAACTGCCTTTGAG 840<br>    |
| OV D 1                     | 721 TGTAAGCAATCCAGGAACTACAAATACTAACACAAGCAACAACAGCAACACTAACAGTCA 780<br>    |
| S B 8                      | 661 TTCAAGAACCTATCGCCGACAAAATAGCGATAACACTTCAAGAACAACTGGGTACCTTC 720<br>     |
| S B 8                      | 601 ATCAGCTAGCGAGTÍGGCTGCTGCAGAAGCCTTCCTATCTGGTCGAGGAAATCTGTCAAA 660<br>    |
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| RESULT 8 AX571763/c LOCUS DEFINITION ACCESSION VERSION KEYWORDS SOURCE ORGANISM  | Qy 2  | Qy 2<br>рь 5   | Оу 2<br>Др 5 | Qy 2<br>Db 5  | Qy 2<br>Db 5   | Qy 2<br>Db 5                                   | Qy 1<br>pb 5  | Qy 1<br>Db 5  | ου 1<br>1<br>1<br>1<br>1<br>1<br>1<br>1                                   | Qy 1<br>Db 5  | Qy 1<br>Db 5  | Qy 1  |
|--|---|--|--------------|---|--|--|---|---|---|---|---|---|
| C AX571763 349980 bp DNA linear PAT 29-NOV-2002 N Sequence 4982 from Patent WO02077021. AX571763 AX571763.1 GI:26003955 Streptococcus pneumoniae M Streptococcus pneumoniae Bacteria; Firmicutes; Lactobacillales; Streptococcaceae; | 2341 GTTGTTAAAAGGAAGTAATCCTTCATCTGTAAGTAAGGAAAAAATAAAC 2389<br> | 2281 TITGACTCTTCAAATTATGGATAACAATAGTATCATGGCAGAAGCAGAAAAATTACTTGC 2340<br> | 221<br>517   | 161 TCAAGTAGAGACTGAAAAAGTAGAAGCCCAACTCAAAGAAGCAGAAGTTTTGCTTGC | 2101 TAAGAACTTCAAAGCGGATGAAGAGCCAGTAGAGGAAACACCTGCTGAGCCAGAAGTCCC 2160<br> | 041 TGGATGGGGCAATGCCAGTGAGCATGTGTTAGGCAAGAAAGA | 981 TTTGTTTGCGACGATTAAGTACTACGTAGAACACCCTGACGAACGTCCACATTCTAATGA 2040<br> | 921 TAAATTTGCTTGGTTTGATGATCACACATACAAAGCTCCAAATGGCTATACCTTGGAAGA 1980<br> | 861 TACAGTTGAGGTTAAAAACGGTAATTTGATTATTCCTCATAAGGATCATTACCATAATAT 1920<br> | 801 CAATCGTGTGAAAGGGGAAAAACGAATTCCACTCGTTCGACTTCCATATATGGTTGAGCA 1860<br> | 741 TCCATCTCCAGACGCAGATGTTAAAGCAAATCCAACTGGAGATAGTGCAGCAGCTATTTA 1800<br> | 681 CCTTTCTGATAAGGAAAAAGTTGCAGCTCAAGCCTATACTAAAGAAAAAGGTATCCTACC 1740<br> |

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ACCESSION
AX571763.1 GI:26003955
KEYWORDS
SURCE
ORGANISM
Streptococcus pneumoniae
ORGANISM
Streptococcus pneumoniae
Bacteria; Firmicutes; Lactobacillales; Streptococcaee;
Streptococcus
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Streptococcus
Chiron Spa (IT); THE INSTITUTE FOR GENOMIC RESEARCH (US)
FEATURES
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|---|---|--|---|--|--|---|---|---|---|--|--|---|--|---|---|---|---|--|
| 901 AGCTAGAGGTGTTGCAGTGCCACGGAGATCATTACCACTTCATCCCTTACTCTCAAAT 960        | 2y 841 TCAACGACATGTAGAATCTGATGGCCTTGTCTTTGATCCAGCACAAATCACAAGTCGAAC 900   |  | YY 721 TGTAAGCAATCCAGGAACTACAAATACTAACACAGCAACAACAGCAACAGCAACAGCTAACAGTCA 780<br>   | Y 661 TTCAAGAACCTATCGCCGACAAAATAGCGATAACACTTCAAGAACAAACTGGGTACCTTC 720 | 2y 601 ATCAGCTAGCGAGTTGGCTGCAGAAGCCTTCCTATCTGGTCGAGGAAATCTGTCAAA 660 | 2y 541 TGGTGATGCTTATATCGTTCCTCATGGAGATCATTACCATTACATTCCTAAGAATGAGTT 600 | 29 481 AGGACGCTATACTACAGATGATGGTTATATCTTTAATGCTTCTGATATCATAGAGGATAC 540 | 27 TCAACATCGTGAAGGTGGAACTCCAAGAAACGATGGTGCTGTTGCCTTGGCACGTTCGCA 480 | 361 TGCCCACGCGGATAACGTCCGTACAAAAGAGGAAAATCAATC              |  |  | 181<br>106770   | Y 121 GCGTGAAGGAATCAATGCTGAGCAAATCGTCATCAAGATAACAGACCAAGGCTATGTCAC 180 | Y 61 TATAGATGGAAAACAAGCGACGCAAAAAACGGAGAATTTGACTCCTGATGAGGTTAGCAA 120 | Y 1 TTCTTACGAGTTGGAACTGTATCAAGCTAGAACGGTTAAGGAAAATAATCGTGTTTCCTA 60 | Query Match 100.0%; Score 2388; DB 6; Length 349980; Best Local Similarity 100.0%; Pred. No. 0; Matches 2388; Conservative 0; Mismatches 1; Indels 0; Gaps 0; | ěq  | to 0.949.980~seq 4982: from 0.900.001 to 1.249.980~seq 4983: from 1.200.001 to 1.249.980~seq |
| ₽ 5   | P &   | ? B &  | S B 8   | Db 09  | B &  | рь .<br>Уу  | gb Qy   | \$ B &  | , B &   | ) B &  | B 8  | , B 8   | B 8  | B 8   | р Q   | B 9   | Db Qy   | Db   |
| 1981 THIGHTIGCGACGATTAAGIACTACGTAGAACACCCTGACGACGTCCACATTCTAATGA 2040<br> | 921 TAMATITISCITISSTITISATISA ICACACATACHANGCITCAMATISSCITATACCTITISSANSA 198 030 TAMATITISCITISGITITISATISATCACACATACANAGCITCCAMATISSCITATACCTTISGAMGA 104 | 001 IACAGI ISAGGITAAANACGGIAATII GAITAI CCICATAAGGAICAI IACCAIRAIA 198<br> | 801 CAATCGTGTGAAAGGGAAAAACGAATTCCACTGGTTCGACTTCCATATATGGTTGAGCA 18 150 CAATCGTGTGAAAGGGGAAAAACGAATTCCACTGGTTCGACTTCCATATATGGTTGAGCA 10 150 CAATCGTGTGAAAGGGGAAAAAACGAATTCCACTCGTTCGACTTCCATATATGGTTGAGCA 10 | TCCATCTCCAGACGCAGATGTTAAAGCAAATCCAACTGGAGATAGTGCAGCAGCACTATTA 180      | CCTTTCTGATAAGGAAAAGTTGCAGCTCAAGCCTATACTAAAGAAAAAGGTATCCTACC 174      | TGAAGGAGTGCATATGTAACGCCTCATATGGGCCATAGTCACTGGATTGGAAAAGATAG 168         | AGCTGATAAGTATACAACGTCAGATGGTTACATTTTTGATGAACATGATAATCAGTGA 16           | ACTTGGCAAACCAAATICTCAAATTGAGTATACTGAAGACGAAGTTGGTATTGCTCAATT 1      | TAAAGAAAAATTGGTAGATTATTGGCATTCCTAGCACCAATTACCCATCCAGAGCG 15 | TARITUTGATTICCAAGCUTTAGACAARTATINGAACGCTTGAATGATGAATGCACTAA 14 | 321 "GATAAAGCATATAATCTGTTAACTGAGGCTCATAAAGCCTTGTTTGAAAATAAGGGTCG 138 | TGTTTCACACACTTTAACTGCTAAAAAGAAAATGTTGCTCCTCGTGACCAAGAATTTTA 1 | GAAAGATTTACCATCTGAAACTGTTAAAAATCTTGAAAGCAAGTTATCAAAACAAGAGAG 12<br>    | AGAAAAGTTGGGGAAGATATGTATTCGAAGAAAAGGCATCTCTCGTTATGTCTTTGC 12          | CCGCAACCTGCACCAAATCTTAAAATAGACTCAAATTCTTCTTTGGTTAGTCAGCTGGT 11      | GGTACCAGATTCAAGGCCAGAACAACCAAGTCCACAACCGACTCCGGAACCTAGTCCAGG 10   | 961 GTCTGAATTGGAAGAACGAATCGCTCGTATTATTCCCCTTCGTTATCGTTCAAACCATTG 1020<br> | 106050 AGCTAGAGGTGTTGCAGTGCCACACGGAGATCATTACCACTTCATCCCCTTACTCCAAAT 105991                   |

| gene   | 308  | TITLE<br>JOURNAL<br>FEATURES   |   |                       |  | AUTHORS   | PUBMED  | TITLE<br>JOURNA  |   |  |   | AUTHOR           | REFERENCE                                      | ORGANISM   | KEYWORDS<br>SOURCE                          | ACCESSION<br>VERSION                           | DEFINITION  | ~1                    | PECIII.T o   |   |  | 3  | Db 1   |   | Db 1   | γo  | р <sub>р</sub> 1   |   | Ş   |
|--|--|--|---|-----------------------|--|---|---|--|---|--|---|------------------|--|--|---|--|---|-----------------------|--|---|--|--|--|---|--|---|--|---|---|
| /mol_type="genomic DNA" /strain="R6" /db_xref="taxon:171101" complement(91738) /gene="spr1056"   | rce 110320<br>/organism="Streptococc   | Dire<br>E Subr   | Zook,C., Baltz,R.H., Jaskunas,S.R., Rosteck,P.R. Jr., Skatrud,P.L. and Glass,J.I. | bertson, G.T.,        | Glimour, K., Glass, J.S., Hann, A., Khoja, H., Kratt, A., Lagace, K., LeBlanc, D.J., Lee, L.N., Lefkowitz, B.J., Lu, J., Matsushima, P., Mchhyon G. McConnor, M. McTontor, V. Myndy, G. Nigao, T. T. | NS Hoskins, J.A., Alborn, W. Jr., Arnold, J., Blaszczak, L., Burgett, S., DeHoff, B.S., Estrem, S., Fritz, L., Fu, DJ., Fuller, W., Geringer, C., | 11544234<br>2 (bases 1 to 10320)                | Genome of the bacterium Streptococcus pneumoniae strain R6  Genome of the bacterium Streptococcus pneumoniae strain R6  J. Bacteriol. 183 (19), 5709-5717 (2001) | oui, rm., wilkler, m.E., Idig, f., roung-betituo, m., Zido, v., Zook, C., Baltz, R.H., Jaskunas, S.R., Rosteck, P.R. Jr., Skatrud, P.L. and Glass T |  | Gilmour,R., Glass,J.S., Khoja,H., Kraft,A., LaGace,R.,<br>LeBlanc,D.J., Lee,L.N., Lefkowitz,E.J., Lu,J., Matsushima,P., |                  | Streptococcus. 1 (bases 1 to 10320)            | Streptococcus<br>Bacteria; Firm                    | Streptococcus pneumoniae                    | DN ĀE008479 AE007317<br>AE008479.1 GT:15458677 | Streptococcus pneumoniae R6 section 95 of 184 of the complete genome. | AE008479 10320 hm DNA |  | GTTGTTAAAAGGAAGTAATCCTTCATCTGTAAGTAAGGAAAAAATAAAC           | GTTGTTAAAAGGAAGTAATCCTTCATCTGTAAGGAAAAAATAAAC 2389                       | 2281 TTTGACTCTTCAAATTATGGATAACAATAGTATTCATGGCAGGAAAGCAGAAAAATTTACTTGC 2340<br> | AGTAACGGATTCTAGTCTGAAAGCCAATGCAACAGAAACTCTAGCTGGTTTACGAAATAA | AGTAACGGATTCTAGTCTGAAAGCCCAATGCAACAGAAACTCTAGCTGGTTTACGAAATAA | 104790 TCAAGTAGAGACTGAAAAAGTAGAAGCCCAACTCAAAGAAGCAGAAGTTTTGCTTGC | 2161 TCAAGTAGAGACTGAAAAAGTAGAAGCCCAACTCAAAGAAGCAGAAGTTTTGCTTGC                  | 2101 TAAGAACTTCAAAGCGGATGAAGAGCCAGTAGAAGGAAACACCTGCTGAGCCAGAAGTCCC 2160        | 104910 TGGATGGGGCAATGCCAGTGAGCATGTGTTAGGCAAGAAAAGACCACAGTGAAGATCCAAA 104851 | 2041 TGGATGGGGCAATGCCAGTGAGCATGTGTTAGGCAAGAAAGA |
|  |  |  |   | CDS                   | gene   |   | repeat_region                                   |  |   |  | CDS   | gene             |  |  |   |  | CDS   | gene                  |  | •   |  |  |  | CDS   | gene   |   |  |   | CDS   |
| KYPYDAIISEELIMKDPNYQLKDEDIISEIKGGYVIKVDGKYYVYLKDAAHADNVRTK<br>EEINRQKQEHSQHREGGTPRNDGAVALARSQGRYTTDDGYIFNASDIIEDTGDAYIVP<br>HGDHYHYIPKNELSASELAAAKAFLSGRGYLSNSRTYRRQNSDNTSRTINWVPSVSNPG<br>TTNTNTSNNSNTNSQASQSNDIDSLLKQLYKLPLSQRHVESDGLIFDPAQITSRTANG<br>VAVPHGDHYHFIPYSQLSPLEEKLARIIPLRYRSNHWVPDSRPEQPSPQSTPEPSPSPS | /\text{trainslation="MNQTYLEKEERMKINKKYLAGSVATLVLSVCAYELGLHQAQTVK} /\text{trainslation="MNQTYLEKEERMKINKKYLAGSVATLVLSVCAYELGLHQAQTVK} ENNRVSYIDGKQATQKTENLTPDEVSKREGINAEQIVIKITDQGYVTSHGDHYHYYNG | <pre>/label=Spr1060 /product="Histidine Motif-Containing protein" /protein_id="AAK99864.1" /protein_id="AAK98682" /db xref="01:19458682"</pre> | /gene- pupa<br>/codon_start=1<br>/transl_table=11                                 | complement (27255292) |  | 80  | complement (25422613) /rpt_family="RUP element" | /db_xref="G1:15458681"<br>/translation="MMESIGIGLVIVSHSKHIAEGVVELISKVAKDVPITYVGGTEGG<br>GIGTERPI   | /product="Hypothetical p<br>/protein id="AAK99863.1"  | <pre>/codon_start=1 /transl_table=11 /label_cart1050</pre> | <pre>/gene="spr1059"</pre>  | t(2151<br>r1059" | <pre>/translation="MNLKMVTDFSD LAELEINK"</pre> | /protein_id="AAK99862.1"<br>/db_xref="GI:15458680" | /label=spr1058<br>/product="Hypothetical pr | /codon_start=1<br>/transl_table=11             | complement(19232081) /gene="spr1058"                                  | complement (19232081) | GAHDLLDSLIERDYDLYAATNGITAIQTGKLAQSGLVPYFNOYFISEOLOTGKEDALF<br>YEKIGQOIAGFSKEKTIMIGDSLTADIQGGNNAGIDTIWYNPHHLENHTQAQPTYEVY<br>SYODLLDCLDKNILEKTIF" | /translation="mfyKflLfDLDHTLLDFDAAEDVALTQLLKEEGVADIQAYKDYYV | /protein_id="AAK99861.1" /protein_id="AAK99861.1" /db xref="GI:15458679" | <pre>/transl_table=11 /label=spr1057 /product="Conserved hype</pre>            | <pre>/gene="spr1057" /codon_start=1</pre>                    | /gene="spr1057"<br>complement (7521465)                       | FDDFLEKNYLKTIWQVSKETPFSI complement (7521465)                    | /CIANSIACION="MIIKWANII<br>FKFFDKKNFSGDLIFTWKSPSLVI<br>MNRNGCMGDFPHDFFDIYLDHVAI | /product="Hypothetical protein" /protein_id="AAK99860.1" /db_xref="GI:1548678" | /codon_start=1<br>/transl_table=11<br>/label=spr1056                        |   |

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BASE COUNT
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       2851 a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KENNRVSYIDGKQATQKTENLTPDEVSKREGINAEQIVIKITDQGYVTSHGDHYHYN GKVPYDAIRSELLMKDPNYKLKDEDIVNEVKGGYVIKUDKYVYVLKDAHADNYRT KEEINRQKQELSCHAKEDENIVLKUGGYVIKUDKYVYVLKDAHADNYRT KEEINRQKQELSCHAKEGINAEQIVIKUDKYVYVLKDAHADNYRT KEEINRQKQELAKEGINAEQIVIKUDGYIFNASDIIEDTGDAYIV PHGHYYYIPKNELASELAALEAFLGGRGNLGNSRTTVRRQNSDNTSRTIMVPSYSN PHGHYYYIPKNELASELAALEAFLGGRGNLGNSRTTVRRQNSDNTSRTIMVPSYSN PGTINTNTSNNSNTNSQASQSNDIDSLLKQLYKLPLSQRHVESDGLVFDPAQITSRTAR GVAVPHGDHYIFIPSSQSQSNDIDSLLKALIKQLYKLPLSQRHVPDSRPEQPSPQPTPBSSPG PQPAPNLKIDSSLVSQLVRKVGGGYVFEEKGISRYVFAKDLPSETVKNLESKLSKQ PQPAPNLKIDSSLVSQLVRKVGGGYVFEEKGISRYVFAKDLPSETVKNLESKLSKQ ESVSHTLTAKKENVAPRDQEFYDKAYNLTTEAHKALFENKGRNSSPQALDKLLEBLND ESTNKEKLVDDLLAFLAPITHPERLGKPNSQIEYTEDEVRIAQLADKYTTSDGYIFDE HDIISDEDBAVTPHKGHSHWIGKOSLSDKEKVAAQAYTEKGGILPSSPDADVKANPT GDSAAAITYNRVKGEKKIPLTVENLYMKHTVEVKNGHLIIPKHHYHNIKFAMFDHTY KAPNGYTLEDLFATIKYYVEHPDERPHSNDGWGNASEHVLGKKHHSEDPNKNFKADEE PVEETPAEPEVPQVFTEKVEAQLKEAFVLAKVTDSSLKANATETLAGLRNNLTILQIM PANGYTLEDLFATIKYYVEHPDERPHSNDGWGNASEHVLGKKHSEDPNKNFKADEE PVEETPAEPEVPQVFTEKVEAQLKEAFVLAKVTDSSLKANATETLAGLRNNLTTLQIM PANGYTARATETLAGLRNNLTTLQIM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            QPAPNPQPAPSNPIDEKLVKEAVRKVGDGYVFEENGVPRYIPAKDLSAETAAGIDSKLAKQEGSUSHKLGAKKTDLPSSDREFYNKAYDLLARIHQDLLDNKGRQVDFEALINILEER LKDVSSDKVKLUDDILAFLAPIRHPEERLGKENDAQITYTDDEIQVAKLAGKYTTEDGYIFDPRDITSDEGJAYVTPHMTHSHWIKKDSLSBAERAAAQAYAKEKGLTPPSTDHQDSGNTEAKGAEAIYNRVKAAKKVPLDRMPYNLQYTVEVKNGSLIIPHYDHYHNIKFEWFDE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DNNSIMAEAEKLLALLKGSNPSSVSKEKIN"
complement(8122. .9855)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GLYEAPKGYSLEDLLATVKYYVEHPNER PHSDNGFGNASDHVQRNKNGQADTNQTEKP
NEEKPQTEKPEEETPREEKPQSEKPESPKPTEEPEESPEESPEESEEBPQVETEKVKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          complement (5417.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      complement (5417. .7903)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            KLREAEDLLGKIQNPIIKSNAKETLTGLKNNLLFGTQDNNTIMAEAEKLLALLKESK"
                                                                                                                                                                                        the PTS"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       complement (9861. .10124)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MAGDQQAVPLLVGMGLDEFSMSATSVLRTRSLMKKLDTAKMEEYANRALTECSTMEEV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               precursor"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    translation="MQLEISNRKRVSMKINKKYLVGSAAALILSVCSYELGLYQARTV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      protein_id="AAK99865.1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="synonym: spr1061"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  product="Pneumococcal histidine triad protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        label=spr1061
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   gene="phtA"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             number="2.7.3.9"
                                                                                                                                                                                                                           of.
밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORIGIN
6848 GTCTGAATTGGAAGAACGAATCGCTCGTATTATTCCCCCTTCGTTATCGTTCAAACCATTG 6789
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| ner)               | atch 99.0%; Score 2365.6  |
|--------------------|---|
| Best Lo<br>Matches | cal Similarity 99.4%; Pred. No. 0; 2374; Conservative 0; Mismatches 15; Ind   |
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| \$ 8               | 61 TATAGATGGAAAACAAGCGACGCAAAAAAACGGAGAATTTGACTCCTGATGAGGTTAGCAA 120  |
| Ş                  | 121 СССПСАВАССАВАТСАВТССТСАВССАВВАТОСТОВТОВЯСАТАВССАВАСССВВСССТВТСТОВ 1   |
| ₽<br>\$            | 88 GCGTGAAGGAATCAATGCTGAGCAAATCGTCATCAAGATAACAGACCAAGGCTATGTCAC 76  |
| δλ                 | ACATGGCGACCACTATCATTATTACAATGGTAAGGTTCCTTATGACGCTATCAT  |
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| Qy                 | 241 TGAAGAATTACTCATGAAAGATCCAAACTATAAGCTAAAAGATGAGGATATTGTTAATGA 300  |
| Db                 | TTACTCATGAAAGATCCAAACTATAAGCTAAAAAGATGAGGATATTGTTAATG   |
| γO                 | 301 GGTCAAGGGTGGATATGTTATCAAGGTAGATGGAAAATACTATGTTTACCTTAAGGATGC 360  |
| Ъ                  | aagggtggatatgttatcaaggtagatggaaaatactatgtttaccttaaggatk   |
| Qy                 | 361 TGCCCACGCGGATAACGTCCGTACAAAAGAGGAAATCAATC   |
| Db                 | SCGGATAACGTCCGTACAAAAGAGGGAAATCAATCGACAAAAACAAGAACATA   |
| 9                  | 421 TCAACATCGTGAAGGTGGAACTCCAAGAAACGATGGTGCTGTTTGCCTTTGGCACGTTCGCA 480  |
| 뫄                  | CAACATCGTGAAGGTGGGACTCCAAGAAACGATGGTGCTGTTGCCTTGGCACGTTCC   |
| · Qγ               | 481 AGGACGCTATACTACAGATGATGGTTATATCTTTTAATGCTTCTGATATCATAGAGGATAC 54  |
| 5                  | 20 AGGACGCIAIACIACAGAIGAIGGIIAIAICIIIAAIGCIICIGAIAICAIAGAGGAIAC /2  |
| γg                 | . υ   |
| ) Db               | 68 TGGTGATGCTTATATCGTTCCTCATGGAGATCATTACCATTACATTCCTAAGAATGAGTT 72  |
| <u> </u>           |   |
| OV                 | 61 TTCAAGAACCTATCGCCGACAAATAGCGATAACACTTCAAGAACAAACTGGGGTACCTTC 72  |
| Db                 | 48 TTCAAGAACCTATCGCCGACAAAATAGCGATAACACTTCAAGAACAAACTGGGTACCTTC 70  |
| δ                  | ZAATCCAGGAACTACAAATACTAACACAAGCAACAGCAACAGCAACAGCTC   |
| Db                 | TCCAGGAACTACAAATACTAACACAAGCAACAACAGCAACACTAACAGT   |
| Ş                  | 781 AGCAAGTCAAAGTAATGACATTGATAGTCTCTTGAAACAGCTCTACAAACTGCCTTTGAG 840  |
| ф                  | GCAAGTCAAAGTAATGACATTGATAGTCTCTTGAAACGCTCTACAAACTGCCTTTGA   |
| δ                  | ATGTAGAATCTGATGGCCTTGTCTTTGATCCAGCACAAATCACAAGTCGAA   |
| Ъ                  | CAACGACATGTAGAATCTGATGGCCTTGTTTTCGACCCAGCGCAAATCACAAGTCG  |
| .8                 | 901 AGCTAGAGGTGTTGCAGTGCCACACGGAGATCATTACCACTTCATCCCTTACTCTCAAAT 96   |
| ָם<br>ס            | 08 AGCTAGAGGTGTTGCAGTGCCACACGGAGATCATTACCACTTCATCCCTTACTCTCAAAT 68  |
| 로 &                | 961 GTCTGAATTGGAAGAACGAATCGCTCGTATTATTCCCCTTCGTTATCGTTCAAACCATTG 1020   |
| j                  | AN INTERPRETARION OF THE PARTY |

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AL449937.1 GI
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Submitted (31-OCT-2000) Research Department,
Severo Ochoa 2, 28760 Tres Cantos, SPAIN
* NOTE: This is a 'working draft' sequence.
* This sequence will be replaced
                                                                                                                                                                                                                                                                                                                                                                                         Dopazo,J., Mendoza,A., Herrero,J., Caldara,F., Polissi,A., Humbert,Y., Friedli,L., Guerrier,M., Grand-Schenk,E., Gandin,C., Francesco,M., Buell,G., Feger,G., Garcia,E., Peitsch,M. and Garcia-Bustos,J.F.
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/mol_type="genomic DNA"
/serotype="19F"
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| 2220 AAGTAACGGATTCTACTCTGAAAGCCAATGCAACAGAAACTCTAGCTGGTTTACGAAATA<br> | - Oy     | 1141 ACGAAAAGTTGGGGAAGGATATGTATTCGAAGAAAAGGGCATCTCTCGTTATGTCTTTGC 1200      | δ          |
|---|----------|---|------------|
| 230   | Db C     | 1081 CCCGCAACCTGCACCAAATCTTAAAATAGACTCAAATTCTTCTTTTGGTTAGTCAGCTGGT 1140     | B 65       |
| 170   | 2 da 6   | 1021 GGTACCAGATTCAAGGCCAGAACCAACCAAGTCCACAACCGACTCCGGAACCTAGTCCAGG 1080<br> | Db Qy      |
|   | 2 B 2    | 961 GTCTGAATTGGAAGAACGAATCGCTCGTATTATTCCCCCTTCGTTATCGTTCAAACCATTG 1020<br>{ | B 8        |
| 980   | Оу       | 901 AGCTAGAGGTGTTGCAGTGCCACACGGAGATCATTACCACTTCATCCCTTACTCTCAAAT 960<br>    | ρ<br>γ     |
| 990   | Db QY    | 841 TCAACGACATGTAGAATCTGATGGCCTTGTCTTTGATCCAGCACAAATCACAAGTCGAAC 900        | g d        |
| 930   | Db QY    | 781 AGCAAGTCAAAGTAATGACATTGATAGTCTCTTTGAAACAGCTCTACAAACTGCCTTTGAG 840       | ρ Q        |
| 870   | Db Qy    | 721 TGTAAGCAATCCAGGAACTACAAATACTAACAGCAACAACAGCAACAGCAACAGTCA 780<br>       | 요 성.       |
| 810   | Db 05    | 661 TTCAAGAACCTATCGCCGACAAAATAGCGATAACACTTCAAGAACAAACTGGGTACCTTC 720        | ₽ <b>Q</b> |
|   | D 6      | 601 ATCAGCTAGCGAGTTGGCTGCAGAAGCCTTCCTATCTGGTCGAGGAAATCTGTCAAA 660           | B 8        |
| 690   | ) Db QY  | 541 TGGTGATGCTTATATCGTTCCTCATGGAGATCATTACCATTACATTCCTAAGAATGÄGTT 600<br>    | д Q        |
| 630   | Db Qy    | 481 AGGACGCTATACTACAGATGATGGTTATATCTTTAATGCTTCTGATATCATAGAGGATAC 540        | D Q        |
| 570   | Db VY    | 421 TCAACATCGTGAAGGTGGAACTCCAAGAAACGATGGTGCTGTTGCCTTTGGCACGTTCGCA 480       | B &        |
| 510   | γ da γ   | 361 TGCCCACGCGGATAACGTCCGTACAAAAGAGGAAATCAATC                               | D 02       |
| 450   | Db<br>CY | 301 GGTCAAGGGTGGATATGTTATCAAGGTAGATGGAAAATACTATGTTTACCTTAAGGATGC 360<br>    | B &        |
| 90  | 2 B &    | 241 TGAAGAATTACTCATGAAAGATCCAAACTATAAGCTAAAAGATGAGGATATTGTTAATGA 300<br>    | P Q        |
| 330   | 5 B 6    | 181 TTCACATGGCGACCACTATCATTATTACAATGGTAAGGTTCCTTATGACGCTATCATCAG 240        | P 65       |
| 270   | . Db     | 121 GCGTGAAGGAATCAATGCTGAGCAAATCGTCAAGATAACAGACCAAGGCTATGTCAC 180<br>       | D Qy       |
| 10  |          |   | В          |

| •  | Query Match Best Local Similarity Matches 1724; Conservat   | EETPI<br>IQNPI<br>BASE COUNT 880 a :   | VDDI<br>DAYV<br>NRVK<br>EDLL <i>L</i>  | TNSQ.<br>IPYSG.<br>NPIDI<br>AKKTI   | QATQ<br>LLMKI<br>QHREC<br>ELSAS  | /traa/<br>/db/<br>/proi<br>/proi   | /gene="<br>/notte="<br>/codon to<br>/trans]   | <b></b>  | /db /   | /mol/orga  | vaccines,  | TITLE Direct Submission JOURNAL Submitted (25-JAN Vaccines 211 Bai   |   | MEDLINE 21246685 PUBMED 11349048                               |  |  | 898<br>000   | SOURCE Streptococcus ORGANISM Streptococcus                          | AF340221<br>ON Streptococcu<br>N AF340221<br>AF340221.1   | T 11   | Qy 2340 CGTTGTTAAAAA<br>          <br>Db 19410 CGTTGTTAAAAA | Qy 2280 ATTTGACTCTTV<br>         <br>Db 19350 ATTTGACTCTTV           |
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|  | 60.0%; Score 1434.4; DB 1; Length 2535;<br>79.0%; Pred. No. 5.1e-296;<br>tive 0; Mismatches 447; Indels 12; Gaps 1; | EETPREEKPOSEKPESPKPTEEPEEESPEESPEESEEPOVETEKVKEKLREAEDLLGK<br>IQNPIIKSNAKETLTGLKNNLLFGTODNNTIMAEAEKLLALLKESK"<br>518 c 533 g 604 t | VDDILAFLAPIRHPERLGKPNAQITYTDDEIQVAKLAGKYTTEDGYIFDPRDITSDEG DAYVTPHMTHSHMIKKDSLSEBAERAAQAYAKEKGLTPPSTBHQDSGNTBAKGAEBAIY NRVKAAKKVPLDRMPYNLQYTVEVKNGSLIPHYDHYHIKKEWEPDEGLYEAPKGYSL EDLLATVKYYVEHPNERPHSDNGFGNASDHVQRNKNGQADTNOTEKPNERKPOTEKPE EDLLATVKYYVEHPNERPHSDNGFGNASDHVQRNKNGQADTNOTEKPNERKPOTEKPE | TNSQASQSNDIDSLLKQLYKLPLSQRHVESDGLIFDPAQITSRTANGVAVPHGDHYHF<br>IPYSQLSPLEEKLARIIPLRYKSNHWVEDSRPEQESPGSTPEPSBSSPGPARNEQEARS<br>NPIDEKLVKEAVRKVGDGYVFEENGVPRYIPAKDLSAETAAGIDSKLAKQESLSHKLG<br>AKKTDLPSSDREFYNRAYDLLARIHODLLDNKGROVDFEALDNLLERLKDVSSDKYKL | QATQKTENLTPDEVSKREGINAEQIVIKITDQGYVTSHGDHYHYYNGKVPYDAIISEE<br>LLMKDPNYQLKDEDIISEIKGGYVIKVDGKYYVYLKDAAHADNYRTKEEINRQKQEHS<br>QHREGGTPRNDGAVALARSQGRYTTDDGYIFNASDIIEDTGDAYIVPHGDHYHYIPKN<br>BLGASELAAAKAFLGGRGNLGNSRTYBRONSDNTSRTWWYPSVSNPGTTNTNTSNNSN | /producT="PhpA"<br>/protein_id="AAK26629.1"<br>/db_xref="GI:13447094"<br>/translation="MKINKYIVGSAAALILGVCSYELGLYOARTVKENNRVSYIDGK | 'gene="phpA"  (gene="histidine motif-containing protein"  (codon start=1)  (trans] table=11 | gene="phpA"<br>2535  | 0 Xref="taxon:1313" -2535   | organism="Streptococcus pneumoniae" mol type="genomic NNA"           | Tey Rodd, West Henrietta, Nr 14586,<br>/Qualifiers                   | sion -(JAN-2001) Department of Bacteriology, Wyeth Lederle           | 2 (bases 1 to 2535) Zhang Y., Masi,A., Barniak,V., Mountzouros,K., Hostetter,M. and | . 69 (6), 382/-3836 (2001)                                     | a uniqu<br>s pneumo<br>hallenge                | Masi,A.W., Barniak, v., Mountzouros,K., Hostetter,M.K. and     | 233 Branish W Manatananan V Watatanan W V                        | oneumoniae<br>oneumoniae<br>outes: Tactobacillales:                  | 2535 bp DNA linear BCT 22-MAY-2001<br>s pneumoniae PhpA (phpA) gene, complete cds.<br>GI:13447093 |  | CGTTGTTAAAAGGAAGTAATCCTTCATCTGTAAGTAAGGAAAAATAAAC 2389<br>  | ATTTGACTCTTCAAATTATGGATAACAATAGTATCATGGCAGAAGCAGAAAATTACTTG 2339<br> |
| 8  | Qy  | Qy<br>Db   | Qy<br>Db   | QY  | Qy<br>Db   | Qy<br>db   | B 8   | Db   | Qy  | Db   | Qγ   | B 2  | <u>а</u>  | Qy   | ₽ &  | 2 6  | \$ \$  | gb Qy  | D QY  | Db VY  | D 5   | S B 8  |
| 1081 CCCGCAACCTGCACCAAATCTTAAAATAGACTCAAATTCTTCTTTGGT 1128 | 1021 GGTACCAGATTCAAGGCCAGAACCAACTCCACAACTCCGGACTCCGGAACCTAGTCCAGG 1080  | 961 GTCTGAAITGGAAGAACGAATCGCTCGTATTATTCCCCTTCGTTATCGTTCAAACCATTG 1020  | 901 AGCTAGAGGTGTTGCAGTGCCACAGGAGATCATTACCACTTCATCCCTTACTCCAAAT 960   | 841 TCAACGACATGTAGAATCTGATGGCCTTGTCTTTGATCCAGCACAAATCACAAGTCGAAC 900<br>  | 781 AGCAAGTCAAAGTAATGACATTGATAGTCTCTTGAAACAGCTCTACAAACTGCCTTTGAG 840<br>   | 721 TGTAAGCAATCCAGGAACTACAAATACTAACACAAGCAACAACAGCAACACTAACAGTCA 780<br>   | 661 TTCAAGAACCTATCGCCGACAAATAGCGATAACACTTCAAGAACAACCTACCT                                   | ATCAGCTAGCGAGTTAGCTGCTGCAAAAGCCTTCCTATCTGGTCGGGGAAATCTGTCAAA | 601 ATCAGCTAGCGAGTTGGCTGCAGAAGCCTTCCTATCTGGTCGAGGAAATCTGTCAAA 660 | 600 TGGTGATGCTTATATCGTTCCTCACGGCGACCATTACCATTACATTCCTAAGAATGAGTT 659 | 541 TGGTGATGCTTATATCGTTCCTCATGGAGATCATTACCATTACATTCCTAAGAATGAGTT 600 | 540 GGGACGCTACACCACAGATGATGGTTATATCTTTAATGCTTCTGATATCATTGAAGATAC 599 |   | TCAACATCGTGAAGGTGGAACTCCAAGAAACGATGGTGCTGTTGTGCTTTGGCACGTTCGCA | 361 TGCCCACGCGGATAACGTCCGTACAAAAGAGGAGAATCAATC | 60 AATCAAGGGTGTTATGTGATTAAGGTAGATGGAAAATACTATGTTTACCTTAAGGATGC | 01 GGTCAAGGGTGGATATGTTATCAAGGATAGATGGAAAATACTATGTTTACCTTAAGGATGC | 241 TGARGAATTACTCATGAARGATCCAAACTATAAGCTAAAAGATGAGGATATTGTTAATGA 300 | 81 TTCACATGGCGACCACTATCATTATTACAATGGTAAGGTTCCTTATGACGCTATCATCAG                                   | GCGTGAAGGAATCAATGCCGAACAAATCGTCATCAAAATAACAGACCAAGGCTATGTCAC |   | 11C1ACGAG11GGACIGAA CAAGCIAGAACGG1TAAGGAAAATAATGG111CCIA             |

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Streptococcus antigens
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SHIRE BIOCHEM INC, (CA)
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AX343073 Sequence 4 from I AX343073 AX343073.1 GI:18 unidentified unidentified unclassified. Streptococcus antigens
Patent: WO 0198334-A 4 27-DEC-2001;
SHIRE BIOCHEM INC. (CA) Hamel, J., Ouellet, C., Charland, N., Martin, D. 934 1. .2647 /note="BVH-11" 538 c 59 /organism="unidentified /mol\_type="genomic DNA" /db\_xref="taxon:32644" Location/Qualifiers GI:18152271 2647 bp Patent WO0198334. 556 ω 619 ct DNA linear and Brodeur, PAT 12-JAN-2002

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| AGCTGTCCCTCATGGTAACCATTACCACTTY AGAACGAATCGCTCGTATTATTCCCCTTCGT  | 944 TCAACGCCATGTAGAATCTGATGGCCTTATTTTCGACCCAGCGCAAATCACAAGT 901 AGCTAGAGGTGTTGCAGTGCCACACGGAGATCATTACCACTTCATCCCTTACTCT                              | CAAGTCAAAGTAATGACATTGATAGTCTCTTGAAACAGCTCTACAAAC<br>  | CTACAAATACTAACACAAGCAACACAGCAACACCTAACAGTCA 7<br>                          | TAÀCACTTCAAGAACAAACTGGGTACCTTC 7  | QY 601 ATCAGCTAGCGAGATTGGCTGCAGAAGCCTTCCTATCTGGTCGAGGAAATCTGTCAAA 660     | QY 541 TGGTGATGCTTATATCGTTCCTCATGGAGATCATTACCATTACATTCCTAAGAATGAGTT 600 | QY 481 AGGACGCTATACTACAGATGATGATGATATATATGCTTCTGATATCATAGAGGATAC 540 | Qy 421 TCAACATCGTGAAGGTGGAACTCCAAGAAACGATGGTGCTTTGCCTTTGGCACGTTCGCA 480  | QY 361 TGCCCACGCGGATAAAGTCCGTACAAAAGAGAGAAATCAATC                      | QY 301 GGTCAAGGGTGGATATGTTATCAAGGTAGATAGATGGAAAATACTATGTTTACCTTAAGGATGC 360 | Qy 241 TGAAGAATTACTCATGAAAGATCCAAACTATAAGCTAAAAGATGAGGATATTGTTAATGA 300  | QY 181 TTCACATGGCGACCACTATCATTACTACAATGGTAAGGTTCCTTATGACGCTATCATCAG 240 | QY 121 GCGTGAAGGAATCAATGCTGAGCAAATCGTCATCAAGATAACAGACCAAGGCTAATGTCAC 180 | OY 61 TATAGATGGAAAACAAGCGACGCAAAAAACGGAGAATTTGACTCCTGATGAGGTTAGCAA 120 | QY 1 TTCTTACGAGTTGGGACTGTATCAAGCTAAGAACGGTTAAGGAAAATAATCGTGTTTTCCTA 60 | Query Match 57.5%; Score 1374.2; DB 6; Length 2647; Best Local Similarity 73.9%; Pred. No. 3.7e-283; Matches 1819; Conservative 0; Mismatches 539; Indels 102; Gaps 2; |
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| 2029 ACATTCTAATGATGGATGGGGCAATGCCAGTGAGCATGTGTTAGGCAAGAAGACCACAG | Db 2024 TTACCATAACATCAAATTTĞAGTGTTTGACGAAGGCCTTTATGAGĞCACCTAAĞGĞĞĞTA 2083  Qy 1969 TACCITGGAAGATTTGTTTGCGACGATTAAGTACTACGTAGAACACCCTGACGAACGTCC 2028 | 1964 CAATCTTCAATATTACCTGTAGAAGTCAAAAACGGTAGTTTAATCATACCTCAATATGACCA 1909 TTACCATAATATTAAATTTGCTTGGTTTGATGATCACACATACAAAGCTCCAAATGGCTA | QY 1789 AGCAGCTATTTACAATCGTGTGAAAAGGGGAAAAACGAATTCCACTCGTTCGACTTCCATA 1848 | Qy 1729 AGGTATCCTACCTCCATCTCCAGACGCAGATGTTAAAGCAAATCCCACTGGAGATAGTGC 1788 | Qy 1669 TGGAAAAGATAGCCTTTCTGATAAGGAAAAAGTTGCAGCCTAAGCCTATACTAAAGAAAA 1728 |   | 1549 TATTGCTCAATTAGCTGATAAGTATACAACGTCAGATGGTTACATTTTTGATGAACATGA    | QY 1489 CCATCCAGACCACTTGGCAAACCAAATTCTCAAATTGAGTATACTGAACACGAAGTTCG 1548 | Oy 1429 TGAATCGACTAATAAAAAAATTGGTAGAAGATTATTGGCATTCCTAGCACCAATTAC 1488 | 1369 ANATANGGOTCGTAATTCTGATTTCCAAGCCTTAGACAATTATTAGAACGCTTGAATGA            | QY 1309 CCAAGAATTTATGATAAAGCATATAATCTGTTAACTGAGGCTCATAAAGCCTTGTTTGN 1368 | Db 1364 CAAGAGAGAGTTTTATCTCATAAGGAGAAAATGTTGCTCCTGGTGA 1308             |  | 1129 TAGTCAGCTGGTACGAAAAGTTGGGGAAGGATATTGTATTGAAGAAAAAGGCATCTCTCG      | 1081 CCCGCAACCTCCACCAATCTTAAAATAGACTCAAATTCTTCTTTGGT                   | Qy · 1021 GGTACCAGATTCAAGGCCAGAACAAACCAAGTCCACAACCGACTCCGGAACCTAGTCCAGG 1080   |

| , 65<br>5  | 子 &   | 유 성  | D QQ  | Db Qy  | d dd  | Query Match<br>Best Local<br>Matches 161   | BASE COUNT  | FEATURES<br>source  | REFERENCE<br>AUTHORS<br>TITLE<br>JOURNAL  | SOURCE   | DEFINITION ACCESSION VERSION KEYWORDS                                   | RESULT 14<br>AX569137  | g Qy   | ₽ Q  | Db Qy  | Db  | дb   | γQ   | Db |
|--|---|--|---|--|---|--|---|---|---|--|---|--|--|--|--|---|--|--|----|
| 98 TGAGGTCAAGGGTGGATATGTTATCAAGGTAGATGGAAAATACTATGTTTACCTTAAGGA 35     | 238 CAGTGAAGAATTACTCATGAAAGATCCAAACTATAAGCTAAAAGATGAGGATATTGTTAA 297  | 178 CACTTCACATGGCGACCACTATCATTATTACAATGGTAAGGTTCCTTATGACGCTATCAT 237 | 118 CAAGCGTGAAGGAATCAATGCTGAGCAAATCGTCATCAAGATAACAGACCAAGGCTATGT 177  | 58 CTATATAGATGGAAAAACGGACGAAAAAACGGAGAATTTGACTCCTGATGAGGTTAG 117   | GGGACTGTATCAAGCTAGAACGGTTAAGGAAAATAATCGTGT<br>                        | / Match 41.6%; Score 993; DB 6; Length 2457;<br>Local Similarity 65.8%; Pred. No. 1.1e-201;<br>les 1611; Conservative 0; Mismatches 696; Indels 141; Gaps 6; | /mol_type="genomic DNA" /db xref="taxon:1313" 836 a 497 c 531 g 593 | Chiron Spa (IT); THE INSTITUTE FOR GENOMIC RESEARCH (US) Location/Qualifiers ce 12457 / Organism="Streptococcus pneumoniae" | 1 Masignani,V., Tettelin,H. and Fraser,C. Streptococcus pneumoniae proteins and nucleic acids Patent: WO 02077021-A 2345 03-OCT-2002; | Streptococcus pneumoniae<br>M Streptococcus pneumoniae<br>Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;<br>Streptococcus. | Sequence 2345 from Patent WOO2077021.  AX569137  AX569137.1 GI:26002635 | AX560137 2457 by DNA 11  | 2299 GGATAACAATAGTATCATGGCAGAAGCAGAAAAATTACTTGCGTTGTTAAAAGGAAGTAA 2358<br> | 2239 GAAAGCCAATGCAACAGAAACTCTAGCTGGTTTACGAAATAATTTGACTCTTCAAATTAT 2298<br> | 2179 AGTAGAAGCCCAACTCAAAGAAGCAGAAGTTTTGCTTGCGAAAGTAACGGATTCTAGTCT 2238<br> | 2126CCAGTAGAGGAAACACCTGCTGAGCCAGAAGTCCCTCAAGTAGAGACTGAAAA 2178        | 2264 GGAAGAAACCCCCTCGAGAAGAGAAACCACAAAGCGAGAAACCAGAGTCTCCAAAAACCAAC 2323 | 2126 2125  |    |
| Q  | Db Qy   | Qy<br>Db   | B Q   | ) D Q  | Db Qy   | Qγ   | Qy<br>Db  | Qγ  | Qy<br>Db  | Qy   | g Qy  | DB Qy  | dg<br>VQ   | DD QY  | g Q  | D Qy  | Db   | Qy   | рь |
| 1378 TCGTAATTCTGATTTCCAAGCCTTAGACAAATTATTAGAACGCTTGAATGATGAATCGAC 1437 | 1318 TTATGATAAAGCATATAATCTGTTAACTGAGGCTCATAAAGCCTTGTTTGNAAATAAGG 1377 |  | 98 TGCGHAMGATTACCATCTGHAMACIATAMACATCTTGHAMGCANGTIATCAMACAMGA 09 AGCCAAGGATCTTCAGCAGAAAACAGCAGCAGGAGTTGATAGCAAACTGGCCAAGCAGGA 09 AGCCAAGGATCTTCAGCAGAAAACAGCAGCAGGAGTTGATAGCAAACTGGCCAAGCAGGA | 38 GGTACGAAAGTTGGGGAAGGAFATGTATTGAAGAAAAGGCAFCTCTCGTTAFGTCTT 13 GGTACGAAAAGTTGGGGAAGGAFATGTATTCTAAAAGGAGCAFCTCTCGTTAFATCCC 49 TGTTCGAAAAGTAGGCGATGGTTATGTCTTTGAGGAGAATGGAGTTTCTCGTTAFATCCC | 1078 AGGCCCGCAACCTGCACCAATCTTAAAATAGACTCAAATTCTTCTTTGGTTAGTCAGCT 1137 |  | 58 AATGTCTGAATTGGAAGAACGAATCGCTCGTATTATTCCCCTTCGTTATCGTTCAAACCA     | 898 AACAGCTAGAGGTGTTGCAGTGCCACACGGAGATCATTACCACTTCATCCCTTACTCTCA 957  | 838 GAGTCAACGACATGTAGAATCTGATGGCCTTGTTTTGATCCAGCACAAATCACAAGTCG 897   | 778 TCAAGCAAGTCAAAGTAATGACATTGATAGTCTCTTGAAACAGCTCTACAAACTGCCTTT 837   | 718 TTCTGTAAGCAATCCAGGAACTACAAATACTAACACAAGCAACAACAAGAACACTAACAG 777    | 658 ADATTCAAGAACCTATCGCCGACAAAATAGCGATAACACTTCAAGAACAAACTGGGTACC 717 | 598 GTTATCAGCTAGCGAGTTGGCTGCTGCAGAAGCCTTCCTATCTGGTCGAGGAAATCTGTC 657       | 538 TACTGGTGATGCTTATATCGTTCCTCATGGAGATCATTACCATTACATTCCTAAGAATGA 597       | 478 GCAAGGACGCTATACTACAGATGATGGTTATATCTTTAATGCTTCTGATATCATAGAGGA 537<br>   | 418 TAGTCAACATCGTGAAGGTGGAACTCCAAGAAACGATGGTGCTGTTGCCTTTGGCACGTTC 477 | 420 TGCAGCTCATGCGGATAATATTCGGACAAAAGAAGATTAAACGTCAGAAGCAGGAACG 479       | 358 TGCTGCCCACGCGGATAACGTCCGTACAAAAGAGGAAATCAATC |    |

| /note="Region: hi<br>feature 1396. 1488<br>/gene="phtB"        | misc_                | RESULT 15 AF318954  | RESUL<br>AF318 |
|--|----------------------|---|----------------|
| _feature 940957<br>/gene="phtB"                                | misc_                | 2409 TATTATGGCAGAAGCTGAAAAACTATTGGCTTTATTAAAGGAGAGTAA 2456  | В              |
|  | m18C_                | 2311 TATCATGGCAGAAGCAGAAAAATTACTTGCGTTGTTAAAAGGAAGTAA 2358  | Qy             |
| /gene  | ı                    | 2349 CAAAGAGACTCTCACAGGATTAAAAAATAATTTACTATTTGGCACCCAGGACAACAATAC 2408  | ф              |
| /note="Region: his   | misc_                | 2251 AACAGAAACTCTAGCTGGTTTACGAAATAATTTGACTCTTCAAATTATGGATAACAATAG 2310  | Qy             |
|  | misc_                | ACTGAGAGAGCTGAAGATTTACTTGGAAAAATCCAGGATCCAATTATCAAGTCCAATGC 234   | Db -           |
| peptide 187<br>/qene="phtB"                                    | sig_p                | 225   | γQ             |
| DNGFGNASDHVQRNKNG<br>EBPEESPEESEEPQVET<br>QDNNTIMAEAEKLLALL    |                      | 2131 AGAGGAAACACCTGCTGAGCCAGAAGTCCCTCAAGTAGAGACTGAAAAAAGTAGAAGCCCA 2190   | D Qy           |
| EAERAAAQAYAXEKGLTI<br>TVEVKNGSLIIPHYDHYI                       |                      | 2169 CCCTCGAGAAGAAAACCGCAAAGCGAGAAACCAGAGTCTCCAAAACCAACAGAGGAACC 2228   | Db             |
| LARIHQDLLDNKGRQVDI<br>NAOITYTDDSTOVAKIA                        |                      | 2122AGAGCCAGT 2130  | Ş              |
| LRELYAKPLSERHVESDO<br>RIIPLRYRSNHWVPDSRI                       |                      |   | ф              |
| SHNHNSRADNAVAAARA(<br>SASELAAAEAYWNGKQG                        | •                    | 2098 AAATAAGAACTTCAAAGCGGATGA 2121  | Qy             |
| DQAGQKAENLTPDEVSKI<br>ELLMKDPNYQLKDSDIVI                       |                      | 2049 TAATGGTTTTGGTAACGCTAGCGACCATGTTCAAAGAAACAAAAATGGTCAAGCTGATAC 2108  | Дb             |
| /db_xref="GI:1274<br>/translation="MKII                        |                      | 2038 TGATGGATGGGGCAATGCCAGTGAGCATGTGTTAGGCAAGAAAGA  | γQ             |
| precursor" /protein_id="AAKO                                   |                      | 1989 GGATCTTTTGGCGACTGTCAAGTACTATGTCGAACATCCAAACGAACG   | DЪ             |
| /transl_table=11<br>/product="pneumoco                         |                      | 1978 AGATTTGTTTGCGACGATTAAGTACTACGTAGAACACCCTGACGAACGTCCACATTCTAA 2037  | Qγ             |
| /note="PhtB; proto<br>/codon_start=1                           |                      | 1929 CATCAAATTTGAGTGGTTTGACGAAGGCCTTTATGAGGCCACCTAAGGGGGTATACTCTTGA 1988  | DЬ             |
| 1>2457<br>/gene="phtB"   | CDS                  | 1918 TATTAAATTTGCTTGGTTTGATGATCACACATACAAAGCTCCAAATGGCTATACCTTGGA 1977  | γQ             |
| 1>2457<br>/gene="phtB"   | gene                 | 1869 ATATACTGTAGAAGTCAAAAACGGTAGTTTAATCATACCTCATTATGACCATTACCATAA 1928  | Db             |
| /serotype="4"<br>/db_xref="taxon:1                             |                      | 1858 GCATACAGTTGAGGTTAAAAACGGTAATTTGATTATTCCTCATAAGGATCATTACCATAA 1917  | Qy             |
|  |                      | 809 CTACAACCGCGTGAAAGCAGCTAAGAAGGTGCCACTTGATCGTATGCCTTACAATCTTCA  | Db             |
| Location/Qualifie:   | FEATURES Sourc       | 1798 TTACAATCGTGTGAAAGGGGAAAAACGAATTCCACTCGTTCGACTTCCATATATGGTTGA 1857  | Q              |
|  | JOURNAL              |   | 망              |
| £O.  | TITLE                | 1738 ACCTCCATCTCCAGACGCAGATGTTAAAGCAAATCCAACTGGAGATAGTGCAGCAGCTAT 1797  | Qγ             |
| _  | REFERENCE            | 689 TAGTTTGTCTGAAGCTGAGAGAGCGGCAGCCCAGGCTTATGCTAAAGAGAAAGGTTTGAC  | Db             |
| Infect. immun. 69 (2), 949 21101045 11159990                   | MEDLINE              | 7 1   | ۷o<br>ا        |
| Identification and char<br>pneumococcal proteins t             | TITLE                | 618 TGATGAAGGAGATGCATATGTAACGCCTCATATGGGCCATAGTCACTGGATTGGAAAAGA 618 TGATGAAGGAGATTGGATATGTAACGCCTCATATTGGGCCATTAGTCACTGGATTGGAAAAGA 618 TGATGAAGGAGATTGGATTAACGCCTCATTGTATGTATGT | }              |
| Dormitzer, M., Dagan, R., Bro<br>Langermann, S., Koenig, S. an |                      | SSS SIIGGUAGCAAGAACAAGAAGAAGGITATATCTTTGATCCTCGTGATATAACCAAG  | ? 5            |
| o 2457)<br>Heinrichs,  | REFERENCE<br>AUTHORS | 558 ATTAGCTGATAAGTATACAACGTCAGATGGTTACATTTTTGATGAACATGTATATAATCAG   | P &            |
|  | ORGANISM             | 1509 ACGTTTAGGAAAAACCAAATGCGCAAATTACCTTACACTGATGATGAGTAGTTCAAGTAGCCAA 1568  | Db             |
|  | KEYWORDS<br>SOURCE   | 1498 GCGACTTGGCAAACCAAATTCTCAAATTGAGTATACTGAAGACGAAGTTCGTATTGCTCA 1557  | γQ             |
| AF318954.1 GI:12744741   | ACCESSION<br>VERSION | 449 TGATAAAGTCAAGTTAGTGGAAGATATTCTTGCCTTCTTAGCTCCGGATTCGTCATCCAGA   | Db             |
|  | DEFINITION           |   | δ ?            |
| AF318954   | TOCITO               | 1389 TCGACAAGTTGATTTTGAGGCTTTGGATAACCTGTTGGAACGACTCAAGGATGTCTCAAG 1448  | Db             |

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misc_feature
1396. .1488
/gene="phtB"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "MKINKYLAGSVAVLALSVCSYELGRYQAGQDKKESNRVAYIDG

BVSKREGINABOIVIKITDQGYVTSHGDHYMYYNGKVPYDAIISE

SDIVNEIKGGYVIKVNGKYYVYLKDAAHADNIHTTKEEIKRQKQER

AARAĞGRYTTDDGYIFNASDIIEDTGDAYIVPHYDHYHYIFKNEL

IGKQGSRPSSSSYNANPAQPRISENHHLTVTPTYHQNQGENISSL

IGKQGSRPSSSSYNANPAQPRISENHHLTVTPTYHQNQGENISSL

IGKQGSRPSSSSYNANPAQPRISENHHLTVTPTYHQNQGENISSL

IGKQGSRPESEPS PQPTPESPSPQPAPSNPIDGKLVKEAVRKYGDGYV

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DLSAETAAGIDSKLAKQESLSHKLGTKKTDLPSSDREYVKAYDL

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**QVSTEKVDEKLREAEDLLGKIQDPIIKSNAKETUTGLKNNLLFGT

**OLITEKVEEKLREAEDLLGKIQDPIIKSNAKETUTGLKNNLLFGT

**NAINTENERVEEKLREAEDLLGKIQDPIIKSNAKETUTGLKNNLLFGT
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Saithersburg, MD 20878, USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 pneumococcal histidine triad protein B artial cds.
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| Oy  598 GTTATCAGCTACCGACTTGGCTGCCTCCTATCTGGTCGAGGAAATCTGTC 657  Db 651 GTTATCAGCTAGCGAGTTAGCTGCTGCAGAAGCCTTTCTGGTCGAGGAAATCTGTC 657  OY  658 AAATTCAAGAACCTATCGCGACAAAATAGCGATAACACTTCAAGAACAACTGGGTACC 717  OB 696 -GAAGCAGGATCTCGTCCTTCTAAGTTATAATGCAAATCCAGCTAACCAA 754  OY  718 TTCTGTAAGCAATCCAGGAACTACAAATACTAACAACAACAGCAACACAACAG 777  Db 755 GATTGTCAGAGAACCACAATCT | 480 CAGTCATAATCATAACTCAAGAGCAGATAATGCTGTTGCTGCAGCCAGAGC  478 GCAAGGACGCTATACTACAGATGATGGTTATATCTTTAATGCTTCTGATATCATAGAGGA  [                     | Qy 298 TGAGGTCAAGGGTGATATGTTATCAAGGTAGATAGTATGTTTACCTTAAGGA 357 | Qy 178 CACTTCACATGGCGACCACTATCATTATTACAATGGTAAGGTTCCTTATGACGCTATCAT 237 | 60 TTCCTATGAGCTTGGACGATACCAAGCTGGTCAGGATAAGAAAGA  | ery Match st Local S ches 1609  | /note="Region: coiled-coil domain"  /gene="phtB" /note="Region: histidine triad"  misc_feature 1909. 1926 /gene="phtB" /note="Region: histidine triad" /gene="phtB" /note="Region: histidine triad" repeat_region 525. 714 /rpt_type=direct repeat_region 1578. 1758 /rpt_type=direct BASE COUNT 832 a 496 c 533 g 593 t 3 others |
|--|--|---|---|---|---|---|
| Db 1689 TAGTTTGTCTGAAGCTGAGAGCGGCGGCCCAGGCTTATGCTTAAGGAAAGGTTTGAC 1748  Qy 1738 ACCTCCATCTCCCAGACGCAGATGTTAAAGCAAATCCAACTGGAGATAGTAGCAGCAGGTTT 1797  | Db 1509 AČGTTTAĞGAĀĀĀĊCĀĀĀTĠCGCĀĀĀŤTACCTĀCĀCĀĞĀTĠĀGĀTĀĞAGĀTĀĞGCĀĀ 1568  Qy 1558 ATTAGCTGATAAGTATCAACGTCAGATGGTTACATTTTTGATGAACATGATATAATCAG 1617 | 1389<br>1438<br>1449<br>1498                                    | Oy 1258 GAGTCTTCACACACTTTAACTGCTAAAAAATGTTGCTCCTGGTGACCAAGAATT 1317     | Db 1095 ĀAĞTČCĞĞAĞCTĞCĞAĞCTĞCAĞTTÇAĞTĞATĞĞĞĞATTĞĞTÇAAAĞAGC 1148  Oy 1138 GGTACGAAAAGTTGGGGAAGGATATGTATTCGAAGAAAĞGGCATCTCTCGTTATGTCTT 1197 | Qy 1018 TTGGGTACCAGATTCAAGGCCAGAACCAAGCTCCACAACCGACTCCGGAACCTAGTCC 1077 | Qy 838 GAGTCAACGACATGTAGAATCTGATGGCCTTGTCTTTGATCCAGCACAAATCACAAGTCG 897   |

protein

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REFERENCE
AUTHORS
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AF318955
                                                                                                                                           Submitted (03-NOV-2000) Molecular Microbiology, West Watkins Mill Road, Gaithersburg, MD 20878, Location/Qualifiers
                                                                                                                                                                                                                                                                                                             Adamou, J.E., Heinrichs, J.H., Erwin, A.L., Walsh, W., Gayle, Dormitzer, M., Dagan, R., Brewah, Y.A., Barren, P., Lathigra, Langermann, S., Koenig, S. and Johnson, S. Identification and characterization of a novel family of pneumococcal proteins that are protective against sepsis Infect. Immun. 69 (2), 949-958 (2001)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CCCTCGAGAAGAGAAACCGCAAAGCGAGAAACCAGAGTCTCCAAAAACCAACAGAGGAACC 2228
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/gene="phtD"
l. .>2517
                                                                     /organism="Streptococcus
/mol_type="genomic DNA"
/serotype="4"
                                  'db_xref="taxon:1313"
. .>2517
                                                                                                                                                                                                                                       Erwin, A.L.,
                                                                                                        pneumoniae"
                                                                                                                                                                                                                                       Walsh,W.,
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Lathigra,R.,
                                                                                                                                                                  MedImmune,
USA
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                                                                                                                         CAAGCGTGAAGGAATCAATGCTGAGCAAATCGTCATCAAGATAACAGACCAAGGCTATGT
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                   GACCTCTCATGGAGACCATTATCATTACTATAATGGCAAGGTCCCTTATGATGCCATCAT
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//db_xref="GI:12744744"
//db_xref="GI:12744744"
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SHNHGGGSNIDQAVVAARAQGRYTTDDGYIFNASDIIEDTANYUPHGOHYHYIFNASH
SHNHGGGSNIDQAVVAARAQGRYTTDDGYIFNASDIIEDTANYUPHGNYHYIFIYSQMSELERRI
LSASELAAABAYMNGKOGSRFSSSSSYNANPAQPRLSENHLTVTPTYHQNQGENISS
LLRELYAKPLSERHVEBDGLIFDPAQITSRTAGGVAVPHGNHYHFIPYEQMSELERRI
ARIIPLAYRSNHWVPDSRPEOQPSPQSTPEPSPSPQPAPNPQPAPSNPIDEKLVKEAVR
KVGDGYVFEENGVSRYIPAKDLSAETAAGIDSKLAKQESLSHKLGAKKTDLPSSDREF
YNKAYDLLARHYDDLLDNKGRQVDFBALDNLLERLKUVPSBKYKLUDDILAFLAPIRH
PERLGKPNAQITYTDDEIQVAKLAGKYTTEDGYIFDPRDITSDEGDAYVTPHMTHSHW
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PNERPHSDNGFGNASDHVRKNKVDQDSKPDEDKEHDEVSEPTHPESDLKENHAGLNPS
ADNIXKPSTDTEETEEBAEDTTDEAEIPQVENSVINAKIADABALLEKVTDPSIRQNA
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1417. .1509
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/transl_table=
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1678. .1695
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                                                                                                      TCGTTATGTCTTTGCGAAAGATTTACCATCTGAAACTGTTAAAAATCTTGAAAGCAAGTT
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                              GGCCAAGCAGGAAAGTTTATCTCATAAGCTAGGAGCTAAGAAAACTGACCTCCCATCTAG
                                                         TCGTTATATCCCAGCCAAGGATCTTTCAGCAGAAACAGCAGCAGGCATTGATAGCAAACT
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                                                                                                 AX568778
Sequence 198
AX568778
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                                           Streptococcus pneumoniae
Streptococcus pneumoniae
Bacteria; Firmicutes; Lactobacillales;
Masignani,V.,
                            Streptococcus.
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   and
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REFERENCE
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Pettelin, H., Nelson, K., Paulsen, I.T., Eisen, J.A., Read, T.D., Peterson, S., Heidelberg, J., DeBoy, R.T., Haft, D.H., Dodson, R.J., Durkin, A.S., Gwinn, M., Kolonay, J.F., Nelson, W.C., Peterson, J.D., Durkin, A.S., Gwinn, M., Kolonay, J.F., Radune, D., Holtzapple, E., Khouri, H., Wolf, A.M., Utterback, T.R., Hansen, C.L., McDonald, L.A., Feldblyum, T.V., Angiuoli, S., Gesuwan, P., Hickey, E.K., Holt, I.E., Loftus, B.J., Ujwal, M.L., Yang, F., Smith, H.O., Venter, J.C., Dougherty, B.A., Morrison, D.A., Hollingshead, S.K. and Fraser, C.M.
                                                                                                                                                                                                                                                                                                                                Direct Submission
Submitted (29-JUN-2001) The Institute
Medical Center Dr. Rockville, MD 20856
Location/Qualifiers
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                           YFTYGYKHSTIEE"
                                                GLIRLRKEKGMPKAGEFKTPLVPLLPILSIIICLSFMLQYNMNTWIAFLVALLVGSII
                                                                                                                                                                                                                                                                                                                                                                                                                                                        3482.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           QGKIGKIQFGAISNADAEAAFKEMN"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /codon_start=1
/transT_table=11
/producT="thioredoxin family protein"
/protein id="AAK75117.1"
/db_xref="GI:14972473"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          KVLGQLDAEKADKKVLAKAQNLLQETLDFVKEENGSAETETKLVEELKAILDKLK"
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1303. .1602
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /translation="MVASASASSTSTQAQEQVDKSELRALSQELDQRLKALATVSDPK
IDATKAVLLDAQKAPEDSALTE"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /gene="SP0999"
1833. .2540
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/protein_id="AAK75114.
/db_xref="GI:14972470"
                                                                                                                                                                                                                                                                                                                                                                                                                               'gene="SP1001"
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2551. .3108
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DSPSAQRYSESDGLVEDPAKI I SRTPNGVA I PHGDHYHF I PYSKLSALEEKL ARMVPI
SGTGSTVSTNAKPNEVVSSLGSLSSNPSSLTTSKELSSASDGY I FNPKDI VEETATAY
I VRHGDHFHY I PKSQQ I GQPTLPNNSLATPS PSILP I NPGTSHEKHEEDGYGFDANR I I
AEDESGFVMSHGDHNHY FFKKDLTEEQ I KAAQKHLEEVKTSHNGLDSLSSHEQDY PSN
AKEMKDLDKKI EEKI AGI MKQ YGVKRES I VVNKEKNA I I Y PHGDHHHADP I DEHKPVB
I GHSHBNYELFKPEGVAKKEBGNKYTGEEL TMVNNLKNSTRNQNDFLHGQTFK
GTSFPELEKKLG I NMLVKL I TPDGKVLEKVSGKVFGEGVGNI I ANFELDQFYLPGQTFK
TI ASKDYPEVS YGVFTTVFTSLA YKAASQTI FY PHAGDTYLFKVNOQPKNEGTDAL
TI ASKDYPEVS YGVFTTVFTSLA YKAASQTI FY PHAGDTYLFKVNOQPKNEGTDAL
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8670. .11789
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5016. .5933
                                                                                                                                                                     VRVFDEFHGNAYLENNYKVGEIKLPIPKLNQGTTRTAGNKIPVTFMANAYLDNQSTYI
VEVPILEKENQTDKPSILPQFKRNKAQENLKLDEKVEEPKTSEKVEKEKLSETGNSTS
NSTLEEVPTVDPVQEKVAKFAESYGMKLENVLFNMDGTIELYLPSGEVIKKNMADFTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                YNKAYDLLAR I HQDLLDNKGRQVDF EALDNLLERLKD VPSDKVKL VDD I LAFLAP I RH
BERLGKPNAQ I TYTDDE I QVAKLAGKYTTEDGY I FDPROI TSDEGDA YVTPHMTISHW
I KKOSLSEAERAAQAY KKEKGLTPESTTHODSGUTEAKGABA I YNR VKAAKKYVELDE
MPYNLQYTVEVKNGSL I I PHYDHYHNI KFEWFDEGLYEAPKGYTLEDLLATVKYYVEH
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SHNHGGGSNDQAVVAARAQGRYTTDDGYIFNASDIIEDTGDAYIVPHGDHYHYIPKNE
LSASELAAAEAYWNGKQGSRPSSSSSYNANPAQPRLSENHNLTVTPTYHQNQGENISS
                                                                                                   EAPQGNGENKPSENGKVSTGTVENQPTENKPADSLPEAPNEKPVKPENSTDNGMLNPE
GNVGSDPMLDPALEEAPAVDPVQEKLEKFTASYGLGLDSVIFNMDGTIELRLPSGEVI
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codon start=1
'codons tart=1
/transI_table=11
/product="conserved hypothetical protein"
/product="canak75121.1"
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ADNLYKPSTDTEETEEEAEDTTDEAEIPQVENSVINAKIADAEALLEKVTDPSIRQNA
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ARIIPLRYRSNHWVPDSRPEQPSPQSTPEPSPSPQPAPNPQPAPSNPIDEKLVKEAVR
KVGDGYVFEENGVSRYIPAKDLSAETAAGIDSKLAKQESLSHKLGAKKTDLPSSDREF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         METLTGLKSSLLLGTKDNNTISAEVDSLLALLKESQPAPIQ"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /protein_id="AAK75121.1"
/db_xref="GI:14972477"
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ELLMKDPNYQLKDADIVNEVKGGYIIKVDGKYYVYLKDAAHADNVRTKGEINRQKQEH
VKDNEKVNSNVAVARSQGRYTTNDGYVFNPADIIEDTGNAYIVPHGGHYHYIFKSDLS
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QAGQKAENLTPDEVSKREGINAEQIVIKITDQGYVTSHGDHYHYYNGKVPYDAIISE
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protein_id="AAK75120.1"
/db_xref="GI:14972476"
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transl_table=
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transl_table=
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|--|---|--|--|---|------|---|-------|--|---|--|--|--|--|---|--|-------------|---|--|---|--|--|------|--|-------|----|--|--|----------------------|
| Q  | P Q   | Db   | νQ   | D Qy  | . pb | 0 6   | ş Q   | Вb   | Qy  | DЬ                                       | Q  | Db Qy  | Db   | γQ  | дь<br>22   | Db          | ργ  | Db   | Ş   | Db   | Qy   | Db & | 5 5  | P 19  | рb | Qy   | Qy<br>db   | Quer<br>Best<br>Mato |
| 1018 TTGGGTACCAGATTCAAGGCCAGAACAACCAAGTCCACAACCGACTCCGGAACCTAGTC | 958 AATGTCTGAAITGGAAGAACGAATCGCTCGTATTATTCCCCTTCGTTATCGTTCAAACC | 6858 AACCGCCAGAGGTGTAGCTGTCCCTCATGGTAACCATTACCACTTTATCCCTTATGA | 898 AACAGCTAGAGGTGTTGCAGTGCCACACGGAGATCATTACCACTTCATCCACTCTACTCTCA | 838 GAGTCAACGACATGTAGAATCTGATGGCCTTGTTCTTTGATCCAGCACAAATCACAAGTCG | 4    | 681 AARICCAGCICAACCAAGAITGICAGAGAACCACAAICIGACIGICACIGICAACIIA<br>778 TCAAGCAAGTCAAAGTAATGACATTGATAGTCTCTTGAAACAGCTCTACAAACTGCC | 7     | 6629ATTGGAATGGGAAGCAGGGATCTCGTCCTTCTTCAAGTTCTATAATGC | 658 AAATTCAAGAACCTATCGCCGACAAAATAGCGATAACACTTCAAGAACAAACTGGGT | 6594 GTTATCAGCTAGCGAGTTAGCTGCTGCAGAAGCCT | 598 GITATCAGCTAGCGAGTTGGCTGCTGCAGAAGCCTTCCTATCTGGTCGAGGAAATCTG | 538 TACTGGTGATGCTTATATCGTTCCTCATGGAGATCATTACCATTACATTCCTAAGAATGA | 6474 CCAAGGACGCTATACAACGGATGATGTTTTATATCTTCAATGCATCTGATATCATTGAT | 478 GCAAGGACGCTATACTACAGATGATGGTTATATCTTTAATGCTTCTGATATCATAGAGG | 418 TAGTCAACATCGTGAAGGTGGAACTCCAAGAAACGATGGTGCTGTTGCCTTGGCACGTT. | 60 TĠĊAĠĊTĊ | 358 TGCTGCCCACGCGGATAACGTCCGTACAAAAAGAGGAAAATCGACAAAAACAAGAGC | 6300 TGAAATCAAGGGTGGTTATGTTATCAAGGTAGATGGAAAATACTATGTTTACCTTAAGG | TGGATATGTTATCAAGGTAGATGGAAAATACTATGTTTACCT1 | 6240 CAGTGAAGAGCTCCTCATGAAAGATCCGAATTATCAGTTGAAAGGATTCAGACATTGTC | 238 CAGTGAAGAATTACTCATGAAAGATCCAAACTATAAGCTAAAAGATGAGGATATTGTT | 80   | I DOJASOT KREDODALI KRAKAJI KAJAKAJI KAJAJAKA STRATOROJ KRODISOTA JASOSKARAKI. I O | 118   | 60 | 58 CTATATAGATGGAAAACAAGCGACGCAAAAAAACGGAGAATTTGACTCCTGATGAGGTTAG | TTCTTACGAGTTGGGACTGTATCAGCTAGAACGGTTAAGGAAAATAATCGTGTTTT | 00 E2                |
| CC 1077  | CA 1017<br>  <br>CA 6977  | ZA 6917  | CA 957   | TCG 897   | n    | TT 837  | G 777 | 30 6680  | CC 717  | 6628                                     | rc 657   | 3A 597<br>  <br>3A 6593  | 3A . 6533  | 3A 537  | TC 477<br> <br>3C 6473   | A-64        | CA 417  | <br>3A 6359  | 3A 357                                      | <br> AA 6299   | AA 297   | 62   | <b>ာ</b> စ   | r 177 | 61 | AG 117   | rc 57<br> -<br>  6059                                    |                      |

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CAGTGAAGATCCAAATAAGAACTTCAAAGCGGATGAAGAGCCAGTAGAGGAAACACCTGC
                                                                                   TCCGCATTCAGATAATGGTTTTGGTAACGCTAGCGACCATGTTCGTAAAAATAAGGTAGA
                                                                                                                         CTATACCTTGGAAGATTTGTTTGCGACGATTAAGTACTACGTAGAACACCCTGACGAACG
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TCGTCATCCAGAACGTTTAGGAAAACCAAATGCGCAAATTACCTACACTGATGATGAGAT
                     TACCCATCCAGAGCGACTTGGCAAACCAAATTCTCAAATTGAGTATACTGAAGACGAAGT
                                                                                              TGATGAATCGACTAATAAAGAAAAATTGGTAGATGATTTATTGGCATTCCTAGCACCAAT
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2 (bases 1 to 232807)
Dopazo, J., Mendoza, A., Herrero, J., Caldara, F., Polissi, A.,
Humbert, Y., Friedli, L., Guerrier, M., Grand-Schenk, E., Gandin, C.,
Francesco, M., Buell, G., Feger, G., Garcia, E., Peitsch, M. and
Garcia-Bustos, J.F.
Direct Submission
Direct Submission
Direct Submission
Direct Submission
Submitted (31-OCT-2000) Research Department, Glaxo Wellcome, S.A
                                                                                                                                                                                                      Dopazo, J., Mendoza, A., Herrero, J., Caldara, F., Humbert, Y., Friedli, L., Guerrier, M., Grand-Schenk, E., Gandin, C., de Francesco, M., Polissi, A., Buell, G., Feger, G., Garcia, E., Pand Garcia-Bustos, J.F.

Annotated draft genomic sequence from a Streptococcus pneutype 19f clinical isolate type 19f clinical isolate type 19f clinical isolate.
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AL449923.1 GI:11545148
HTG; HTGS_PHASE2.
Streptococcus pneumoniae
Streptococcus pneumoniae
Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
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Best Local Similarity 65.6%;
Matches 1616; Conservative
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* NOTE: This is a 'working draft' sequence

* This sequence will be replaced

* by the finished sequence as soon as it is available

* the accession number will be preserved.

1. 232807
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TCAAGCAAGTCAAAGTAATGACATTGATAGTCTCTTGAAACAGCTCTACAAACTGCCTTT
                                             GATTGTCAGAGAACCACAATCT---
                                                                                                                                                             TTTATCTGCCAGTGAATTAGCTGCTGCCCAAGCCTATTGGAATGG-
                                                                                                                                                                               GTTATCAGCTAGCGAGTTGGCTGCTGCAGAAGCCTTCCTATCTGGTCGAGGAAATCTGTC
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/mol type="genomic DNA"
/serotype="19f"
/db_xref="taxon:1313"
/clone="G54"
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| Qy 58 CTATATAGATGGAAAACAAGCGACGCAAAAAAACGGAGAATTTGACTCCTGATGAGGTTAG 117 | OY 1 TTCTTACGAGTTGGGACTGTATCAAGCTAGAACGGTTAAGGAAAATAATCGTGTTTC 57 | Query Match 41.3%; Score 987.6; DB 6; Length 2290;<br>Best Local Similarity 67.7%; Pred. No. 1.5e-200;<br>Matches 1481; Conservative 0; Mismatches 645; Indels 60; Gaps 5; | source 1. 2290 /organism="unknown" BASE COUNT 766 a 474 c 498 g 547 t 5 others ORIGIN | Fannon,M.R. and Rosen,C.A. Streptococcus pneumoniae antigens and vaccines Patent: US 6159469-A 65 12-DEC-2000; Location/Qualifiers | ified.<br>es 1 to 2290)<br>H., Kunsch,C.A.                           | ARI20270<br>ARI20270.1 GI:14103846<br>Unknown.                       | RESULT 21 AR120270 AR120270 AR20270 DEFINITION Sequence 65 from patent US 6159469. | 202767 TAA   | 202707 CCAGGACAATACTATTATGGCAGAAGCTGAAAAACTATTGGCTTTATTAAAGGAGAG 202<br>2356 TAA 2358 | 202647 TATCAAGTCCAATGCCAAAGAGACTCTCACAGGATTAAAAAATTACTTAC            | 202587 AAAGGTTGAAGAAAAACTGAAGAGAGATTTACTTGGAAAAATCCAGGATCCAAT 2036 TCTGAAAGCCAATGCAACAGAAACTCTAGCTAGGTTTACGAAATAATTTGACTCTTCAAAT |   | 202467 TGAGGAAGAACCCCTCGAGAAGAAAACCGCAAAGCGAGAAACCAGAGTCTCCAAAACC 2126CCAGTAGAGGAAACACCTGCTGAGCCAGAAGTCCCTCAAGTAGAGACTGA | 202407 TCAAGCTGATACCAATCAAACGGAAAAAACCAAAACGAGGAAAACCTCAGACAGA       | 202347 TCCGCATTCAGATAATGATTTTGGTAACGCTAGCGATGATGAGAAAAAAAA            | 202287 GTATACTCTTGAGGATCTTTTGGCGACTGTCAAGTACTATGTCGAACATCCAAACGAACG  | QY 1906 TCATTACCATAATATTAAATTTGCTTGGTTTGATGATGACACATACAAAGCTCCAAATGG 1965 |   |
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| 1126 GGTTAGTCAGCTGGTACGAAAAGTTGGGGAAGGATATGTATTCGAAGAAAAGGGCATCTC 1185  | AGGICCGCAACCTGCACCAATCTTAAATTAGATTCAATTCTTCTTF                    | 8 TTGGGTACCAGATTCAAGGCCAGAAACCAAGTCCACAACCCAGATCCGCAACCTAGTCC  | 8 AATGTCTGAATTGGAAGAACGAATCGCTCGTATTATTCCCCTTCGTTATCGTTCAAACCA<br>                    | 8 AACAGCTAGAGGTGTTGCAGTGCCACACGGAGATCATTACCACTTCATCCCCTTACTCTCA  | 838 GAGTCAACGACATGTAGAATCTGATGGCCTTGTCTTTGATCCAGCACAAATCACAAGTCG 897 | 778 TCAAGCAAGTCAAAGTAATGACATTGATAGTCTCTTGAAACAGCTCTACAAACTGCCTTT 837 | 718 TICTGTAAGCAATCCAGGAACTACAAATACTAACAAGCAACAAGAGCAACAGCAACACTAACAG 777           | 658 AAATTCAAGAACCTATCGCCGACAAAATAGCGATAACACTTCAAGAACAAACTGGGTACC 717 | 598 GTTATCAGCTAGCGAGTTGGCTGCTGCAGAAGCCTTCCTATCTGGTCGAGGAAATCTGTC 657                  | 538 TACTGGTGATGCTTATATCGTTCCTCATGGAGATCATTACCATTACATTCCTAAGAATGA 597 | 478 GCAAGGACGCTATACTACAGATGATGATGATATCTTTAATGCTTCTGATATCATAGAGGA 537<br>   | 418 TAGTCAACATCGTGAAGGTGGAACTCCAAGAAACGATGGTGCTGTTGCCTTTGGCACGTTC 477 | 358 TGCTGCCCACGCGGATAACGTCCGTACAAAAGAGGAAATCAATC   | 298 TGAGGTCAAGGGTGGATATGTTATCAAGGTAGATGGAAAATACTATGTTTACCTTAAGGA 357 | 238 CAGTGAAGAATTACTCATGAAAGATCCAAACTATAAGCTAAAAGATGAGGGATATTGTTAA 297 | 178 CACTTCACATGGCGACCACTATCATTACTACAATGGTAAGGTTCCTTATGACGCTATCAT 237 | CAAGCGTGAAGGAATCAATGCTGAGCAAAATCGTCATCAAGATAACAGACCAAGGCTATGT             | 64 TTATATAGATGGTGATCAGGCTGGTCAAAAGGCAGAAAACTTGACACCAGATGAAGTCAG 123 |

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TACTGGTGATGCTTATATCGTTCCTCATGGAGATCATTACCATTACCATTACCATTCCTAAGAATGA
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Best Local Similarity
Matches 1481; Conserv
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1 (bases 1 to 2290)

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1 (TITLE

Streptococcus pneumoniae antigens and vaccines

OURNAL

HUMAN GENOME SCIENCES INC

PN JP 2001505415-A/33

PD 24-APR-2001

PF 30-OCT-1097 JP

PR 31-OCT-107
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PF 30-CCT-1997 JP 1998520667

PR 31-CCT-1996 US 60/029960

PI CHARLES A KUNSCH, GIL H CHOI, SYDNOR L JOHNSON, ALEX HROMOCKYJ PC C12N15/31, C12N5/18, C12N1/21, C07K14/315, C12Q1/68, A61K39/09, PC G01N33/68

PC G01N33/68

CC Strandedness: Double;

CC Topology: Linear.
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BD063279
BD063279.1 GI:22608882
JP 2001505415-A/33.
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                  GCAAGGACGCTATACTACAGATGATGGTTATATCTTTAATGCTTCTGATATCATAGAGGA
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CCAAGGACGTTATACAACGGATGATGGGTATATCTTCAATGCATCTGATATCATTGAGGA
                                                                   CAGTCATAATCAT
                                                                                       TAGTCAACATCGTGAAGGTGGAACTCCAAGAAACGATGGTGCTGTTTGCCTTTGGCACGTTC
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ilarity 67.7%;
Conservative
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/mol_type="genomic DNA"
/db_xref="taxon:32644"
474 c 498 g 54'
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Pred. No. 1.5e-200;
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                                                                                                                                                                                                                                          TGATGAATCGACTÀATAAAGAAAAATTGGTAGATGATTTATTGGCATTCCTAGCACCAAT 1485
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TGATATAACCAGTGATGAGGGGGATGCCTATGTAACTCCACATATGACCCATAGCCACTG: 1638
                       TGATATAATCAGTGATGAAGGAGATGCATATGTAACGCCTCATATGGGCCCATAGTCACTG
                                                                             TCAAGTAGCCAAGTTGGCAGGCAAGTACACAACAGAAGACGGTTATATCTTTGATCCTCG
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Matches 1473; Conservative
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Sequence 5 from
AX343074
AX343074.1 GI:1
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Streptococcus antigens
Patent: WO 0198334-A 5
SHIRE BIOCHEM INC. (CA)
                                            TTCTTACGAGTTGGGACTGTATCAAGCTAGAACGGTTAAGGAAAA---TAATCGTGTTTC
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              CTATATAGATGGAAAAACAAGCGACGACAAAAAAACGGAGAATTTGACTCCTGATGAGGTTAG
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/mol_type="genomic DNA"
/db_xref="taxon:32644"
/note="BVH-11-2"
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1. .2639
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Patent WO0198334.
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Pred. No. 4.4e-199;
0; Mismatches 638;
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| 1126 GGTTAGTCAGCTGGTACGAAAAGTTGGGGAAGGATATTCGAAGAAAAGGGCATCTC 1185<br>     -   | 078 AGGCCCGCAACCTGCACCAAATCTTAAAATAGACTCAAATTCTTCTTT 1<br>      | ### TTGGGTACCAGATTCAAGGCCAGAACAACCAAGTCCACAACCGACTCCGGAACCTAGTCC 1 | 88 AATGTCTGAATTGGAAGAACGAATCGCTCGTATTATTCCCCTTCGTTATCGTTCAAACCA 1         | 98<br>28  | 38 GAGTCAACGACATGTAGAATCTGATGGCCTTGTCTTTGATCCAGCACAAATCACAAGTCG 8 | 78 TCAAGCAAGTCAAAGTAATGACATTGATAGTCTCTTGAAACAGCTCTACAAACTGCCTTT 8          | 18 TTCTGTAAGCAATCCAGGAACTACAATACTAACAGCAACAACAGCAACACAGCAACACAGCAACACACTAACAG 7 | 58 AAATTCAAGAACCTATCGCCGACAAAATAGCGATAACACTTCAAGAACAAACTGGGTACC 71 | GTTATCAGCTAGCGAGTTGGCTGCCAGAAGCCTTCCTATCTGGTCGAGGAAATCTGTC 65           | 38 TACTGGTGATGCTTATATCGTTCCTCATGGAGATCATTACCATTACATTCCTAAGAATGA 59<br>    | 78 GCAAGGACGCTATACTACAGATGATGGTTATATCTTTAATGCTTCTGATATCATAGAGGA 5 | 18 TAGTCAACATCGTGAAGGTGGAACTCCAAGAAACGATGGTGCTGTTGCTTGGCACGTTC 4              | 58 TGCTGCCCCACGCGGATAACGTCCGTACAAAAGAGGAAATCAATC                         | AG LORANGARE LLE LERIGRARIAGAT E CORANI LA LORANGARI LOR | 38 CAGTGAAGAATTACTCATGAAAGATCCAAACTATAAGCTAAAAGATGAGGATATTGTTAA 29        | 78 CACTTCACATGGCGACCACTATCATTATTACAATGGTAAGGTTCCTTATGACGCTATCAT 23       | 118 CAAGCGTGAAGGAATCAATGCTGAGCAAATCGTCATCAAGATAACAGACCAAGGCTATGT 177<br>      |
|--|---|--|---|---|---|--|---|--|---|---|---|---|--|--|---|--|---|
| RESULT 24 AE008464 | Qy 2146 TGAGCCAGAAG 2156               Db 2288 TGAATCTGATG 2298 | 086 CAGTGAAGATCC<br>       <br>228 CCAAGATAGTAJ                    | Qy 2026 TCCACATTCTAATGATGGATGGGCCAATGCCAGTGAGCATGTGTTAGGCAAGAAAACCCA 2085 | Qy 1966 CTATACCTTGGAAGATTTGTTTGCACGATTAACTACTAGAACAACACCCTGACGAACG 2025 |   | Qy 1846 ATATRATGGTTGAGCATACAGTTGAGATTAAAAACGGTAATTTGATTATTCCTCATAAGGA 1905 | Qy 1786 TGCAGCAGCTATTTACAATCGTGTGAAAAGGAAAAAAAAA                                |  | Qy 1666 GATTGGAAAAGATAGCCTTTCTGATAAGAAAAGTTGCAGCTCAAGCCTATACTAAAGA 1725 | Qy 1606 TGATATAATCAGTGATGAAGGAGATGCATATGTAACGCCTCATATGGGCCATAGTCACTG 1665 |   | Qy 1486 TACCCATCCAGAGCGACTTGGCAAACCAAATTCTCAAATTGAGTATACTGAAGACGAAGT 1545<br> | Qy 1426 TGATGAATCACTAATAAAGAAAAATTGGTAGATGATTTATTGGCATTCCTAGCACCAAT 1485 | Qy 1366 TGNAAATAAGGGTCGTAATTCTGATTTCCAAGCCTTAGACAATTATTAGAACGCTTGAA 1425<br>   | OY 1306 TGACCAAGAATTTTATGATAAAGCATATAATCTGTTAACTGAGGCTCATAAAGCCTTGTT 1365 | Qy 1246 ATCAAACAAGAGAGTGTTTCACACACTTTAACTGCTAAAAAAGAAAATGTTGCTCCTCG 1305 | QY 1186 TCGTTATGTCTTTGCGAAAGATTTACCATCTGAAACTGTTAAAAATCTTGAAAGCAAGTT 1245<br> |

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REFERENCE
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AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (27-JUL-2001) Infectious Diseases Research, Eli Lilly and Company, Lilly Research Labs, Indianapolis, IN 46285-0438, USA Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         J. Bacte
21429245
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J. Bacteriol. 183 (19), 5709-5717 (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    and Glass,J.I
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Streptococcus pneumoniae R6
Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1544234
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      organism="Streptococcus pneumoniae R6"
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12. .1615
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ESDEKENHVGLNPSADNLYKPSTDTEETEEEAEDTTDEAEI PQVEHSVINAKIAEAEA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NKAYDLLARIHQDLLDNKGRQVDFEALDNLLERLKDVSSDKVKLVDDILAFLAPIRHP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ʻrecursor"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  'label=spr0908
|product="Pneumococcal histidine triad protein
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transl_table=11
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9403. .9543

gene="spr0909"

'transī\_table=11 'label=spr0909 |product="Hypothetical protein"

gene="spr0909" codon\_start=1 transl\_table=1

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Matches 1461;
                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
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                                                                                                                                                   TTATATAGATGGTGATCAGGCTGGTCAAAAGGCAGAAAATTTGACACCAGATGAAGTCAG
                   GACCTCTCATGGAGACCATTATCATTACTATAATGGCAAGGTTCCTTATGATGCCATCAT
                                        CACTTCACATGGCGACCACTATCATTACTACAATGGTAAGGTTCCTTATGACGCTATCAT
                                                                                                                                                                                   CTATATAGATGGAAAACAAGCGACGCAAAAAACGGAGAATTTGACTCCTGATGAGGTTAG
                                                                                                                  CAAGCGTGAAGGAATCAATGCTGAGCAAATCGTCATCAAGATAACAGACCAAGGCTATGT 177
                                                                                                                                                                                                                                      TTCTTACGAGTTGGGACTGTATCAAGCTAGAACGGTTAAGGAAAA---TAATCGTGTTTC
                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                   /gene="pepT"
/note="synonym: spr0913"
complement (11045. .12265)
                                                                                                                                                                                                                                                                                                                                                                                                                                                          /translation="MPVTPNNGVSAVDDGYVFNPNDIVRDTGDAYIVRHGDHYHYIPK SLINNPPSHSNTEEVGSSSSSVLSNPSLHVHHEEEDGHGFDANRIISEDSEGFVLPHG DHNHYIKVQTKGYEAALKKIPBSLQSNYPPGTFDEKAVLAKVDQLLADSRSIYKDKPI EQRQIELALGQPTESLKKIKVS"
                                                                                                                                                                                                                                                                                                                                                                                                                                            complement (11045. .12265)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /product="Pneumococcal histidine triad precursor, truncation" /protein id="AAK99714.1" /db_xref="GI:15458517"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /translation="MLEITLKSPYQFAHILFQSTIVPHGGHYHFIPESDLSAGELAVA
KV"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /translation="mfQELICLAQKTFYFFLAICRRLLVAIYHVFLKQESYNTRLQGL
TEIRNPDKTMSVQDAIRFAQQRGFNML"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      complement (10187. .10402)
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/codon_start=1
/transl_table=11
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/transl_table=11
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.0373. .11002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             gene="phtE-truncation"
note="synonym: spr0910"
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/db_xref="GI:15458516"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                label=spr0912
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protein_id="AAK99715.1"
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label=spr0910
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Pred. No. 3e-195;
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TGACCAAGAATTTTATGATAAAGCATATAATCTGTTAACTGAGGCTCATAAAGCCTTGTT 1365
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                                                               ATCAAAACAAGAGAGTGTTTCACACACTTTAACTGCTAAAAAAAGAAAATGTTGCTCCTCG 1305
                                                                                                                                                                                          GGTTAGTCAGCTGGTACGAAAAGTTGGGGAAGGATATGTATTCGAAGAAAAGGGCATCTC 1185
                                                                                                                                                                                                                                                        AGGCCGCAACCTGCACCAAATCTTAAAATAGACTCAAATTCTTC------TTT 1125
                                                                                                                                                                                                                                                                                                         TTGGGTACCAGATTCAAGACCAGAACAACCAAGTCCACAATCGACTCCGGAACCTAGTCC 3776
                                                                                                                                                                                                                                                                                                                                                                          ACTGTCACCTTTGGAAGAAAAATTGGCTCGTATTATTCCCCTTCGTTATCGTTCAAACCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                             AACAGCTAGAGGTGTTGCAGTGCCACACGGAGATCATTACCACTTCATCCCTTACTCTCA
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                                                                                                                                    TCGTTATGTCTTTGCGAAAGATTTACCATCTGAAACTGTTAAAAAATCTTGAAAGCAAGTT 1245
                                                                                                                                                                     GGTCAAAGAAGCTGTTCGAAAAGTAGGCGATGGTTATGTCTTTGAGGAGAATGGAGTTCC 3896
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KEYWORDS
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ORGANISM
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AF340222
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AF340222 AF340222 . 1 GI:134470
artificial sequences.
1 (bases 1 to 2166)
Zhang, Y., Masi, A.W., |
Green, B.A.
                                                                  synthetic synthetic
                                                                                                                                                                                                                                                                                                                                                                                                          CTATACCTTGGAAGATTTGTTTGCGACGATTAAGTACTACGTAGAACACCCTGACGAACG
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                 Mountzouros, K.,
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                 Hostetter, M.K.
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Matches 1436; Conser
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                  ATCGTTCCTCATGGAGATCATTACCATTACATTCCTAAGAATGAGTTATCAGCTAGCGAG
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                                                                 ACGGATGATGGTTATATCTTCAATGCATCTGATATCATTGAGGACACGGGTGATGCTTAT
                                                                                     ACAGATGATGATTATATCTTTAATGCTTCTGATATCATAGAGGATACTGGTGATGCTTAT
                                                                                                                              GGTGGTTCT----AACGATCAAGCAGTAGTTGCAGCCAGAGCCCAAGGACGCTATACA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (25-JAN-2001) Department of Bacteriology, Vaccines, 211 Bailey Road, West Henrietta, NY 14586,
                                                        /translation="MKDPNYQLKDSDIVNEIKGGYVIKVDGKYYVYLKDAAHADNIRT
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KTDLFSSDREFYNKAYDLLARHQDLLDNKGRQVDFBALDNLLERLKDVPSDKVKLVD
DILAFLAPIRHPERLGKPNAQITYTDDEIQVAKLAGKYTTEDGYIFDPRDITSDEGDA
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TPREEKFQSEKPESSKPTEFPESPESSPESSEEPQVETEKVEKLREABDLLGKIQDPIIK
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/note="N-terminal truncated
/notif-containing protein"
SNAKETLTGLKNNLLFGTQDNNTIMAEAEKLLALLKESK"
450 c 462 g 515 t
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/mol_type="genomic DNA"
/db_xref="taxon:32630"
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/db_xref="GI:13447096"
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GAGGGGGATGCCTATGTAACTCCACATATGACCCATAGCCACTGGATTAAAAAAGATAGT
                                                                                                                    TTAGGAAAACCAAATGCGCAAATTACCTACACTGATGAGGATTCAAGTAGCCAAGTTG
                                                                                                                                                                                   AAAGTCAAGTTAGTGGATGATATTCTTGCCTTCTTAGCTCCGATTCGTCATCCAGAACGT
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VERSION KEYWORDS SOURCE ORGANISM LOCUS
DEFINITION
ACCESSION REFERENCE JOURNAL MEDLINE TITLE AUTHORS Annotated draft genomic sequence from a Streptococcus pneumoniae type 19F clinical isolate Microb. Drug Resist. 7 (2), 99-125 (2001) 21335329 HTG; HTGS\_PHASE2 Streptococcus pneumoniae Streptococcus pneumoniae Bacteria; Firmicutes; Lactobacillales; Streptococcus pneumoniae AL449929 AL449929.1 GI:11545154 Dopazo,J., Mendoza,A., Herrero,J., Caldara,F., Humbert,Y., Friedli,L., Guerrier,M., Grand-Schenk,E., Gandin,C., de Francesco,M., Polissi,A., Buell,G., Feger,G., Garcia,E., P SPNEU1907 and Garcia-Bustos, J.F. 75874 bp pneumoniae clone G54, DNA \*\*\* Streptococcaceae, linear SEQUENCING HTG 11-JUL-2001 IN PROGRESS \*\*\*. Peitsch, M.

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| 885 AAATCACAAGTCGAACAGCTAGAGGTGTTGCAGTGCCACACGGAGATCATTACCACTTCA 944       | 825 ACAAACTGCCTTTGAGTCAACGACATGTAGAATCTGATGGCCTTGTCTTTGATCCAGGAC 884 | 765 GCAACACTAACAGTCAAGCTCAAAGTAATGACATTGATAGTCTCTTGAAACAGCTCT 824 | 705 CAAACTGGGTACCTTCTGTAAGCAATCCAGGAACTACAAATACTAACACAAGCAACAACA 764  | + >   | 585 TTCCTAAGAATGAGTTATCAGCTAGCGAGTTGGCTGCTGCAGAAGCCTTCCTATCTGGTC 644   | 525 ATATCATAGAGGATACTGGTGATGCTTATATCGTTCCTCATGGAGATCATTACCATTACA 584 | 465 CCTTGGCACGTTCGCAAGGACGCTATACTACAGATGATGGTTATATCTTTAATGCTTCTG 524     | 405 AAAAACAAGAGCATAGTCAACATCGTGAAGGTGGAACTCCAAGAAACGATGGTGCTGTTG 464 | 345 TTTACCTTAAGGATGCTGCCCACGCGGATAACGTCCGTACAAAAGAGGAAATCAATC    | 285 AGGATATTGTTAATGAGGTCAAGGGTGGATATGTTATCAAGGTAGATGGAAAATACTATG 344<br> | 225 ATGACGCTATCATCAGTGAAGAATTACTCATGAAAGATCCAAACTATAAGCTAAAAAAAGATG 284 | Match 35.0%; Score 835.8; DB 2; Length 75874;<br>Local Similarity 67.0%; Pred. No. 3.9e-168;<br>Les 1290; Conservative 0; Mismatches 578; Indels 58; Gaps 5; | 22476   |  | * Inis sequence w<br>* by the finished<br>* the accession n<br>Location | Submitted (31-OCT-2000)<br>Severo Ochoa 2, 28760 T.<br>* NOTE: This is a 'work | Humbert, Y., Friedli, L., Francesco, M., Buell, G., Garcia-Bustos, J.F. Direct Submission | 11442348<br>2 (bases 1 to 75874)<br>Dopazo,J., Mendoza,A., F  |
| d<br>V   | D 43   | 9 da 49   | 2 B 89  | Db Qy   | g Qy   | Qy<br>Db   | Db Qy  | Db Qy  | рь   | Qy<br>Qy   | Db QY   | ) Db QY  | D .   | S B S  | Db QY   | D 4  | ov b s  | \$ B  |
| 1952 AAAGCTCCAAATGGCTATACCTTGGAAGATTTGTTTGCGACGATTAAGTACTACGTAGAA 2011<br> | 39 ATACCTCATTATGACCATTACCATAACATCAAATTTGAGTGGTTTGACGAAGGCCTTTAT      |   | 73 CAACTGGAGATAGTGCAGCAGCTAT-TTACAATCGTGTGAAAGGGGAAAACGAATTCCA 1 75 CTGAGGCAAAAGGAGCAAATTCCA 1 76 CTGAGGCAAAAGGAGCAAGCTATCTTACAACCGCTGAAAGCAGCTAAGAAGGTGCCG 7 | 13 CCTATACTAAAGAAAAAGGTATCCTACCTCCATCTCCAGACGCAGATGTTAAAGCAAATC | 1653 GCCATAGTCACTGGATTGGAAAAGATAGCCTTTCTGATAAGGAAAAAGTTGCAGCTCAAG 1712 | 93 TTTTTGATGAACATGATAATCAGTGATGAAGGAGATGCATATGTAACGCCTCATATGG        | 1533 CTGAAGACGAAGTTCGTATTGCTCAATTAGCTGATAAGTATTACAACGTCAGATGGTTACA. 1592 | 1473 TCCTACCACCAATTACCCATCAGACGACTTGGCAAACCAAATTCTCAAATTGACTATA 1532 | 13 TAGAACGCTTGAATGAATGAATCGACTAATAAAGAAAAATTGGTAGATGATTTATTGGCAT | 1353 ATAAAGCCTTGTTTGNAAATAAAGGGTCGTAATTCTGATTTCCAAGCCTTAGACAAATTAT 1412  | 93 ATGITIGETCCTCGTGGACCAAGAATTTTATGATAAAGCATAATCTGTTAACTGAGGCTC         | 33 TTGANAGCAAGTTATCAAACAGAGAGTGTTTCACACACTTTAACTGCTAAAAAAGAAA  | 59 AGAATGGAGTTTCTCGTTATATCCCAGCCAAGGATCTTTCAGCAGAAACAGCAGCAGGCA | 1116ATTCTTTGGTTAGTCAGCTGGTACGAAAAGTTGGGGAAAGGATATGTATTCGAAG 1172 |   | 39 ATCGTTCAAACCATTGGGTACCAGATTCAAGACCAGACC                                     | 945 TCCCTTACTTCAAATSTCTSAATTGGAAGAACGAATCGCTGGTATTATTCCCCTTCGTT 1004                      | 59 AAATCACAAGTCGAAACCGCCAGAGGTGTAGCTGTCCCTCATGGTAATCACTTTACCACTTTA 45 TCCCTTTACTCTTCAAATTCTCTCAAATTCCAATCAATC |

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Submitted (31-OCT-2000) Research Department,
Severo Ochoa 2, 28760 Tres Cantos, SPAIN
* NOTE: This is a 'working draft' sequence.
* This sequence will be replaced
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Dopazo, J., Mendoza, A., Herrero, J., Caldara, F., Polissi, A.,
Humbert, Y., Friedli, L., Guerrier, M., Grand-Schenk, E., Gandir
Francesco, M., Buell, G., Feger, G., Garcia, E., Peitsch, M. and
Garcia-Bustos, J.F.
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Francesco,M., Polissi,A., Buell,G., Feger,G., Garcia,E., Peitsch,
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Kunsch, C.A., Choi, G.H., Dillon, P.S., Rose
Fannon, M.R. and Dougherty, B.A.
Streptococcus pneumoniae polynucleotides
Patent: US 6420135-A 243 16-JUL-2002;
Location/Qualifiers
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18 (Kunsch,C.A., Choi,G.H., Dillon,P.J., Rosen,C.A., Bara,S.C., Fannon,M. and Dougherty,B.A.

Polymucleotide of Streptococcus pneumoniae and sequence patent: JP 2001501833-A 243 13-FEB-2001;

HUMAN GENOME SCIENCES INC

OS Unidentified
PN JP 2001501833-A/243

PD 13-FEB-2001
PF 30-OCT-1997 UP 1998520718
PR 31-OCT-1996 US 60/029960
PI CHARLES A KUNSCH,GIL H CHOI,PATRICK J DILLON,CRAIG A ROSEN, PI STEVEN C BARASH,
DI MITCHAFT FRANCY.
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PC C12N1.
PC C12N5.
Q06F15/40
CC Stran
CC Topol
FH Key
FT Source
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     unidentified unidentified
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JP 2001501833-A/243.
                                                                                                                                                                                          Similarity
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 TAAGAGGGAGGGGATCAACGCCGAACAAATTGTTATCAAGATTACGGATCAAGGTTATGT
                    CAAGCGTGAAGGAATCAATGCTGAGCAAATCGTCATCAAGATAACAGACCAAGGCTATGT
                                                                           CTATATAGATGGAAAACAAGCGACGCAAAAAAACGGAGAATTTGACTCCTGATGAGGTTAG
                                                                                                                                       TTCTTACGAGTTGGGACTGTATCAAGCTAGAACGGTTAAGGAAAA---
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                                                         TTATATAGATGGTGATCAGGCTGGTCAAAAGGCAGAAAACTTGACACCAGATGAAGTCAG
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C12N15/09, A01K67/027, C07K14/315, C07K16/12, C12N1/15, C12N1/19,
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                                                                                                                                                                                                                                                /organism="unidentified"
/mol_type="genomic DNA"
/db_xref="taxon:32644"
451 c 511 g 61
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                                                                                                                                                                                         27.4%;
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                                                                                                                                                                           Score 653.8; DB 6;
Pred. No. 3.3e-129;
0; Mismatches 413;
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AGCCAÁGGATCTTTCÁGCAGAÁACAGCAGCAGCATTGATAGCAÁACTGGCCAÁGCÁGGA
                                    TGCGAAAGATTTACCATCTGAAACTGTTAAAAATCTTGAAAGCAAGTTATCAAAACAAGA 1257
                                                                                                                                                  AAGTCCGCAACCAGCTCCAAGCAATCCAATTGATGAGAA-----ATTGGTCAAAGAAGC
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Sequence
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Choi,G.H., Kunsch,C.A., Barash,S.C., D
Fannon,M.R. and Rosen,C.A.
Streptococcus pneumoniae antigens and
Patent: US 6159469-A 181 12-DEC-2000;
Location/Qualifiers
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                                                                                                                                                                             TAATGTTGCTGTAGCAAGGTCTCAGGGACGATATACGACAAATGATGGTTATGTCTTTAA
                                                         CAATCGTCAAAAACAAGAACATGTCAAAGATAATGAGAAGGTTA
                                                                                                                                                                                                                                                       GGTTCCTTATGACGCTATCATCAGTGAAGAATTACTCATGAAAGATCCAAAACTATAAGCT
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Kunsch,C.A., Choi,G.H., Johnson,S.L. and Hromockyj,A.

Streptococcus pneumoniae antigens and vaccines

Patent: JP 2001505415-A 91 24-APR-2001;

HUMAN GENOME SCIENCES INC

PN JP 2001505415-A/91
                                                                                                                                                                                                                                                                                                                                                                                       Streptococcus pneumoniae
BD063337
BD063337.1 GI:22608940
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                                                                                                                                                                                                                                                                                                                                                              unidentified
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I CHARLES A KUNSCH,GIL H CHOI,SYDNOR L JOHNSON,ALEX HROMOCKYJ
C12N15/31,C12N5/18,C12N1/21,C07K14/315,C12Q1/68,A61K39/09, PC
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                                     /organism="unidentified"
/mol_type="genomic_DNA"
/db_xref="taxon:32644"
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Streptococcus pneumoniae proteins and nucleic
Patent: WO 02077021-A 1987 03-OCT-2002;
Chiron Spa (IT): THE INSTITUTE FOR GENOMIC RE
Location/Qualifiers
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                                       GGCTGGAAAAAATATGCAACCGAGTCAGTTAAGCTATTCTTCAACAGCTAGTGACAA---
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                                                                                          TCACTACATTCCCAAAAGCGATTTATCTGCTAGTGAATTAGCAGCAGCTAAAGCACATCT
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/mol_type="genomic DNA"
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Submitted (03-NOV-2000)
West Watkins Mill Road,
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/protein_id="AAK06761.1"
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gLLMKDPNYQLKDADIVNEVKGGYIIKVDGKYYYVLKDAAHADNVRTKDEINRQKQEH
VKDNEKVNSNVAVARSQGRYTTNDGYVFNPADIIEDTGNAYIVPHGGHYYIPKSDLS
ASELAAAKAHLAGKNMQPSQLSYSTASDNNTQSVAKGSTSKPANKSENIQSLLKEDY
BSPSAQRYSESDGLVFDPAKIISRTPNGVAIPHGDHYHFIPYSKLSALEEKIARMVPI
                                                                                                                                                                                                                                                                                                                                        /organism="Streptococcus
/mol_type="genomic DNA"
/serotype="4"
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(phtE) gene, complete cds.
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/transl_table=11
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 ATATTATGTCTACCTGAAAGATGCAGCTCATGCTGATAATGTTCGAACTAAAGATGAAAT
                   ATACTATGTTTACCTTAAGGATGCTGCCCACGCGGATAACGTCCGTACAAAAGAGGGAAAT
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IVRHGDHFH/IPKSNOJGQPTLPNNSLATPSPSLFINPGTSHEKHEEDGYGFDANRII
AEDESGFVMSHGDHNHYFFKKDLTERQIKAAQKHLEEVKTSHNGLDSLSSHQQDYPSN
AKEMKDLDKKLEEKIAGIMKQYGVKRESIVVNKEKNAIIYPHGDHHADPIJDHKPVG
IGHSHSNYELFKPEGEVAKKEGNKVYTGEELTNVVNLLKNSTFNNQNFTLANGQKRVS
FSFPFBLEKKLGINMLVKLITPDGKVLEKVSGKVFGEGVANAFTELDQPYLFGGTFK
YTIASKDYPBVSYDGTFTVPTSLAYKMAGQTIFXTAGNKIPVTFMANAYLDNQSTYI
VRVFDEFHGNAYLENNYKVGEIKLPFKLNQGTTRTAGNKIPVTFMANAYLDNQSTYI
VRVFDEFHGNAYLENNYKVGEIKLPFKLNQGTTRTAGNKIPVTFMANAYLDNQSTYI
VEVPILEKENGTDKPSILPGFKRNKAQENIKLDBKVEEFFTSEKVERKSKLSETGNSTS
NSTLEEVFTVDPVQEKVAKFAESYGMKLNDENDGTIELYLPSGEVIKKNMADFTG
EAPQCNGENKSSENGKVSTGTVENQFTENKPADSLFEAPNEKPVKEKKSENSTNAMADFTG
EAPQCNGENKSSENGKVSTGTVENQFTENKPADSLFEAPNEKPVKENSTNAMADFTG
EAPQCNGENFALDPALEEAPAVDPVQEKLEKFTASYGLGLDSVIFNMDGTIELRLPSGEVI
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522. .789
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/note="Region: histidine
1414. .1491
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1569. .1749
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247. .264
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1648. .1665
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526 c 612
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1381. .1398
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REFERENCE
AUTHORS
TITLE
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ORIGIN
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AX343070
LOCUS
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ORGANISM
                                                                                                                                                                                                                                                                                                                                 DEFINITION
ACCESSION
                                                                                                                                                                                                                                                                                                    KEYWORDS
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                                                                                                                                                                  FEATURES
Query Match 16.1%;
Best Local Similarity 65.3%;
Matches 631; Conservative
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Sequence 1
AX343070
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Patent: WO 0198334-A 1
SHIRE BIOCHEM INC. (CA)
                                                                                                                                                                                                                                                                      unidentified unidentified
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                                                                                                                                                                                                                                                           unclassified
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/db_xref="taxon:32644"
/note="BVH-3"
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from Patent WO0198334.
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Score 385.4; DB 6;
Pred. No. 7.6e-72;
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Patent: WO 0198334-A 2 27-DEC-2001;
SHIRE BIOCHEM INC. (CA)
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                                                                                          ATCTGGTCGAGGAAATCTGTCAAATTCAAGAACCTATCGCCGACAAAATAGCGATAACAC
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Kunsch (C.A., Choi,G.H., Dillon,P.S., Rosen,C. Fannon,M.R. and Dougherty,B.A.
Streptococcus pneumoniae polynucleotides and Patent: US 6420135-A 192 16-JUL-2002;
Location/Qualifiers
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                        CAATCGACAAAAACAAGAGCATAGTCAACATCGTGAAGGTGGAACTCCAAGAAACGATGG
                                                                                                                  TARAGACGCTGATATTGTCAATGAAGTCAAGGGTGGTTATATCATCAAGGTCGATGGAAA 6388
                                                                                                                                            AAAAGATGAGGATATTGTTAATGAGGTCAAGGGTGGATATGTTATCAAGGTAGATGGAAA 336
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   CAATCGTCAAAAACAAGAACATGTCAAAGATAATGAGAAGGTTA---
                                                           ATATTATGTCTACCTGAAAGATGCAGCTCATGCTGATAATGTTCGAACTAAAGATGAAAT
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FH Key
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Polynucleotide of Streptococcus pneumoniae Patent: JP 2001501833-A 192 13-FEB-2001;
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Polynucleotide of Streptococcus
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pp 30-OCT-1997 JP 1998520718
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px CHARLES A KUNSCH,GIL H CHOI, PATRICK J DILLON, CRAIG
STEVEN C BARASH,
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                                                        C12N5/10, C12P21/02, C12Q1/68, G06F17/30, C12N15/00, C12N5/00,
                                                                         C12N1/21
                                                                                     MICHAEL FANNON, BRIAN A DOUGHERTY
C12N15/09, A01K67/027, C07K14/315, C07K16/12, C12N1/15, C12N1/19,
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Topology:
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                       TCCAGCACAAATCACAAGTCGAACAGCTAGAGGTGTTGCAGTGCCACACGGAGATCATTA
                                                                 GGAACTCTATGATTCACCTAGCGCCCAACGTTACAGTGAATCAGATGGCCTGGTCTTTGA
                                                                                         ACAGCTCTACAAACTGCCTTTGAGTCAACGACATGTAGAATCTGATGGCCTTGTCTTTGA
                                                                                                                              AGCAAAAGGATCAACTAGCAAGCCAGCAAATAAATCTGAAAATCTCCAGAGTCTTTTGAA
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Pred. No. 7.4e-72;
0; Mismatches 276;
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Kunsch,C.A., Choi,G.H., Dillon,P.S., Rose
Fannon,M.R. and Dougherty,B.A.
Streptococcus pneumoniae polynucleotides
Patent: US 6420135-A 355 16-JUL-2002;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Unclassified
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TACTGGTGATGCTTATATCGTTCCTCATGGAGATCATTACCATTACCATTACCTAAGAATGA
                                                  CCAAGGACGTTATACAACGGATGATGGGTATATCTTCAATGCATCTGATATCATTGAGGA
                                                                   GCAAGGACGCTATACTACAGATGATGGTTATATCTTTAATGCTTCTGATATCATAGAGGA
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Pred. No. 5.6e-71;
0; Mismatches 131;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       S Kunsch,C.A., Choi,G.H., Dillon,P.J., Rosen,C.J.
Fannon,M. and Dougherty,B.A.
Polynucleotide of Streptococcus pneumoniae and
Patent: JP 2001501833-A 355 13-FEB-2001;
HUMAN GENOME SCIENCES INC
Unidentified
PN JP 2001501833-A/355
PD J-FEB-2001
PF 30-OCT-1997 JP 198520718
PR 31-OCT-1996 US 60/029960
PI CHARLES A KUNSCH,GIL H CHOI,PATRICK J DII
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R 31-OCT-1996 US 60/029960

I CHARLES A KUNSCH, GIL H CHOI, PATRICK J DILLON, CRAIG STEVEN C BARASH,
                                                                                                      CACTTCACATGGCGACCACTATCATTATTACAATGGTAAGGTTCCTTATGACGCTATCAT
TGAGGTCAAGGGTAGGTATGTTATCAAGGTAGATGGAAAATACTATGTTTACCTTAAGGA
                                                       CAGTGAAGAATTACTCATGAAAGATCCAAACTATAAGCTAAAAGATGAGGATATTGTTAA
                                                                                    GACCTCTCATGGAGACCATTATCATTACTATAATGGCAAGGTTCCTTATGATGCCATCAT
                                                                                                                                             TAAGAGGGAGGGGATCAACGCCGAACAAATTGTTATCAAGATTACGGATCAAGGTTATGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C12N5/10, C12P21/02, C12Q1/68, G06F17/30, C12N15/00, C12N5/00,
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/mol_type="genomic DNA"
/db_xref="taxon:32644"
178 c 211 g 25
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Patent: WO 0198334-A 9
SHIRE BIOCHEM INC. (CA)
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                                                                                                                                                                                  Submitted (29-JUN-2001) The Institute for Genomic Research, 9712
Medical Center Dr, Rockville, MD 20850, USA
Location/Qualifiers
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CLILEPHYSFYSVMGYEKFLESKOIQFLVIKDWYQEEALLNYWADEIAKILKEEVKQD
SFKVIFSAHSVPIFALDFGDPYIDQIFENSKLVAEKLGLSSEQYTNTWQSESDIGIPW
IKPDVLEYLREQTEHPDHYIFVPISFISEHIEVLFDNDVECYDLCQEFGVNYHRPPMP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /translation="mtyphildrfltyvkvntrsdehsttpstqsqvdpatnvlipe
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peikhceirugfgpdeeigugankfdaedfdvdfayffudgflgelgelgvetfsaagael
hfqgrnvhpgtakgqmvnalqlaidfhnqlpendrpeltegyqgfyhlmdvtgsveea
rasyiirdfekdafearkasmqsiadkmneelgsdrutlnltdqyynmkeviekdmtp
                                                                                                                                                                                                                           NTDSRLIDALVNTVRVNENQEFKEFLPEEETFDELVPSDETKNILAESQDLQMPEFVK
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                                                                                                                                                                                                                                                                                                                                                     /translation="MKKAILMMTFGSPEEIIFEGVADFFTNIRRGVRPQDHEIQTLYD
NYVRIGGTPLQKITRQEVALVEARLGSEYSVYFANKFSSPFIPDVIGQMEADGIEQCI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ERAVDTI IGI VAYKG"
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NATAESNIETASDENKPSNTRDSKPAESTSENETTESSTTTGNQEKPVE"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /trānslation="MSKANQLLEQIHEEGIRQSLAEEVENLKAATNKADADLDEVNSQ
VKDVLTRIASALQQEKENAEQDPQTLVLYQKLYDILMSLHSYLESNNGSDADFDKVDA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /gene="SP1007"
1612. .2241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /translation="MICLAQKTFYFFLAICRRLLVAIYHVLLKQESYNPRLQGLTEIR
NPDKTMFVQDAIRFAQQHGFNML"
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                                                                                                                                                   complement (4791.
                                                                                                                                                                                                 complement (4791.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="identified
TIGR00109"
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/transl_table=11
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                                                                                                  note="identified
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /gene="SP1013"
6827. .7903
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5804. .6313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="similar to GB:X73124 SP:P39602 PID:413958
GB:AL009126; identified by sequence similarity; |
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NPALKAAKVERLAQLSWHGVGYGNFLSAINFIFVGTALFFIIKGIEKAQKLTGIKEE
KTDEKKKPTELEVLQEIKALLEKK"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /product="tRNA-Thr"
6827. .7903
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6413. .6485
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                                                                                                                                                                                                                                                                                                                                              /gene="SP1014"
7959. .8894
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                                                                                                                                                                                                                                                                                                                       'gene="SP1014"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /gene="SP1011"
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                                                                                                                                                                                                                                                                                                'note="identified
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                                                                                                                                               TITLE
JOURNAL
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Sequence
AR219026
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Kunsch, C.A., Choi, G.H., Dillon, P.S., Rose
Fannon, M.R. and Dougherty, B.A.
Streptcocccus pneumoniae polynucleotides
Patent: US 6420135-A 258 16-JUL-2002;
                                                                                                                                                                                                                                                Unknown
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/note="This region contains an authentic frame shift and is not the result of a sequencing artifact; similar to GP:2804700; identified by sequence similarity; putative; IS1167, transposase, authentic frameshift"
a 1815 c 2088 g 3151 t
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70.5%;
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Pred. No. 1.7e-41;
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(C.A., Kunsch, C.A., Choi,G.H., Dillon,P.J., Rosen,C.A., Kunsch,C.A., Choi,G.H., Dillon,P.J., Rosen,C.A., Fannon,M. and Dougherty,B.A.

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OS Unidentified
PN JP 2001501833.A/25
PD 13-FEB-2001
PF 30-OCT-1997 JP 199
PR 31-OCT-1996 US
PI CHARLES A KUNSCH,G
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R 31-OCT-1996 US 66/029960

I CHARLES A KUNSCH,GIL H CHOI,PATRICK J DILLON,CRAIG A ROSEN,
STEVEN C BARASH,
I MICHAEL FANNON,BRIAN A DOUGHERTY
C C12N15/09,A01K67/027,C07K14/315,C07K16/12,C12N1/15,C12N1/19,
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           CTGCTGAGCCAGAAGTCCCTCAAGTAGAGACTGAAAAAGTAGAAGCCCCAACTCAAAGAAG
                                                                                               AGAAACCGCAAAGCGAGAAACCAGAGTCTCCAAAACCAACAGAGGAACCAGAAGAATCAC
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| 21394 ABACAGCTCAAGAATCTATGAGGCAATTGAACCAAAAGCAATTGTTAAACCTGAAGATT 21335 | 347 AGGCTCATAAAGCCTTGTTTGNAAATAAGGGTCGTAATTCTGATTTCCAAGCCTTAGACA |   | 22) AMARI CHI SANANGANGHI AT CAMAMARANGANG ISTI CAMAMARI INTERIOR CHAMACA IL AMAMARI INTERIOR CHAMACA IL AMAMARI INTERIOR CHAMACA IL AMAMARI INTERIOR CAMACA | 82 62 6   | 1107 TAGACTCAAATTCTTCTTTGGTTAGTTCACCGAAAAGTTGGGGAAGGATGTAT 1166   | 104/ CAAGUCHAACCGACTCCGGAACCTAGTCCAGGCCCGCACCTGCACCACACATATAAA 1106         | 987 GHATHATICCCCTTCGTTATCGTCAAACCATTGGGTACCAGATTCAAGGCCAGAACAAC 1046   | GAGATCATTACCACTTCATCCCTTACTCTCAAATGTCTGAATTGGAAGAACGAATCGCTC | 867 TTGTCTTTGATCCAGCACAAATCACAAGTCGAACAGCTAGAGGTGTGTGCAGTGCCACACG 926                                       | 807 GTCTCTTGAAACAGCTCTACAAACTGCCTTTGAGTCAACGACATGTAGAATCTGATGGCC 866   | 747 CTAACACAAGCAACAACAGCAACACTAACAGTCAAGGCAAGTCAAAGTAATGACATTGATA 806   | 722   | 672 ATCGCCGACAAAATAGCGATAACACTTCAAGAACAAACTGGGTACCTTCT 721                               | 631 | 573 ATTACCATTACATTCCTAAGAATGAGTTATCAGCTAGCGAGTTGGCTGCTGCAGAAGC 630 | 513 TTAATGCTTCTGATATCATAGAGGATACTGGTGATGCTTATATCGTTCCTCATGGAGATC 572      | 461GTTGCCTTGGCACGTTCGCAAGGACGCTATACTACAGATGATGGTTATATCT 512                   |

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                                                     Colaser, P., Rusniok, C., Chevalier, Zouine, M., Couve, E., Lalioui, L., Trieu-Cuot, P. and Kunst, F. Genome sequence of Streptococcus invasive neonatal disease
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Glaser, P., Rusniok, C. and Frangeul, L.
Direct Submission
Submitted (31-MAY-2002) Glaser P., Institut Pasteur, Genwicroorganismes Pathogenes, 25, rue du Docteur Roux, 757 Cedex 15, FRANCE. E-mail: pglaser@pasteur.fr Phone: +33 89 96, Fax: +33 (0)1 45 68 87 86
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                    enzyme II"
                                                                                                                                                                                                                                                                                                                                                                                                                                                               complement (1983.
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77529 460 GTAGCAAACGAACAAATGTTCGTACAAAGGAACAAATCCAAAAGCAACGCGAAGAATGGT 77589

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419

359

77709

77649

GTGAAGAATTGATTATGAAAGACCCTAGCTATGTCTTTAATAAAGCTGATGTCATTAATG GTGAAGAATTACTCATGAAAGATCCAAACTATAAGCTAAAAGATGAGGATATTGTTAATG 299 CTTCTCATGGAGACCATTACCATTACTACAATGGGAAAGTGCCATATGATGCCATCATTA CTTCACATGGCGACCACTATCATTATTACAATGGTAAGGTTCCTTATGACGCTATCATCA **AAGAAGAAGGCATATCTGCAGAACAAATCGTTGTTAAAATTACTGACGACGGTTATGTGA** AGCGTGAAGGAATCAATGCTGAGCAAATCGTCATCAAGATAACAGACCAAGGCTATGTCA 179 

239

77829

77889

77769

ATATAGATGGAAAACAAGCGACGCAAAAAACGGAGAATTTGACTCCTGATGAGGTTAGCA 119

Conservative

°.

Mismatches 1045;

Indels

127;

Gaps

11;

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terminator
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9755...
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9770. .10747
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CTCAAATTGAGTATACTGAAGACGAAGTTCGTATTGCTCAATTAGCTGATAAGTATACAA 1577
                                      TATTATTTGGAATTGCACAAGCGACAGACTATAAGAATGGTACATTTGTAATTCCTCATA
                                                                            ATTTATTGGCATTCCTAGCACCAATTACCCATCCAGAGCG---ACTTGGCAAACCAAATT
                                                                                                                                                AATTATTAGAACGCTTGAATGA-----TGAATCGACTAATAAAGAAAAATTGGTAGATG
                                                                                                                                                                                                       CAGCTCAAGAATTTCTTTCAGGAAAATCTGAAGCAAATCAAGACAAAACCAAAAACAGGTA
                                                                                                                                                                                                                                             AGGCTCATAAAGCCTTGTTTGNAAATAAGGGTCGTAATTCTGATTTCCAAGCCTTAGACA
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                                                                                                                                                                                                                                                                                                                       AAGAAAATGTTGCTCCTCGTGACCAAGAATTTTATGATAAAGCATATAATCTGTTAACTG
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                                                                                                                                                                                                                               Koenig,S., Heinrichs,J., Johnson,L.S. and Adamou,J.E. Homologs of a pneumococcal protein and fragments for vaccines Patent: WO 0114421-A 1 01-MAR-2001; MEDIMMUNE, INC. (US)
                                                                                                                                                                                                                                                                                                                                                                               Streptococcus pyogenes
Streptococcus pyogenes
Bacteria; Firmicutes; Lactobacillales;
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Sequence 1 from Patent WO0114421.
AX088372 GI:13397243
                                                                                                                                                                                                                                                                                                                                                            Streptococcus.
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                                                                     /organism="Streptococcus
/mol_type="genomic DNA"
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486 c 518 g 628
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i Streptococcus pyogenes M1
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                                Ferretti,J.J., McShan,W.M., Adjic,D., Savic,D., Savic,G., Primeaux,C., Sezate,S.S., Surcorov,A.N., Kenton,S., Lai,H., Qian,Y., Jia,H.G., Najar,F.Z., Ren,Q., Zhu,H., Song,L., Wh Yuan,X., Clitton,S.W., Roe,B.A. and McLaughlin,R.E. Complete genome sequence of an M1 strain of Streptococcus Proc. Natl. Acad. Sci. U.S.A. 98 (8), 4658-4663 (2001)
                                                                                                                                                                                     Streptococcus pyogenes
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Bacteria; Firmicutes; I
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RerrettL,J.J., McShan, W.M., Adjic,D., Savic,D., Savic,G., Lyon,K.,

Primeaux,C., Sezate,S.S., Surorov,A.N., Kenton,S., Lai,H., Lin,S.,

Qian,Y., Jia,H.G., Najar,F.Z., Ren,Q., Zhu,H., Song,L., White,J.,

Yuan,X., Clifton,S.W., Roe,B.A. and McLaughlin,R.E.
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NPGQGHQPDNGGYHPAPPRNASQNAHHIIPRGDEFKKFKTEKLLDDHKLDLKYRHVESDH
GLIFEPTQVIKSNAPGYVPHGDHYHIIPRGDLSPLEMELADRYLAGGTEDDDSGSDH
SKPSDKEVTHTFLGHRIKAYGKGLDGKPYDTSDAYVFSKESIHSVDKSGVTAKHGDHF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="Best Blastp hit = gb|AAB58414.1| (AF000561) interacting peptide 21; TIP21; Transcription Termin Factor I Interacting Peptide 21 [Homo sapiens]"
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complement (71.
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ADKSNENQQPSEASKEEEKESDDFIDSLPDYGLDRATLEDHINQLAQKANIDPKYLIF
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GAKEOHTDEDVIVDNTTPEVATSATFSTEDRRATTLASKEPKTSQPVYRERIAYTYNDED
GAKEOHTDEDVIVDNTTPEVATSATFSTEDRRATTLASKEPKTSQPVYRERIAYTYNDED
GAKEOHTDEDVIVDNTTPEVATSATFSTEDRRATTLASKEPKTSQPVYRERIAYTYNDED
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                     REGYREYKSDPVICANCPLLSVCTTSKNYQKVVTRHIWKDYLAQPRNTTISAIRERKA
SPKWKIRLD"
                                                                  FINREVEKQAKFMSEQLEIEINRDREKHGKKPLGPAKELEPVAKKISTTDPESGWFHK
GDHKEVFAYSAQVACDKYGWALAYSVEAGNIHDSQAFPALFAKLEPLKPQFIIADSGY
NVPSIAKFLIDKEITPVLPYTRPRGKKDLLRPKELIYDEHFDCVICPEHQALTYRTTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RDLNDPSQVKTLQEKAGKGAGTTVVAVIDAGFDKNHEAWRLTDKTKARYQSKEDLEKAK
KEHGITYGEWVNDKVAYYHDYSKDGKTAVDQEHGTHVSGILSGNAPSETKEPYRLEGA
MPEAQLLLMRVEIVNGLADYARNYAQAIIDAVNLGAKVINMSFGNAALAYANLPDETK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /product="C5A peptidase precursor"
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/db_xref="G1:13623022"
/translation="MRKQKLPFDKLAIALMSTSILLNAQSDIKANTVTEDTPATEQA
/translation="MSKCYKLPFDKLAIALMSTSILLNAQSDIKANTVTEDTPATSKATI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /trānslation="mrraennkhsrysirklsvgvtsiaiaslflgkvayavdgipfi
$LTQKTTATTSSNWHH.DKDGLIPLGISJEAAKEEFKKEVEESKLSEAQKETYKQKIK
TAPDKDKLLFTYHSEYMTAVKULPASTESTTQDVEAFVQETQASASDSHVTGDSTSVT
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                                                                                                                           /db xref="GI:13623023"
/translation="MLHKEKPDYNRNQYGFYTLDQLVPDEHFLRQVEAVIDFDFIYDL
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VPHFTTYGKNYSRRFQEKGLIESIFTHIVGLCINTLDFTEIFIDGTHIKAAANNRKV
VPHFTTYGKNYSRRFQEKGLIESIFTHIVGLCINTLDFTEIFIDGTHIKAAANNRKV
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HSNKPEQDGSDQAPDKKPETKPEQDGSGQAPDKKPETKPEQDGSGQTPDKKPETKPEQ
DGSGQTPDKKPETKPEKDSSGQTPGKTPQKGQPSRTLEKRSSKRALATKASTKDQLPT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="synonym: SPy2010" complement(5322. .8867)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VRAHESGKYLPSTGEKAQPLFIATMTLMSLFGSLLVTKRQKETKK"
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TPPAVTKDSDKPSSAAEKPAASSLVSEQTVQQPTSKRSSDKKEEQEQSYSPNRSLSRQ
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/gene="SPy2009"
                                                                                                                                                                                                                                                                                                                      putative transposase
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LSPLEAAPSGNKTYLENLRANLEVLYQQLK"
                                                                                                                                                                                                                         /transl_table=11
/product="transposase - IS1562"
/protein_id="AAK34692.1"
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note="Best Blastp hit =
                                                                                                                                                                                                                                                                                                                                                                                                           'gene="SPy2013"
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protein_id="AAK34690.1"
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transl_table=
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|Streptococcus agalactiae]"
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Streptococcus pyogenes]"
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streptococci
Unpublished
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Streptococcus pyogenes htpA gene for histidine
                                                                                                                                                                           Streptococcus pyogenes
Streptococcus pyogenes
Bacteria; Firmicutes; Lactobacillales;
                                                                                                                                                                                                                                                                                                           group A streptococci,
AB073859
                                                                          Terao,Y., Kawabata,S. and Hamada,S. Characterization of a novel histidine triad
                                                                                                                                                     Streptococcus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CAAGCGTGAAGGAATCAATGCTGAGCAAATCGTCATCAAGATAACAGACCAAGGCTATGT 177
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Pred. No. 2.3e-35;
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                                                                                                                                                                              Streptococcaçeae;
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    TAGTCAACATCGTGAAG---
                                        AGGTAGCAAGCGCAAAAACATTCGAACCAAACAACTTGCTGAGCAAGTAGCCAAAGG
                                                                            TGAGGTCAAGGGTGGATATGTTATCAAGGTAGATGGAAAATACTATGTTTTACCTTAAGGA
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VGYMMPKDGKDYFYARDQLDLTQIAFAAQELMLKOKKHYRYDIVDTGIEBRLAVDVSS
LPMHAGNATVDTGSSEVIPHIDHIHVVPYSWLTRDQIATIKYVMQHPEVRPDIVKKPR
HEESGSVIPNVTPLDKRAGMPNWQIIHSAEEVQKALAEGRFATPDGYIFDPRDVLAKE
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/mol type="genomic DNA"
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/protein_id="BAB71774.1"
/db_xref="GI:16610230"
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/transl_table=
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/strain="SSI-9"
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Smoot,J.C., Barbian,K.D., Van Gompel,J.J., Smoot,L.M.,
Smoot,J.C., Barbian,K.D., Sturdevant,D.E., Ricklefs,S.M.,
Chaussee,M.S., Sylva,G.L., Sturdevant,D.E., Ricklefs,S.M.,
Porcella,S.F., Parkins,L.D., Beres,S.B., Campbell,D.S., Smith,T.M.,
Zhang,Q., Kapur,V., Daly,J.A., Veasy,L.George. and Musser,J.M.
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Smoot, J.C., Barbian, K.D., Van Gompel, J.J., Smoot, L.M.,
Chaussee, M.S., Sylva, G.L., Sturdevant, D.E., Ricklefs, S.M.,
Porcella, S.F., Parkins, L.D., Beres, S.B., Campbell, D.S., Smith, T.M.,
Zhang, O., Kapur, V., Daly, J.A., Veasy, L.G. and Musser, J.M.
Genome sequence and comparative microarray analysis of serotype M18
group A Streptococcus strains associated with acute rheumatic fever
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Streptococcus pyogenes MGAS8232
Bacteria; Firmicutes; Lactobacillales;
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Streptococcus pyogenes
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complement(95. .259)
/gene="spyM18.2063"
complement(95. .259)
/gene="spyM18.2063"
/note="best blastp match
                                                      /product="hypothetical protein"
/protein id="AAL98534.1"
/db_xref="GI:19749145"
/translation="MNIEVKEKISFVFFINSLESGAIILLCFNITLSKEIIINNFLDI
LADYRMKIET"
                                                                                                                                                                                                                                                                                                                                                                                  location/Qualifiers
                  gene="SMEZ"
                                                                                                                                                                                                                                                                                                          mol_type="genomic
strain="MGAS8232"
note="synonym: spyM18_2064"
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SYQLGWFPIGISSPIGTLSQDITLADRIKHLMLPVFTLSILGIANVTLHTRTKMMSVL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               pyogenes] "
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="best blastp match gb|AAC67218.1| (U78968)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3388.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DKRINVGKQGVHSHGHDWSLLTNIAEWTWDESTK"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            KWTWVLLDENTALAALESGDVDMIYATPELASKKVKGTRLLDIPSNDVRGLSLPYVKK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DLHDDFKFSNGEPVTADDVKFTYDMLKADGKAWDLTFIKNVEVVGKNQVNIHLTBAHS
TFTAQLTBIPIVRKKHYNDKYKSNPIGSGPYMVKBYKAGEQAIFVRNPYWHGKKPYFK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        complement (1334...1468)
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complement (1334...1468)
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SEGKVI AYTYGGMTPYQKTSI PKNI PVNLWI NGKQI SVPYNE I STNKTTVTAQEI DLK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FYNNPTVTKYLDKAMTSSDLDKANEYWKLAQWDGKTGASTLGDLPNVWLVSLNHTYIG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    hypothetical protein [Streptococcus pyogenes M1 GAS]"
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transl_table=11
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transl_table=11
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                            spyM18_2068"
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Z [Streptococcus pyogenes M1 GA
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protein [Streptococcus pyogenes MI GAS]"
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transmembrane transport protein [Streptococcus pyogenes
                                                                                                                                                                                                                                                      complement (7059.
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I gasgsgeksllaha i molipknaavtgdmi yrgqsltskri kqlrgkemtli pqsvo
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Sdtvsli i adeptpglhpdalqmvldqlrsfadkgi svifi thdi vaasqi adriti
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transl_table=
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SEELLMTDPNYRFKQSDVINEILDGYVIKVNGNYYVYLKPGSKRKNIRTKQQIAEQVA

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REFERENCE
AUTHORS
TITLE
                                                                             SOURCE
ORGANISM
                                                                                                                                         ACCESSION
VERSION
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                                                        SAG290952

Vereptococcus agalactiae lmb gene for Streptococcus agalactiae lmb gene for protein, partial ORFy and partial in AJ290952

AJ290952

AJ290952.1 GI:13548638

adhesin; insertion sequence IS1548; protein; lmb gene; orfy.

Streptococcus agalactiae

Westreptococcus agalactiae

Bacteria; Firmicutes; Lactobacillale
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 Granlund, M., Michel, F. and Norgren, M. Mutually exclusive distribution of IS1548 and
                                                Streptococcus.
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HGNHYHY1PKKDLSPSELAAAQAYWSQKQGRGARPSDYRPTPAPGRRKAP1PDVTPNP
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Pred. No. 5.1e-35;
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                                                                                                                                                                 DNA linear BCT 07-JUI for laminin-binding surface insertion sequence IS1548.
                                                             Streptococcaceae,
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J. Bacteriol. 183 (8), 2560-2569 (2001)
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Direct Submission
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AGATGGAAAACAAGCGACGCAAAAA-----ACGGAGAATTTGACTCCTGATGAGGTTAG 117
                                    TTACCAGCTTGGTAAGCATCATATGGGTCTAGCAACAAAGGACAATCAGATTGCCTATAT
                                                                       TTACGAGTTGGGACTGTATCAAGCTAGAACGGTTAAGGAAAATAATCGTGTTTCCTATAT
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                                                                                                                                                                                                                                     /codon_start=1
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KGTKEAKEKGLAQVAHLSKEEVJAFVNEAKRQGRFTTDIGYIFSTDIIDLGDAYLVP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /translation="MKKGFFLMAMVVSLVMIAGCDKSANPKQPTQGMSVVTSFYPMYA
MTKEVSGDLNDVRMIQSGAGIHSFEPSVNDVAAIYDADLFVYHSHTLEAWARDLDNLI
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KQLGISGISPEQEPSPRQLKEIQDFVKEYNVKTIFAEDNVNPKIAHAIAKSTGAKVKT
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366 c 4
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/mol_type="genomic DNA"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /protein_id="CAC35984.1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /codon_start=1
/transI_table=11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "SPLEAAPSGNKTYLENLRANLEVLYQQLK"
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insertion_seq="IS1548"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     note="ORFy"
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note="serotype III"
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Pred. No. 1.2e-34;
0; Mismatches 231
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|      | leted: November 13, 2003, 23:47:14<br>8825 secs                 | Search completed:<br>Job time : 8825 s | or<br>es |
|------|---|--|----------|
|      | c 1769  | 1769                                   | g        |
|      | C 634   | 634                                    | Ş        |
| 1768 | CTATCATTATATTCCTAAAAAGGATTTGTCTCCAAGTGAGCTAGCT                  | 1709                                   | Д        |
| 633  | TTACCATTACATTCCTAAGAATGAGTTATCAGCTAGCGAGTTGGCTGCTGCAGAAGCCTT    | 574                                    | Ş        |
| 1708 | TAGTCCGACAGATATCATTGATGTTTAGGAGATGCTTATTTAGTACCTCATGGTAATCA     | 1649                                   | 망        |
| 573  | TAATGCTTCTGATATCATAGAGGATACTGGTGATGCTTATATCGTTCCTCATGGAGATCA    | 514                                    | Ş        |
| 1648 | TGCGGCAGTCAATGAAGCAAAAAGACAAGGACGCTATACTACAGACGATGGCTATATTTT    | 1589                                   | 망        |
| 513  | TGGTGCTGTTGCCTTGGCACGTTCGCAAGGACGCTATACTACAGATGATGATGGTTATATCTT | 454                                    | ρ        |
| 1588 | AACTAAAGAAGCTAAAGAAAAAGGTTTAGCTCAAGTGGCCCATCTCAGTAAAGAAGAAGT    | 1529                                   | Вb       |
| 453  | TAGTCAACATCGTGAAGGTGGAACTCCAAGAAACGA                            | 418                                    | δ        |
| 1528 | AGGTAGTAAGCGCAAAAATTCGAACCAACAAATTGCTGAGCAAGTAGCCAAAGG          | 1469                                   | 밁        |
| 417  | TGCTGCCCACGCGGATAACGTCCGTACAAAAGGGGAAATCAATC                    | 358                                    | δ        |
| 1468 | TGAAATCTTAGACGGTTATGATTAAAGTCAATGGCAACTATTATGTTTACCTCAAGCC      | 1409                                   | 멍        |
| 357  | TGAGGTCAAGGGTGGATATGTTATCAAGGTAGATGGAAAATACTATGTTTACCTTAAGGA    | 298                                    | و        |
| 1408 | TAGTGAAGAGTTGTTGATGACGGATCCTAATTACCGTTTTAAACAATCAGACGTTATCAA    | 1349                                   | Dp.      |
| 297  | CAGTGAAGAATTACTCATGAAAGATCCAAACTATAAGCTAAAAGATGAGGATATTGTTAA    | 238                                    | ð        |
| 1348 | GACCTCACACGGTGACCATTATCATTTTTACAATGGGAAAGTTCCTTATGATGCGATTAT    | 1289                                   | Дb       |
| 237  | CACTTCACATGGCGACCACTATCATTATTACAATGGTAAGGTTCCTTATGACGCTATCAT    | 178                                    | Ş        |
| 1288 | TGCTGAAGAAGGCATCTCTGCTGAACAGATCGTAGTCAAAATTACTGACCAAGGCTATGT    | 1229                                   | 멼        |
| 177  | CAAGCGTGAAGGAATCAATGCTGAGCAAATCGTCATCAAGATAACAGACCAAGGCTATGT    | 118                                    | Ş        |
| 1228 |   | 1169                                   | 망        |

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                                                                                                                               protective or therapeutic
                                                                                                    Claim 1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            amplification methods), also for isolating Streptococcus genes or their allelic variants. The protein can be used similarly to detect specific antibodies in standard immunoassays, especially for diagnosing or monitoring infections. Antibodies which bind the protein are used to detect corresponding antigens, to purify the protein and for passive immunisation (optionally coupled to a toxin). Vaccines are administered, e.g. by injection, orally or through the skin, typically at 0.01-1000 (especially 10-300) mu g/ml per dose.
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P-PSDB; ABU01598.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gene; ds; bacterial meningitis; pneumonia; sepsis; otitis media; ear infection; antiinflammatory; antibacterial; immunostimulant;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      S. pneumoniae type 4 strain coding region #1174
The invention relates to a protein comprising or having at least identity to any of the 2469 amino acid sequences, identified in t specification (available on a computer readable format), or its f
                                                                                                                                                                                                                                                                                                                                                                                   WO200277021-A2
                                                                                                                                                                                                                                                                                                                                                                                                               Streptococcus pneumoniae type 4 strain
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                                                                                                     New proteins and nucleic acid molecules from Streptococcus pneumoniae, useful as medicaments for treating or preventing a disease or infection due to streptococcus bacteria, such as pneumonia, sepsis, otitis media
                                                                                                                                                                                                              Masignani V,
                                                          Claim 6; SEQ ID No 2347; 56pp; English
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CC of the printed second data for this patent did not form part
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Best Local S
Matches 2388
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CC The present invention describes a computer readable medium which has CC the nucleotide sequences SEQ ID NO:1 to 391 (AAV52134 to AAV52524) CC recorded on it, or a representative fragment or a sequence at least 95% CC identical to SEQ ID NO: 1 to 391. The nucleotide sequences depicted in CC SEQ ID NO: 1 to 391 (AAV52134 to AAV52524) are genomic fragments from CC Streptococcus pneumoniae. The present invention also describes an CC isolated nucleic acid molecule encoding a homologue of any of the CC fragments of the S.pneumoniae genome (SEQ ID NO:1 to 391) where the CC nucleic acid molecule is produced by a process comprising: (a) screening CC a genomic DNA library using as a probe a target sequence defined by any CC of the sequences in SEQ ID NO:1 to 391, identifying members of the CI library which contain sequences that hybridise to the target sequence is not isolating the nucleic acid molecules from the members; or (b) isolating CC mRNA, DNA or cDNA produced from an organism, amplifying nucleic acid molecules whose nucleotide sequence is homologous to amplification
                                   primers derived from the fragment of the S. pneumoniae genome to prime the amplification and isolating the amplified sequences. The computer readable medium can be used in a computer-based system for identifying fragments of the S. pneumoniae genome of commercial importance, or expression modulating fragments of the S. pneumoniae genome. Products from the present invention can be used in diagnosis kits and assays, and pharmaceutical compositions and vaccines for S. pneumoniae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Computer-readable medium with recorded Streptococcus pneumoniae polynucleotide sequences - useful in diagnostic kits and assays pharmaceutical compositions and vaccines for Streptococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 1; Page
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    pneumoniae
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Rosen CA;
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Sequence 8195 BP; 2688 A; 1622 C; 1777 G; 2105 H 3 other;

DB 19;

Length

8195;

Query Match Best Local Similarity

S 밁 δ 밁 á 밁 Ş 밁 á 밁 Ş 밁 Ş Matches 3173 3353 3293 3233 3113 3053 181 2388; 301 121 361 241 61 GCGTGAAGGAATCAATGCTGAGCAAATCGTCATCAAGATAACAGACCAAGGCTATGTCAC GGTCAAGGGTGGATATGTTATCAAGGTAGATGGAAAATACTATGTTTACCTTAAGGATGC 360 TGAAGAATTACTCATGAAAGATCCAAACTATAAGCTAAAAGATGAGGATATTGTTAATGA 300 TTCACATGGCGACCACTATCATTACTACAATGGTAAGGTTCCTTATGACGCTATCATCAG 240 GCGTGAAGGAATCAATGCTGAGCAAATCGTCATCAAGATAACAGACCAAGGCTATGTCAC TATAGATGGAAAACAAGCGACGCAAAAAACGGAGAATTTGACTCCTGATGAGGTTAGCAA TATAGATGGAAAACAAGCGACGCAAAAAAACGGAGAATTTGACTCCTGATGAGGTTAGCAA 120 TTCTTACGAGTTGGGACTGTATCAAGCTAGAACGGTTAAGGAAAATAATCGTGTTTCCTA TTCTTACGAGTTGGGACTGTATCAAGCTAGAACGGTTAAGGAAAATAATCGTGTTTCCTA TTCACATGGCGACCACTATCATTATTACAATGGTAAGGTTCCTTATGACGCTATCATCAG TGAAGAATTACTCATGAAAGATCCAAACTATAAGCTAAAAGATGAGGATATTGTTAATGA 3352 100.0%; Score 2388; ilarity 100.0%; Pred. No. 0; Conservative 0; Mismatches <u>بر</u> Indels 0, Gaps 3232 180 3172 3112 3292 60 0

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| TGATAAAGCATATTAATCTCTTAACTGAGGCTCATRAAGCCTTGTTTGNAAATAAGGGTCG 1380  RESULT 6  ABS56454/c TGATAAAGCATATAATCTGTTAACTGAGGCTCATAAAGCCTTGTTTGAAAATAAGGGTCG 4432  TAATTCTGATTACCAAGCCTTAGACAAATTATTAGAACGCTTGAATGATGAATCGACTAA 1440  XX TAATTCTGATTTCCAAGCCTTAGACAAATTATTAGAACGCTTGAATGATGAATCGACTAA 4492  TAATTCTGATTTCCAAGCCTTAGACAAATTATTAGAACGCTTGAATGATGAATCGACTAA 4492  TAATTCTGATTTCCAAGCCTTAGACAAATTATTAGAACGCTTGAATGATGAATCGACTAA 4492  TAAATATCTGATTTCCAAGCCTTAGACAAATTATTAGAACGCTTGAATGATCGACTAA 4492  TAAAGAAAAATTGGTAGATGATTATTGGCAATTACCCCAATTCCCCAGGCCG 1500  XX TAAAGAAAAATTGGTAGATGGATTATTGGCAATTACCCCAATTCCCCAGGCCG 1500  XX TAAAGAAAAATTGGTAGATGATTATTGGCAATTCCTAGCACCCAATTACCCCATCCAGAGCG 1500  XX TAAAGAAAAAATTGGTAGATGATTATTGGCAATTCCTAGCACCCAATTACCCCATCCAGAGCG 1500  XX  TAAAGAAAAAATTGGTAGATGATTATTGGCAATTCCTAGCACCCAATTACCCCATCCAGAGCG 1500  XX  TAAAGAAAAAATTGGTAGATTATTGGCAATTCCTAGCACCCAATTACCCCATCCAGAGCG 1500  XX  TAAAGAAAAAATTGGTAGATTATTGGCAATTCCTAGCACCCAATTACCCCATCCAGAGCG 1500  XX  TAAAGAAAAAATTGGTAGATTATTATTGGCAATTACCCCAATTACCCCATCCAGAGCG 1500  XX  TAAAGAAAAAATTGGTAGAATTATTATTGGCAATTACCCCAATTACCCCATCCAGAGCG 1500  XX  TAAAGAAAAAATTGGTAGAATTATTATTGGCAATTACCCCAATTACCCCATCCAGAGCG 1500  XX | TATTCGAAGAAAAGGCATCTCTCGTTATGTCTTTGC 1200   |   | 952 QY 952 QY 00 Db 952 QY 60 Db  | 660 |  |
|--|---|---|---|-----|--|
| 6<br>4/C<br>\$56454 standard; DNA; 2162598 BP.<br>\$56454;<br>-FEB-2003 (first entry)<br>reptococcus pneumoniae type 4 strain complete genome.   | 2221 AGIANCGGATTCTAGTCTAGAGCCAATGCAACGGAACTCTAGCTGGTTTACGAAATTAA 5273 AGTAACGGATTCTAGTCTGAAAGCCAATGCAACGCAACTCTAGCTGGTTTACGAAATTAA 5273 AGTAACGGATTCTAGTCTGAAAGCCAATGCAACAGAAACTCTAGCTGGTTTACGAAATAA 52281 TTTGACTCTTCAAATTATGGATAACAATAGTATCATGGCAGAAGCAGAAAAATTACTTGC [ | TAAGATTAAGATTAAGATTAAGATTAAGATTAAGATTAAGATTAAGATTAAGATTAAGATTAAAAGATTAAAAGATTAAAAGATTAAAAGATTAAAAGATTAAAAGATTAAAAGATTAAAAGATTAAAAGATTAAAAGATTAAAAGATTAAAAGATTAAAAGATTAAAAGATTAAAAGATTAAAAGATTAAAAAA | 4913 TACAGTTGAGATTAAAAACGGTAATTTGATTACTCTCATAAGGATCACTGAGAGATTACCATAATATTTGATTACCATAAACGATTAAAAACGGTAAAACGGTAAATTTGATTACCATAAAGATTTGCTTGGTTTGATGATGACAACAAAAGCTCCAAAAGGCTATACCATAAGAGAT1921 TAAATTTGCTTGGTTTGATGATGATCACACAATACAAAAGCTCCAAATGGCTATACCTTGGAAGAACATTTTGGTTTGCGACGATTAAGTACCACACATACAAAAGCCTCGAAACGTCCAACATTCTAATGAACAACTTTGTTTTGCGACGACGATTAAGTACCTACGTAGAACACCCTGACGAACGTCCACATTCTAATGAACATTTGTTTG |     | 4493 TAAAGAAAAATTGGTAGATGATTTATTGGCATTCCTAGCACCAATTACCCAGAGCG 4493 TAAAGAAAAATTGGTAGATGATTATTGGCATTACCTAGCACCCAATTACCCAGAGCG 1501 ACTTGGCAAACCCAAATTCTCCAAATTGAGTATACTGAAGACGAAGTTCGTATTGCTCAATT |

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                                                                                                                                                                                                                                                                target sequence not defined in the specification, for amplifying a target sequence contained within a Streptococcus nucleic acid sequence, where the first primer is substantially complementary to the target sequence and the second primer is substantially complementary to the complement of the target sequence, and where the parts of the primers complement of the target sequence, and where the parts of the primers having substantial complementarity define the termini of the target sequence to be amplified, assay comprising contacting a test compound with the protein, and determining whether the test compound binds to the protein and a Streptococcus pneumoniae bacterium, where one or more genes encoding the proteins has been rendered inactive. The proteins, nucleic acid molecules, antibody and compositions are useful as medicaments for treating or preventing a disease or infection due to streptococcus bacteria, particularly S. pneumoniae, such as pneumonia, sepsis, otitis media or ear infection. They are also useful in developing vaccines, diagnostics and antibotics. The methods are useful for identifying immunodominant proteins. The methods are useful for Streptococcus pneumoniae type 4 strain genome sequence is the printed specification but was obtained in alcotronic.
                                                                                                                                                                                                 Query Match
Best Local :
                                                                                                                                                                                 Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention relates to a protein comprising or having at least 50% identity to any of the 2469 amino acid sequences, identified in the specification (available on a computer readable format), or its fragment, expressed from 2469 of 2489 identified DNA coding regions from the Streptococcus pneumoniae type 4 strain genomic sequence appearing as Streptococcus pneumoniae type 4 strain genomic sequence appearing as Sh856454. Also included are an antibody with binds one of the proteins, treating a patient by administering the protein, DNA or antibody (in a composition), a kit comprising first and second primers, which are the nucleic acid cited above or fragments between nucleotides and second primers.
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                                                                                                                                                                                                                                                            Sequence
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                                                                                                                                                                                                                                                                                                                        of the printed specification, but was obtained in electronic format directly from WIPO at
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                    1006890
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                                                                                                                                                                                                                                                                                                 wipo.int/pub/published_pct_sequences
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                                                        TATAGATGGAAAACAAGCGACGCAAAAAACGGAGAATTTGACTCCTGATGAGGTTAGCAA 120
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                                                                GTCTGAATTGGAAGAACGAATCGCTCGTATTATTCCCCCTTCGTTATCGTTCAAACCATTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Streptococcus pneumoniae; BVH-3; BVH-11; BVH-28; antigen; vaccine; prophylaxis; therapy; infection; diagnosis; meningitis; bacteraemia; otitis media; pneumonia; immunisation; bactericidal; ds.
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| 1249 AAAACAAGAGAGAGTTTTCACACACTTTTAACTGCTAAAAAAGAAAATGTTTGCTCCTCGTGA 1308 | 1189 THATGTCTTTGCGAAAGATTTACCATCTGAAACTGTTAAAAATCTTGAAAGCAAGTTATC 1248<br> | 1129 TAGTCAGCTGGTACGAAAAGTTGGGGAAGGATATGTATTCGAAGAAAAGGGCATCTCTCG 1188 | 1081 CCCGCAACCTGCACCAAATCTTAAAATAGACTCAAATTCTTCTTTGGT 1128 | 1021 GGTACCAGATTCAAGGCCAGAACCAAGTCCACAACTGCGCACTCCGGAACCTAGTCCAGG 1080 | 961 GTCTGAATTGGAAGAACGAATCGCTCGTATTATTCCCCTTCGTTATCGTTCAAACCATTG 1020 | 901 AGCTAGAGGTGTTGCAGTGCCACACGGAGATCATTACCACTTCATCCCTTACTCTCAAAT 960 | 841 TCAACGACATGTAGAATCTGATGGCCTTGTCTTTGATCCAGCACAAATCACAAGTCGAAC 900 | 781 AGCAAGTCAAAGTAATGACATTGATAGTCTCTTGAAACAGCTCTACAAACTGCCTTTGAG 840 | 721 TGTAAGCAATCCAGGAACTACAAATACTAACACAAGCAACAACAGCAACACACTAACAGTCA 780 | 661 TTCAAGAACCTATCGCCGACAAAATAGCGATAACACTTCAAGAACAAACTGGGTACCTTC 720 | 601 ATCAGCTAGCGAGTTGGCTGCAGAAGCCTTCCTATCTGGTCGAGGAAATCTGTCAAA 660 | 541 TGGTGATGCTTATATCGTTCCTCATGGAGATCATTACCATTACATTCCTAAGAATGAGTT 600 | 481 AGGACGCTATACTACAGATGATGGTTATATCTTTAATGCTTCTGATATCATAGAGGATAC 540 | 421 TCAACATCGTGAAGGTGGAACTCCAAGAAACGATGGTGCTGTTGCCTTTGGCACGTTCGCA 480 | 361 TGCCCACGCGGATAACGTCCGTACAAAAGAGGAAATCAATC | 301 GGTCAAGGGTGGATATGTTATCAAGGTAGATGGAAAATACTATGTTTACCTTAAGGATGC 360<br> | 240 CTCTCATGGAGACCATTATCATTACTATAATGGCAAGGTCCCTTATGATGCCATCATCAG 299  241 TGAAGAATTACTCATGAAAGATCCAAACTATAAGCTAAAAGATGAGGATATTGTTAATGA 300 |
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| 239 GAAGCCAATGCAACAGAACTCTAGCTGGTTACGAAATAATTTGACTCTCAAATGATTAT<br>       | 2179<br>2340   | 2280   | 2126   | 216  | 2029 A<br>2100 G  | 2040   | 1980   | 1920   | 1860   | 1800   | 1740  | 1680   | 1549 T   | 1560  | 1500 1  | 1440 7   | 1309 (   |

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| 41 TGAAGAATTACTC   | 181 TTCACATGGCGACCACTATCATTACTACAATGGTAAGGTTCCTTATGACGCTATCATCAG 240   | 121 GCGTGAAGGAATCAATGCTGAGCAAATCGTCATCAAGATAACAGACCAAGGCTATGTCAC 180<br> | 61 TATAGATGGAAAACAAGCGACGCAAAAAACGGAGAATTTGACTCCTGATGAGGTTAGCAA 120 | 1 TTCTTACGAGTIGGGACTGTATCAAGCTAGAACGGTTAAGGAAAATAATCGTGTTTCCTA 60  | 57.5%; Score 1374.2;<br>Similarity 73.9%; Pred. No. 0;<br>9; Conservative 0; Mismatches | present sequence encodes the gen.  56 G; 619 T; 0 other;              | recombinant production of the prote gens may then be used as vaccines for treptococcal infections in mammals ult in, e.g. meningitis, otitis medi | The present invention describes nucleic acids (I) encoding protein antigens (II) from Streptococcus pneumoniae. The protein antigens have bactericidal activity. The nucleic acids, encoding the protein | Streptococcal antigens useful for vaccinating against e.g. meningitis, otitis media, bacteremia and/or pneumonia - Example 6; Fig 15; 106pp; English. | Hamel J, Brodeur BR, Pineau I, Martin D, Rioux C, Charland N; WPI; 2000-452397/39. | 23-DEC-1998; 98US-0113800. (BIOC-) BIOCHEM PHARMA INC.               | 06-UUL-2000.<br>20-DEC-1999; 99WO-CA01218.                           | Streptococcus pneumoniae. WO200039299-A2.                                | Streptococcus pneumoniae; BVH-3; BVH-11; BVH-28; antigen; vaccine; prophylaxis; therapy; infection; diagnosis; meningitis; bacteraemia; otitis media; pneumonia; immunisation; bactericidal; ds. | Streptococcus pneumoniae BVH-11 gene SEQ ID NO:12.                  | 21-NOV-2000 (first entry)   | AAA65736 standard; DNA; 2647 BP. AAA65736;    | IIT 8  | 2299 GGATAACAATAGTATCATGGCAGAAGCAGAAAAATTACTTGCGTTGTTAAAAGGAAGTAA 2358<br>      -  - |
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| Ş  | B 8  | ₽ \$   | . B &   | \$ B &   | da dy   | Db Qy   | g &   | Db Qy  | dg<br>VQ  | Dy<br>Qy   | gg Qy  | DP QV  | dd<br>VQ   | g<br>V   | Db  | Ş   | g &   | B &  | Db   |
| 1309 CCAAGAATTTTATGATAAAGCATATAATCTGTTAACTGAGGCTCATAAAGCCTTGTTTGN 1368 | 1249 AAAACAAGAGAGTGTTTCACACACTTTAACTGCTAAAAAAGAAAATGTTGCTCCTCGTGA 1308 | 1304 TTATATCCCAGCCAAGAATCTTTCAGCAGAAACAGCAGCAGGCATTGATAGCAAACTGGC 1363   | CAAAGAAGCTGTTCGAAAAAGTAAGGCGATGGTTATGTCTTTGAGGAGAATGGAGTTTCTCCG     | 108 CCCCAACCISCACCAAAICIIAAAAIAACICAA 1184 TCCGCAACCIGCACCAATCCTCAACCAGCCAATGCAATCCAATTGATGAGAAATTGGT 1243 1184 TCCGCAACCTGCAACATCCTCAACCAGCCAATGCAATACAAAAACCAATTGGT 1243 | GSTACCAGATTCAAGGCCAGAACAACCCAAGTCCACAACCGACTCCGGAACCTAGTCCAGG                           | 961 GTCTGAATTGGAAGAACGAATCGCTCGTATTATTCCCCTTCGTTATCGTTCAAACCATTG 1020 | 901 AGCTAGAGGTGTIGCAGTGCCACACGGAGATCATTACCACTTCATCCCTTACTCCAAAT 960<br>   | 841 TCAACGACATGTAGAATCTGATGGCCTTGTTCTTTGATCCAGCACAAATCACAAGTCGAAC 900  | 781 AGCAAGTCAAAGTAATGACATTGATAGTCTCTTGAAACAGCTCTACAAACTGCCTTTGAG 840  | 721 TGTAAGCAATCCAGGAACTACAAATACTAACACÁAGCAACAACAGCAACACTAACAGTCA 780<br>           | 661 TTCAAGAACCTATCGCCGACAAAATAGCGATAACACTTCAAGAACAAACTGGGTACCTTC 720 | 601 ATCAGCTAGCGAGTTGGCTGCTGCAGAAGCCTTCCTATCTGGTCGAGGAAATCTGTCAAA 660 | 541 TGGTGATGCTTATATCGTTCCTCATGGAGATCATTACCATTACATTCCTAAGAATGAGTT 600<br> | 481 AGGACGCTATACTACAGATGATGGTTATATCTTTAATGCTTCTGATATCATAGAGGATAC 540   | 524 TCAGCATCGTGAAGGAGGACTTCAGCAAACGATGGTGCGGTAGCCTTTGCACGTTCACA 583 | 421 TCAACATCGTGAAGGTGGAACTCCAAGAAACGATGGTGCTGTTGGCTTTGGCACGTTCGCA 480 | 361 TGCCCACGCGGATAACGTCCGTACAAAAGAGGAAATCAATC | 301 GJICAAGGGTGGAKATGTKATCAAGGTRGATGGAAAATACTATGTTKACCTKAAGGATGC 360 |  |

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                                                                     CAAGTCCAATGCCAAAGAGACTCTCACAGGATTAAAAAAATAATTTACTATTTGGCACCCA
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                                                                                                                                                                         GGTTGAAGAAAACTGAGAGAGGCTGAAGATTTACTTGGAAAAATCCAGGATCCAATTAT
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2563

Query Match Best Local Similarity Matches 1819; Conserv

Conservative

0;

Mismatches

539; DB 24;

102;

Gaps

2

57.5%; 73.9%;

Score 1374.2; Pred. No. 0;

Length

Sequence 2647

BP;

934 A; 538 C; 556 G; 619

T; 0 other

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RESULT 9
ABK15103
ID ABK1
XX ABK1
XX ABK1
XX ABK1
XX DNA
XX DNA
XX DNA
XX DNA
XX PPT CDS
FT C
                                                 The invention describes an isolated polypeptide (I) with 70-90% CC identity to Streptococcus pneumonia protein BVH-3, BVH-11, variants of CC BVH-3 or BVH-11, or chimeric sequences derived from them. A vaccine (II) CC comprising (I) is useful for therapeutic or prophylactic treatment of CC individual susceptible to these disorders. (II) is also useful for therapeutic or prophylactic or prophylactic treatment of any streptococcal bacterial CC infection (e.g., caused by Streptococcus pneumonia infection in an CC infection (e.g., caused by Streptococcus pneumoniae, group A CC Streptococcus such as Streptococcus pneumoniae, group A Streptococcus sureus) in an individual susceptible to the infection. CC as Streptococcus aureus) in an individual susceptible to the infection. CC techniques. The Streptococcus polypeptides are useful in a diagnostic CC test for S. pneumoniae infection. (III) is useful for designing DNA CC probes for use in detecting the presence of Streptococcus in a biological sample suspected of containing the bacteria. The DNA probes may also be cused for detecting circulating S. pneumonia nucleic acid in a sample for CC diagnosing streptococcal infections. This sequence encodes the Streptococcus pneumoniae protein BVH-11, used to create the antigenic CC peptides described in the method of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New Streptococcus pneumoniae BVH-3 and BVH-11 variant and epitope-bearing polypeptides, useful as vaccine components or preventing streptococcal infections such as otitis media
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| ACCAG       | 1021 GGTACCAGAGTTCAAGGCCAGAACCAACTACAGTCCACAACTCCGGAACCTAGTCCAGG 1080 | 961 GTCTGAATTGGAAGAACGAATCGCTCGTATTATTCCCCTTCGTTATCGTTCAAACCATTG 1020 | 901 AGCTAGAGGTGTTGCAGTGCCACACGGAGATCATTACCACTTCATCCCTTACTCTCAAAT 960  | 841 TCAACGACATGTAGAATCTGATGGCCTTGTCTTTGATCCAGCACAAATCACAAGTCGAAC 900 | 781 AGCAAGTCAAAGTAATGACATTGATAGTCTCTTGAAACAGCTCTACAAACTGCCTTTGAG 840               | 721 TGTAAGCAATCCAGGAACTACAAATACTAACACAAGCAACAACAACAACAACAACAACAACAACAGTCA 780  | 661 TTCAAGAACCTATCGCCGACAAAATAGCGATAACACTTCAAGAACAAACTGGGTACCTTC 720   | 601 ATCAGCTAGCGAGTTGGCTGCAGAAGCCTTCCTATCTGGTCGAGGAAATCTGTCAAA 660   | 541 TGGTGATGCTTATATCGTTCCTCATGGAGATCATTACCATTACCATTACATTCCTAAGAATGAGTT 600  | 481 AGGACGCTATACTACAGATGATGGTTATATCTTTAATGCTTCTGATATCATAGAGGATAC 540 | 421 TCAACATCGTGAAGGTGGAACTCCAAGAAACGATGGTGCTGTTGCCTTGGCACGTTCGCA 480 | 361 TGCCCACGCGGATAACGTCCGTACAAAAAAAGAGGAAAATCAATC  | 301 GGTCAAGGGTGGATATGTTATCAAGGTAGATGGAAAATACTATGTTTACCTTAAGGATGC 360     | 241 TGAAGAATTACTCATGAAAGATCCAAACTATAAGCTAAAAGATGAGGATATTGTTAATGA 300    | 181 TTCACATGGCGACCACTATCATTATTACAATGGTAAGGTTCCTTATGACGCTATCATCAG 240        | 121 GCGTGAAGGAATCAATGCTGAGCAAATCGTCATCAAGATAACAGACCAAGGCTATGTCAC 180  | 61 TATAGATGGAAAACAAGCGACGCAAAAAACGGAGAATTTGACTCCTGATGAGGTTAGCAA 120        | 1 TTCTTACGAGTTGGGACTGTATCAAGCTAGAACGGTTAAGGAAAATAATCGTGTTTCCTA 60 |
| Qy 5        | β δ   | Db Q  | S B &   | ? B \$   | ?  | S B &  | ? ₽ \$   | S B &   | S B &   | D 65   | S & &  | S & &  | ? B &  | B &   | ? B &   | S B &   | P &  | S B S   |
| 2126 2125   | 2089   TGAAGATCCAAATAAGAACTTCAAAGCGGATGAAGAGGAGAAAAACCTGA<br>         | 2023 ACATIC FRATIGATISMA ISMA ISMA ISMA ISMA ISMA ISMA ISMA           | THE TRANSPORT OF THE PROPERTY |  | 1964 CAATCTTCAATATACTGTTGCTTTGCTTTGATGATCACACAGTACAAAACGCTCCAAAACCTCATATGACCA 2023 | 1994 AGANGCINIILKAMICGIGIGAMAGGAMAAACGAMIICCACIGIICGACIICCAIA 1948 1904 AGANGCTATCTACAACCGCGGAAAGCAGCTAAGAAGGTGCCACTTGATCGTATGCCTTA 1963 1904 AGANGCTATCTACAACCGCGGAAAGCAGCTAAGAAGGTGCCACTTGATCGTATGCCTTA 1963 | 120 AGGITTERED STEERCE STANDARD CANADARD CONTROL CONTR | 1739 ACCEPATICE ACCEPACION AND CONTARA ACCEPANA ACCEPANA CONTRARA CONTRARA ACCEPANA CONTRARA ACCEPANA ACCEPANA CONTRARA ACCEPANA | 1609 TATAATCAGTGATGAAGGAGTGCATATGTAACGCCTCATATGGGCCATAGTCACTGGAT 1668   1009 TATAATCAGTGATGAAGGAATGCATATGTAACGCCCTCATATGGGCCATAGTCACTGCAT 1668   1100 | 1549 PATIGCTCAATTACCIGATAAGTACACGTCACATGTTACATTTTIGATGACATGA 1608    | 1909 CHAICCHAMACCHAMACCHAMAILCICHAMACCHAMAGICCA 1548                 | 1429 CANTOLOGO STREEGALLAGEN AGEST ATTECTS OF THE CONTROL STREET O | 1369 AAAIRAAGUSTOKINAITICGAKITICCAAGCCTTKGACAAATTATTAGAACGCTTGAATGA 1428 | 1909 CHAMBANIIIIA WAIAANGCAIAIAANICIGIIAACIWAGGCICAIAAAGCCIIGIIIGN 1368 | 1300 CGANGAATTTTTTAAACGATATAAGCTTTTAAACGTTAAGAAAAACTGACCTCCCATCTTAGTGA 1423 | 1107 11A ISTOLITIS COMPANSA II INCOMICA (ISMARCIS II AND II AND II INCOMPANSA II INCOMICA (ISMARCIS II AND II | 1129 TANICANG ING MANANG ING SANGGAN AND AND AND AND AND AND AND AND AND A | 1081 CCCGCAACCTGCACCAAATCTTAAAATAGACTCAAATTCTTCTTTGGT 1128        |

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                                                                     The DNA sequences can be used for producing an immune response to Streptococcus pneumoniae in a mammal. Antibodies against the proteins can be used to inhibit S. pneumoniae-mediated C3 degradation.

3-mediated inflammation and rejection in xenotransplantation can be inhibited by expressing the nucleic acid sequences on the surface of a organ of an animal. In particular, the polypeptides are useful for stimulating the immune system and are effective to immunize or treat a mammalian subject against Streptococcus pneumoniae infection or
                                                                                                                                                                                                                                                                                   The present sequence, isolated from Streptococcus pneumoniae, envinuman C3-degrading protein (see Ay91939) of about 92 kDa. This sequence may encompass a smaller Ay91939) of both coding sequencemay encompass a smaller 20 kDa polypeptide coding sequence may encompass a Smaller Ay91939 and coding sequencemay encompass a smaller and control of the coding sequencemay encompass a smaller and coding sequencemay encompass a smaller and coding sequencemay encompass as the coding sequencemay encompass.
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31-MAR-1999;
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Gilbert (MICR-) MICROBIAL TECHNICS LTD CFG, Hansbro PM.

2000-195300/17. DB; AAY81662.

27-JUL-1998; 19-MAR-1999;

98GB-0016337. 99US-0125164.

New Streptococcal protein, useful as a vaccine, for dia pneumococcal diseases and for screening agents capable or inhibiting expression of the protein for diagnosis of capable of antago antagonizing

Page 99; 108pp; English

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AAY81501 to AAY81679 represent specifically claimed protein sequences isolated from Streptococcus pneumoniae. AAA05407 to AAA05590 represent specifically claimed nucleotide sequences isolated from S. pneumoniae. The sequences have antibacterial and antiinflammatory properties. The protein sequences, and fragments of them, are useful as immunogens and/or antigens. The nucleotide sequences can be used in vaccines and in diagnostic assays. The proteins and nucleotides can be useful for the detection and diagnosis of S. pneumoniae. The protein sequences are also useful for screening an agent capable of antagonising, inhibiting or interfering with the function or expression of the proteins in which the agent is useful for treatment or prophylaxis of S. pneumoniae infection

| PAGE 18 P. 839 A, 514 C, 538 G, 550 T, 0 other;  281 BP, 839 A, 514 C, 538 G, 550 T, 0 other;  142 DP, 850 M, 1514 C, 538 G, 550 T, 0 other;  142 DP, 850 M, 1514 C, 538 G, 550 T, 0 other;  142 DP, 850 M, 1514 C, 538 G, 550 T, 0 other;  142 DP, 850 M, 1514 C, 538 G, 550 T, 0 other;  143 DP, 850 M, 1514 C, 538 G, 550 T, 0 other;  144 DP, 850 M, 1514 C, 538 G, 550 T, 0 other;  145 CORRESPONDING CONTROLLED C | OY 898 AACAGCTAGAGGTGTTGCAGTGCCAGCGAGATCAGAGTCGCAGGCAAATCACAAGTCGCAGAGATCATTACCACTTCATCCCTTACTCTCAGCCAGGTGTAGAGATCATTACCACTTTATCATTCAT | 778 .<br>798 .<br>838 . |     | 6 6 5 5<br>7 5 5 9 4 4 4 | Qy 478 GCAAGGACGCTATACTACAGATGATGGTTATATCTTTAATGCTTCTGATATCATAGAGGA | 418 | Db 360 TGAAATCAAGGGTGGTTATGTCATCAAGGTAGAACGGAAAATACTATGTTTACCTTAAGGA  Qy 358 TGCTGCCACGCGGATAACGTCCGTACAAAAAAACAAATCAATGACAAAAAAAA | Oy 238 CAGTGAAGAATTACTCATGAAAGATCAAAACTRIAAGCTAAAAGATGAGATATTGTTAA Db 300 CAGTGAAGAACTACCATGAAAGATCAAGCTAAAAGATGAGAATATTGTTAA OY 298 TGAGGTCAAGGGTGGATATGTTAATCAAGGTAGAAATTACTATGTTTACCTTAAGGA OY 298 TGAGGTCAAGGGTGGATATGTTATCAAGGTAGAAATACTATGTTTACCTTAAGGA | 178<br>240            | Qy 118 CAAGCGTGAAGGAATCAATGCTGAGCAAATCGTCAAGATAACAGACCAAGGCTATGT | 58<br>120     | 1 TTCTTACGAGTTGGGACTGTATCAAGCTAGAACG | Query Match Best Local Similarity 66.0%; Score 1003.8; Best Local Similarity 66.0%; Pred. No. 4.8e Marches 1623; Conservative 0: Mismatches | CC and meningitis. AAA05591 to AAA05614 represent CC exemplification of the present invention.  XX SO Semmence 2481 Bp: 839 A: 514 C: 538 G: 590 T: C |
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|  | 957  | 837<br>857<br>897       | 757 | 653<br>657<br>698        | 537 Db 597 Oy   | 477 | 419  | 359   | CCTTATGACGCTATCAT 237 | 177  | TGAGGTTAG 117 | TCGTGTTTC 57                         | 7 3 000007,<br>243; Length 2481;<br>693: Indels 144: Gaps 6:  | primers used in the   |

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 The invention relates to a protein comprising or having at least 50% identity to any of the 2469 amino acid sequences, identified in the specification (available on a computer readable format), or its fragment, expressed from 2469 of 2489 identified DNA coding regions from the Streptococcus pneumoniae type 4 strain genomic sequence appearing as ABS56454. Also included are an antibody which binds one of the
                                                                                     Claim
                                                                                                                               New proteins and nucleic acid molecules from Streptococcus pneumoniae, useful as medicaments for treating or preventing a disease or infection
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                                                                                                                                                                                                                                                                                                                                                                        Streptococcus pneumoniae
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                                                                                                                       as medicaments for treating streptococcus bacteria, such
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                                                                                                                                                                                                                                   CHIRON SPA.
INST GENOMIC RES
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CC proteins, treating a patient by administering the protein, DNA or Cantibody (in a composition), a kit comprising first and second primers, CC which are the nucleic acid cited above or fragments between nucleotides CC 8-100 of a sequence not defined in the specification, for amplifying a CC target sequence ont defined in the specification, for amplifying a CC target sequence contained within a Streptococcus nucleic acid sequence, CC the first primer is substantially complementary to the target sequence and the second primer is substantially complementary to the target complement of the target sequence, and where the parts of the primers CC having substantial complementarity define the termini of the target sequence to be amplified, assay comprising contacting a test compound CC with the protein, and determining whether the test compound to the protein and a Streptococcus pneumoniae bacterium, where one or more CC genes encoding the proteins has been rendered inactive. The proteins, cutleic acid molecules, antibody and compositions are useful as CC medicaments for treating or preventing a disease or infection due to Streptococcus bacteria, particularly S. pneumoniae, such as pneumonia, compositions are useful for CC streptococcus bacteria, particularly S. pneumoniae, such as pneumonia, compositions, otitis media or ear infection. They are also useful in developing vaccines, diagnostics and antibiotics. The methods are useful for CC the 2489 identified coding region from the genomic sequence is one of the printed specification, but was obtained in electronic formation in the sequence.

CC format directly from WIPO at ftp.wipo.int/pub/published\_pct\_sequences. \_developing the

CACTTCACATGGCGACCACTATCATTATTACAATGGTAAGGTTCCTTATGACGCTATCAT CAAGCGTGAAGGAATCAATGCTGAGCAAATCGTCATCAAGATAACAGACCAAGGCTATGT CTATATAGATGGAAAACAAGCGACGCAAAAAAACGGAGAATTTGACTCCTGATGAGGTTAG TAAGAGGGAGGGGATCAACGCCGAACAAATTGTTATCAAGATTACGGATCAAGGTTATGT TTATATAGATGGTGATCAGGCTGGTCAAAAGGCAGAAAACTTGACACCAGATGAAGTCAG TTCCTATGAGCTTGGACGTTACCAAGCTGGTCAGGATAAGAAGAGTCTAATCGAGTTGC TTCTTACGAGTTGGGACTGTATCAAGCTAGAACGGTTAAGGAAAA---TAATCGTGTTTC Score 993; DB Pred. No. 2.6e-0; Mismatches C; 531 G; 593 DB .6e-240; T; 0 25; 696; Indels 141; Gaps 119 179 57 239 σ

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Streptococcus pneumoniae; infection; vaccine; coiled coil region; histidine triad residue; Sp36; antibody; otitis media; nasopharyngeal infection; bronchial infection; bronchitis; sepsis meningitis; lobar pneumonia; ds.
                                                                                                                  Streptococcus
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                                                                                                                                                                                                                                                                                                                                                                                                                         standard;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
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Gene; ds; bacterial meningitis; pneumonia; sepsis; otitis media; ear infection; antiinflammatory; antibacterial; immunostimulant; auditory; respiratory; gene therapy; vaccine.
                                                                S. pneumoniae type 4 strain coding region #993.
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Matches 1478;

Conservative

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Mismatches 636;

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Gaps

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CC Streptococcus pneumoniae type 4 strain genomic sequence appearing as CC ABS56454. Also included are an antibody which binds one of the CC proteins, treating a patient by administering the protein, DNA or CC antibody (in a composition), a kit comprising first and second primers, CC which are the nucleic acid cited above or fragments between nucleotides CC which are the nucleic acid cited above or fragments between nucleotides CC where the first primer is substantially complementary to the target complement of the target sequence, and the second primer is substantially complementary to the target CC emplement of the target sequence, and where the parts of the primers CC having substantial complementarity define the termini of the target sequence to be amplified, assay comprising contacting a test compound CC with the protein, and determining whether the test compound CC sequence to be amplified, assay comprising contacting a test compound CC mucleic acid molecules, antibody and compositions are useful as CC mucleic acid molecules, antibody and compositions are useful as CC medicaments for treating on preventing a disease or infection due to streptococcus bacteria, particularly S. pneumoniae, such as pneumoniae, sepsis, otitis media or ear infection. They are also useful for CC the 2489 identified coding region from the genomic sequence.
    Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The invention relates to a protein comprising or having at least 50% identity to any of the 2469 amino acid sequences, identified in the specification (available on a computer readable format), or its fragment, expressed from 2469 of 2489 identified DNA coding regions from the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New proteins and nucleic acid molecules from Streptococcus pneumoniae, useful as medicaments for treating or preventing a disease or infectio due to streptococcus bacteria, such as pneumonia, sepsis, otitis media or ear infection
                                                             Sequence
                                                                                                                           of the printed specification, but format directly from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Masignani V,
                                                                                                    ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                               Note: The sequence data for this patent did not form part
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Streptococcus pneumoniae; infection; vaccine; coiled coil region; histidine triad residue; Sp16; antibody; otitis media; nasopharyngeal infection; bronchial infection; bronchitis; sepsis; meningitis; lobar pneumonia; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Disclosure; Page 57-58; 70pp; English.
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                 GACCTCTCATGGAGACCATTATCATTACTATAATGGCAAGGTCCCTTATGATGCCATCAT
                                                 CACTTCACATGGCGACCACTATCATTATTACAATGGTAAGGTTCCTTATGACGCTATCAT
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auditory; respiratory; gene therapy; vaccine
                                  ds;
                                                                   Streptococcus
                                                                                                        10-FEB-2003
                                                                                                                                                                          ABS56454 standard;
            bacterial meningitis; pneumonia; sepsis; otinfection; antiinflammatory; antibacterial;
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                                                                                                      (first
                                                                  pneumoniae type 4 strain complete genome
                                                                                                                                                                        DNA; 2162598
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                                  otitis media;
                  immunostimulant;
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TAAGAGGGAGGGGATCAACGCCGAACAAATCGTCATCAAGATTACGGATCAAGGTTATGT CAAGCGTGAAGGAATCAATGCTGAGCAAATCGTCATCAAGATAACAGACCAAGGCTATGT TTATATAGATGGTGATCAGGCTGGTCAAAAGGCAGAAAACTTGACACCAGATGAAGTCAG

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                                                                                                                                                            Query Match
Best Local (
                                                                                                                                         Matches 1478;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   identity to any of the 2469 amino acid sequences, identified in the specification (available on a computer readable format), or its fragment, expressed from 2469 of 2489 identified DNA coding regions from the streptococcus pneumoniae type 4 strain genomic sequence appearing as ABS56494. Also included are an antibody which binds one of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New proteins and nucleic acid molecules from Streptococcus pneumoniae, useful as medicaments for treating or preventing a disease or infection due to streptococcus bacteria, such as pneumonia, sepsis, otitis media or ear infection -
                                                                                                                                                                                                                              Sequence 2162598 BP; 654373 A; 427176 C; 431369
                                                                                                                                                                                                                                                                                               of the printed specification, but was obtained in electronic format directly from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The invention relates to a protein comprising or having at least 50% identity to any of the 2469 amino acid sequences, identified in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 17; SEQ ID No 4979; 56pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2003-040579/03
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 27-MAR-2001; 2001GB-0007658
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             27-MAR-2002; 2002WO-IB02163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Streptococcus pneumoniae type 4 strain
                                                                                                                                                                                                                                                                     ftp.wipo.int/pub/published_pct_sequences
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(GENO-) INST GENOMIC
         58
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                                                                                                                                                              Similarity
CTATATAGATGGAAAAACAAGCGACGCAAAAAACGGAGAATTTGACTCCTGATGAGGTTAG
                                                TTCTTACGAGTTGGGACTGTATCAAGCTAGAACGGTTAAGGAAAA---TAATCGTGTTTC
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                                                                                                                                                            41.4%;
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                                                                                                                                       0;
                                                                                                                                     Score 990; DB 25;
Pred. No. 2.8e-238;
0; Mismatches 636;
                                                                                                                                                                                                                              G; 649680 T; 0 other;
                                                                                                                                                                              Length 2162598;
                                                                                                                                       57;
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                                                                                                                                       Gaps
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| 1186 TCGTTATGTCTTTGCGAAAGATTTACCATCTGAAACTGTTAAAAATCTTGAAAGCAAGTT 1245 | 1126 GGTTAGTCAGCTAGTACGAAAAGTTGGGGGAAGGATATGTATTCGAAGAAAGGGCATCTC 1185 | 1078 AGGCCCGCAACCTGCACCAAATCTTAAAATAGACTCAAATTCTTCTTT 1125 | 1018 TTGGGTACCAGATTCAAGGCCAGAACCAACCAAGTCCACAACCGACTCCGGAACCTAGTCC 1077  | 1017           | 957<br>838925  | 897 | 778 TCAAGCAAGTCAAAGTAATGACATTGATAGTCTCTTGAAACAGCTCTACAAACTGCCTTT 837 | 777<br>838748   | 658 AAATTCAAGAACTATCGCCGACAAAATAGCGATAACACTTCAAGAACAAACTGGGTACC 717       | 598 GTTATCAGCTAGCGAGTTGGCTGCTGCAGAAGCCTTCCTATCTGGTCGAGGAAATCTGTC 657      | 538 TACTGGTGATGCTTATATCGTTCCTCATGGAGATCATTACCATTACATTCCTTAAGAATGA 597 | 478 GCAAGGACGCTATACTACAGATGATGGTTATATCTTTAATGCTTCTGATATCATAGAGGA 537      | 477<br>838481   | 358 TGCTGCCCACGCGGATAACGTCCGTACAAAAGAGGAAATCAATC                         | 298 TGAGGTCAAGGGTGGATATGTTATCAAGGTAGATGGAAAATACTATGTTTACCTTAAGGA 357 8308 TGAAATCAAGGGTGGTTATCAAGGTAGATGGAAAATACTATGTTTACCTTAAGGA 838367 | 238 CAGTGAAGAATTACTCATGAAAGATCCAAAACTATAAAGATGAAGATGAGGATATTGTTAA 297  238 CAGTGAAGAATTACTCATGAAAGATCCAAAACTATAAAGATGAAGATGAGGATATTGTTAA 297  8348 CAGTGAAGACTCCTCATGAAAGATCAATTATTCTAAAGATTGAAGATTTTATAA 238367 | 178 CACTTCACATGGCGACCACTATCATTATTACAATGGTAAGGTTCCTTATGACGCTATCAT 237       |
|--|--|--|--|----------------|--|-----|--|---|---|---|---|---|---|--|--|--|--|
| AC AAV27356; AC AAV27356; XX DT 02-OCT-1998 (first entry) XX           | RESULT 17<br>AAV27356<br>ID AAV27356 standard; DNA; 2290 BP.           | Db 840126 TGAATCTGATG 840136                               | 2086 CAGTGAAGATICAAA TAAGAACI ILAMAGCOGA ISAAGATAAGTGAAGTAAGTGAAGCCAACTCACCC 840066 CCAAGACAGTAAACCTGATGAAGATAAGGAACATGATGAAGTAAGT | 2026<br>840006 | CTATACCTTGGAGATTTGTTTGCGACGATTAGTACTACGAGACACCCTGAGGAACACCCTGAGGACGACGACGACGACGACGACGACGACGACGACGACG |     | ATATATGGTTGAGCATACAGTTGAGGTTAAAAACGGTAATTTGATTATTCCTCATAAGA          | QY 1786 TGCAGCAGCTATTTACAATCGTGTGAAAGGGGAAAAACGAATTCCACTCGTTCGACTTCC 1845 | Qy 1726 AAAAGGTATCCTACCTCCATCTCCAGACGCAGATGTTAAAGCAAATCCAACTGGAGATAG 1785 | QY 1666 GATTGGAAAAGATAGCCTTTCTGATAAGGAAAAAGTTGCAGCTCAAGCCTATACTAAAGA 1725 |   | Qy 1546 TCGTATTGCTCAATTAGCTGATAAGTATACAACGTCAGATGGTTACATTTTTGATGAACA 1605 | OY 1486 TACCCATCCAGAGCGACTTGGCAAACCAAATTCTCAAATTGAGTATACTGAAGACGAAGT 1545 | Qy 1426 TGATGAATCGACTAATAAAGAAAAATTGGTAGATGATTATTGGCATTCCTAGCACCAAT 1485 | Qy 1366 TGNAAATAAGGGTCGTAATTCTGAFTTCCAAGCCTTAGACAAATTATTAGAACGCTTGAA 1425  | Qy 1306 TGACCAAGAATTTTATGATAAAGCATATAATCTGTTAACTGAGGCTCATAAAGCCTTGTT 1365  | Qy 1246 ATCAAAACAAGAGAGTGTTTCACACACTTTAACTGCTAAAAAAAGAAAATGTTGCTCCTCG 1305 |

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                                                                                                                                                                                                                                                                                                   CC The present sequence encodes a protein from Streptococcus pneumoniae.
CC The nucleic acid sequence encoding the Streptococcus pneumoniae protein
CC can be useful in vaccines for inducing protective antibodies against
CC Streptococcus pneumoniae, for treatment or prevention of infection e.g.
CC pneumonia, otitis media or meningitis. Probes based on the nucleic acid
CC are used to detect Streptococcus infection (by usual hybridisation or
CC amplification methods), also for isolating Streptococcus genes or their
CC allelic variants. The protein can be used similarly to detect specific
CC antibodies in standard immunoassays, especially for diagnosing or
CC monitoring infections. Antibodies which bind the protein are used to
CC detect corresponding antigens, to purify the protein and for passive
CC immunisation (optionally coupled to a toxin). Vaccines are administered,
CC e.g. by injection, orally or through the skin, typically at 0.01-1000
CC (especially 10-300) mu g/ml per dose.
                                                                                                                                                                                                                                       Query Match
Best Local
                                                                                                                                                                                                                           Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       pneumoniae
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 acid encoding antigenic peptide(s) from Streptococcus iae or their epitope-containing fragments, useful in
                                                                                                                                                                                                                                        Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HUMAN
                                                                                                                                                                                                                                                                                 2290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Page
                                                                                                           TTATATAGATGGTGATCAGGCTGGTCAAAAGGCAGAAAACTTGACACCAGATGAAGTCAG
                                                                                                                                       CTATATAGATGGAAAACAAGCGACGCAAAAAAACGGAGAATTTGACTCCTGATGAGGTTAG
                                                                                                                                                                                               TTCTTACGAGTTGGGACTGTATCAAGCTAGAACGGTTAAGGAAAA---TAATCGTGTTTC
GACCTCTCATGGAGACCATTATCATTACTATAATGGCAAGGTTCCTTATGATGCCATCAT
                    CACTTCACATGGCGACCACTATCATTACTACAATGGTAAGGTTCCTTATGACGCTATCAT
                                                    TAAGAGGGAGGGGATCAACGCCGAACAAATNGTNATCAAGATTACGGATCAAGGTTATGT
                                                                             CAAGCGTGAAGGAATCAATGCTGAGCAAATCGTCATCAAGATAACAGACCAAGGCTATGT
                                                                                                                                                                   Hromockyj A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      pneumonia;
                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    or their epitope-containing fragments, we therapeutic vaccines, and for diagnosis
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Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New Streptococcus pneumoniae antigens, useful for detecting Streptococcus and for preventing or attenuating disease caustreptococcus infection -
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Streptococcus pneumoniae; BVH-3; BVH-11; BVH-28; antigen; vaccine; prophylaxis; therapy; infection; diagnosis; meningitis; bacteraemia; otitis media; pneumonia; immunisation; bactericidal; ds.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The present invention describes nucleic acids (I) encoding protein antigens (II) from Streptococcus pneumoniae. The protein antigens have bactericidal activity. The nucleic acids, encoding the protein antigens, may be used for the recombinant production of the proteins they encode. The protein antigens may then be used as vaccines for the prevention and treatment of Streptococcal infections in mammals (especially humans) which result in, e.g. meningitis, otitis media, bacteraemia and/or pneumonia. The present sequence encodes the S. pneumoniae BVH-11-2 protein antigen.
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                                                       GATTGGAAAAGATAGCCTTTCTGATAAGGAAAAAGTTGCAGCTCAAGCCTATACTAAAGA
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  New Streptococcus pneumoniae BVH-3 and BVH-11 variant and epitope-bearing polypeptides, useful as vaccine components or preventing streptococcal infections such as otitis media
                                                                                                                                                                                                                                                            20-JUN-2000;
                                                                                                                                                                                                                                                                                                       19-JUN-2001; 2001WO-CA00908
                                                                                                                                                                                                                                                                                                                                                       27-DEC-2001
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                                                                                                                                                                                                               SHIRE BIOCHEM
                                                                                                 AAU75934
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/note= "The gene is flanked by sequences from the vector SP64, no information on which is
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  therapeutic or prophylactic treatment of any streptococcal bacterial infection (e.g., caused by Streptococcus progenes, group B Streptococcus such as Streptococcus progenes, group B Streptococcus such as Streptococcus agalactiae, S. dysgalactiae, S. uberis, S. nocardia or staphylococcus aureus) in an individual susceptible to the infection. A polynucleotide (III) encoding (I) is useful in DNA immunisation techniques. The Streptococcus polypeptides are useful in a diagnostic test for S. pneumoniae infection. (III) is useful for designing DNA probes for use in detecting the presence of Streptococcus in a biological sample suspected of containing the bacteria. The DNA probes may also be used for detecting circulating S. pneumonia nucleic acid in a sample for diagnosing streptococcus infections. This sequence encodes the Streptococcus pneumoniae protein BVH-11-2, used to create the antigenic peptides described in the method of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The invention describes an isolated polypeptide (I) with 70-90% identity to Streptococcus pneumonia protein BVH-3, BVH-11, variants BVH-3 or BVH-11, or chimeric sequences derived from them. A vaccine comprising (I) is useful for therapeutic or prophylactic treatment omeningitis, otitis media, bacteraemia or pneumonia infection in an individual susceptible to these disorders. (II) is also useful for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
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                                                                     CACGGGTGATGCTTATATCGTTCCTCACGGCGACCATTACCATTACATTCCTAAGAATGA
                                                                                                                                                               CCAAGGACGTTATACAACGGATGATGGGTATATCTTCAATGCATCTGATATCATTGAGGA
                                                                                                                                                                                                          GCAAGGACGCTATACTACAGATGATGGTTATATCTTTAATGCTTCTGATATCATAGAGGA
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Pred. No. 3.2e-237;
0; Mismatches 638;

    - AACTCAAGAGCAGATAATGCTGTTGCTGCAGCCAGAGC

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GATTAAAAAAGATAGTTTGTCTGAAGCTGAGAGCGGCAGCCCAGGCTTATGCTAAAGA
                      GATTGGAAAAGATAGCCTTTCTGATAAGGAAAAAGTTGCAGCTCAAGCCCTATACTAAAGA
                                                                                                         TGATATAATCAGTGATGAAGGAGATGCATATGTAACGCCTCATATGGGCCATAGTCACTG
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                                                                            TGATATAACCAGTGATGAGGGGGATGCCTATGTAACTCCACATATGACCCATAGCCACTG
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This DNA sequence encodes a 79 kDa protein (see AAY05753) of Streptococcus pneumoniae serotype 4 that is capable of degrading human complement protein C3 (HCPC3). It was identified in the S.

Claim 54; Page 52-54; 66pp; English

New isolated human complement C3-degrading

proteinase

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RESULT 21
AAX25394
ID AAX25
XX AAX25
XX AAX25
XX AAX25
XX Human
DE Strep
XX Human
IX Human
IX
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                                                                                                                                                                                                                                                      WPI; 1999-254719/21.
P-PSDB; AAY05753.
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                                                                                                                                                                                                                                                                                                                                                                                                         (AMCY ) AMERICAN CYANAMID CO
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Best Local Simi
Matches 1436;
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                      GCTGTCCCTCATGGTAACCATTACCACTTTATCCCTTATGAACAAATGTCTGAATTGGAA
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Streptococcus pneumoniae. The present invention also describes an isolated nucleic acid molecule encoding a homologue of any of the fragments of the S.pneumoniae genome (SEQ ID NO:1 to 391) where the streptococcus pneumoniae genome (SEQ ID NO:1 to 391) where the streptococcus pneumoniae genome (SEQ ID NO:1 to 391) where the streptococcus pneumoniae genome (SEQ ID NO:1 to 391) where the streptococcus pneumoniae genome (SEQ ID NO:1 to 391) where the streptococcus pneumoniae genome (SEQ ID NO:1 to 391) where the streptococcus pneumoniae genome (SEQ ID NO:1 to 391) where the streptococcus pneumoniae genome (SEQ ID NO:1 to 391) where the streptococcus pneumoniae genome (SEQ ID NO:1 to 391) where the streptococcus pneumoniae genome (SEQ ID NO:1 to 391) where the streptococcus pneumoniae genome (SEQ ID NO:1 to 391) where the streptococcus pneumoniae genome (SEQ ID NO:1 to 391) where the streptococcus pneumoniae genome (SEQ ID NO:1 to 391) where the streptococcus pneumoniae genome (SEQ ID NO:1 to 391) where the streptococcus pneumoniae genome (SEQ ID NO:1 to 391) where the streptococcus pneumoniae genome (SEQ ID NO:1 to 391) where the streptococcus pneumoniae genome (SEQ ID NO:1 to 391) where the streptococcus pneumoniae genome (SEQ ID NO:1 to 391) where the streptococcus pneumoniae genome (SEQ ID NO:1 to 391) where the streptococcus pneumoniae genome (SEQ ID NO:1 to 391) where the streptococcus pneumoniae genome (SEQ ID NO:1 to 391) where the streptococcus pneumoniae genome g
                                                                           The present invention describes a computer readable medium which has the nucleotide sequences SEQ ID No:1 to 391 (AAV52134 to AAV52524) recorded on it, or a representative fragment or a sequence at least identical to SEQ ID NO: 1 to 391. The nucleotide sequences depicted is SEQ ID NO:1 to 391 (AAV52334 to AAV52524) are genomic fragments from
                                                                                                                                                                                                                                      Claim
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nucleic acid molecule is produced by a process comprising: (a) screening a genomic DNA library using as a probe a target sequence defined by any of the sequences in SRQ ID NO:1 to 391, identifying members of the SRQ isolating the nucleic acid molecules from the members; or (b) isolating the nucleic acid molecules from the members; or (b) isolating CRNA, DNA or CDNA produced from an organism, amplifying nucleic acid molecules whose nucleotide sequence is homologous to amplification primers derived from the fragment of the S. pneumoniae genome to prime the amplification and isolating the amplified sequences. The computer readable medium can be used in a computer-based system for identifying fragments of the S. pneumoniae genome. Products from the present invention can be used in diagnosis kits and assays, and pharmaceutical compositions and vaccines for S. pneumoniae.
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2359 BP; 786 A; 451 C; 511 G; 611 T; 0 other;

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Length

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Rioux Q Charland z

against Ø ġ meningitis,

The present invention describes nucleic acids (I) encoding protein antigens (II) from Streptococcus pneumoniae. The protein antigens have bactericidal activity. The nucleic acids, encoding the protein antigens, may be used for the recombinant production of the proteins they encode. The protein antigens may then be used as vaccines for the prevention and treatment of Streptococcal infections in mammals (especially humans) which result in, e.g. meningitis, otitis media, bacteraemia and/or pneumonia. The present sequence encodes the S. pneumoniae NEW12 protein antigen. T; 0 other;

Score 548.4; DB 21; Pred. No. 5.3e-128; 432; Indels Length 102; Gaps 2

CTTCGTTATCGTTCAAACCATTGGGTACCAGATTCAAGGCCAGAACAACCAAGTCCACAA CCGACTCCAGACCTAGTCCAAGTCCGCAACCTGCACCAAATCCTCAACCAGCTCCAAGC ccgactccggaacctagtccaggcccgcaacctgcaccaaatcttaaaatagactcaa--GGTTATATCTTTGATCCTCGTGATATAACCAGTGATGAGGGGGGATGCCTATGTAACTCCA GGTTACATTTTTGATGAACATGATATAATCAGTGATGAAGGAGATGCATATGTAACGCCT GAGTATACTGAAGACGAAGTTCGTATTGCTCAATTAGCTGATAAGTATACAACGTCAGAT TTGGCATTCCTAGCACCAATTACCCATCCAGAGCGACTTGGCAAACCAAATTCTCAAATT AACCTGTTGGAACGACTCAAGGATGTCTCAAGTGATAAAGTCAAGTTAGTGGATGATATT AAATTATTAGAACGCTTGAATGAATGAATCGACTAATAAAGAAAAATTGGTAGATGATTTA 1465 AGAATTCACCAAGATTTACTTGATAATAAAGGTCGACAAGTTGATTTTGAGGCTTTGGAT GAGGCTCATAAAGCCTTGTTTGNAAATAAGGGTCGTAATTCTGATTTCCAAGCCTTAGAC AAAACTGACCTCCCATCTAGTGATCGAGAATTTTACAATAAGGCTTATGACTTACTAGCA AAAGAAAATGTTGCTCCTCGTGACCAAGAATTTTATGATAAAGCATATAATCTGTTAACT GCAGGCATTGATAGCAAACTGGCCAAGCAGGAAAGTTTATCTCATAAGCTAGGAGCTAAG AAAAATCTTGAAAAGCAAGTTATCAAAAACAAGAGAGTGTTTCACACACTTTAACTGCTAAA TITGAGGAGAATGGAGTTTCTCGTTATATCCCCAGCCAAGAATCTTTCAGCAGAAACAGCA TTCGAAGAAAAGGCATCTCTCGTTATGTCTTTGCGAAAGATTTACCATCTGAAACTGTT AATCCAATTGATGAGAAATTGGTCAAAGAAGCTGTTCGAAAAGTAGGCGATGGTTATGTC CTTCGTTATCGTTCAAACCATTGGGTACCAGATTCAAGACCAGAAGAACCAAGTCCACAA ATTCTTCTTTGGTTAGTCAGCTGGTACGAAAAGTTGGGGAAGGATATGTA 2067 2367 1645 2307 1585 1525 2127 1405 2007 1947 1225 1827 1115 1767 1057 2247 2187 1285 1887 1165

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CC The present sequence encodes a protein from Streptococcus pneumoniae.

CC The nucleic acid sequence encoding the Streptococcus pneumoniae protein

CC can be useful in vaccines for inducing protective antibodies against

CC Streptococcus pneumoniae, for treatment or prevention of infection e.g.

CC pneumonia, otitis media or meningitis. Probes based on the nucleic acid

CC are used to detect Streptococcus infection (by usual hybridisation or

CC amplification methods), also for isolating Streptococcus genes or their

CC allelic variants. The protein can be used similarly to detect specific

CC antibodies in standard immunoassays, especially for diagnosing or

CC monitoring infections. Antibodies which bind the protein are used to

CC detect corresponding antigens, to purify the protein and for passive

CC immunisation (optionally coupled to a toxin). Vaccines are administered,

CC e.g. by injection, orally or through the skin, typically at 0.01-1000

CC (especially 10-300) mu g/ml per dose.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Nucleic acid encoding antigenic peptide(s) from Streptococcus pneumoniae - or their epitope-containing fragments, useful in protective or therapeutic vaccines, and for diagnosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
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                                               CAATCGACAAAAAACAAGAGCATAGTCAACATCGTGAAGGTGGAACTCCAAGAAACGATGG 456
                                                                                                    ATACTATGTTTACCTTAAGGATGCTGCCCACGCGGATAACGTCCGTACAAAAGAGGAAAT 396
                                                                                                                                            TAAAGACGCTGATATTGTCAATGAAGTCAAGGGTGGTTATATCATCAAGGTCGATGGAAA
                                                                                                                                                                   AAAAGATGAGGATATTGTTAATGAGGTCAAGGGTGGATATGTTATCAAGGTAGATGGAAA 336
                                                                                                                                                                                                                                 GGTTCCTTATGACGCTATCATCAGTGAAGAATTACTCATGAAAGATCCAAACTATAAGCT
                                                                                                                                                                                                                                                                               AATTACAGATCAGGGCTATGTAACGTCACACGGTGACCACTATCATTACTATAATGGGAA
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/note= "no stop codon given"
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65.3%;
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Pred. No. 5.3e-87;
0; Mismatches 276; ]
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                                                                                          The present invention describes nucleic acids (I) encoding protein antigens (II) from Streptococcus pneumoniae. The protein antigens have bactericidal activity. The nucleic acids, encoding the protein antigens, may be used for the recombinant production of the proteins they encode. The protein antigens may then be used as vaccines for the prevention and treatment of Streptococcal infections in mammals (especially humans) which result in, e.g. meningitis, otitis media, bacteraemia and/or pneumonia. The present sequence encodes the S. pneumoniae BVH-3A protein antigen.
                                                                                                                                                                                                                                                                                                                              Streptococcal antigens useful for vaccinating against otitis media, bacteremia and/or pneumonia -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Streptococcus pneumoniae; BVH-3; BVH-11; BVH-28; antigen; vaccine; prophylaxis; therapy; infection; diagnosis; meningitis; bacteraemi otitis media; pneumonia; immunisation; bactericidal; ds.
                                                          Sequence 1455
                                                                                                                                                                                                                                                                                          Disclosure;
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                                                                                                                                                                                                                                                                            polypeptides in vaccines to protect against a wide variety of S. pneumoniae. New vaccine compositions are described which comprise streptococcus pneumoniae polypeptide (or fragments) of 80 . dmino acids in length that comprise at least one histidine triad residue (HxxHxH) or a coiled-coil region, or an antibody directed against these features. The vaccine is useful in protecting against infection by Streptococcus pneumoniae. The vaccine composition comprising antibodies to is useful for passive immunization for treating pneumococcal infections which includes otitis media, nasopharyngeal
                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                                               Although a number of proteins have been suggested as being involved in the pathogenicity of Streptcococus pneumoniae, there still remains a need to identify polypeptides having epitopes in common from various strains of S. pneumoniae in order to utilise such
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure; Page 60-61;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       comprises
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Vaccine useful for prophylaxis and treatment of pnemococcal infections such as otitis media, nasopharyngeal and bronchial infections,
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The protein sequences, and fragments of them, are useful as immunogens and/or antigens. The nucleotide sequences can be useful as immunogens and for antigens. The proteins and nucleotides can be useful for the detection and diagnosis of S. pneumoniae. The protein sequences are also useful for screening an agent capable of antagonising, inhibiting or interferring with the function or expression of the proteins in which the agent is useful for treatment or prophylaxis of S. pneumoniae infection and deningities. AAA05591 to AAA05591 represent primers used in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New Streptococcal protein, useful as a vaccine, for diagnosis pneumococcal diseases and for screening agents capable of anta or inhibiting expression of the protein -
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                                              TTCAAGAACAAACTGGGTACCTTCTGTAAGCAATCCAGGAACTACAAATACTAACAAAG
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identity to any of the 2469 amino acid sequences, identified in the specification (available on a computer readable format), or its fragment, expressed from 2469 of 2489 identified DNA coding regions from the Streptococcus pneumoniae type 4 strain genomic sequence appearing as ABS56454. Also included are an antibody which binds one of the proteins, treating a patient by administering the protein, DNA or antibody (in a composition), aki comprising first and second primers, which are the nucleic acid cited above or fragments between nucleotides 8-100 of a sequence not defined in the specification, for amplifying a target sequence contained within a Streptococcus nucleic acid sequence, where the first primer is substantially complementary to the target
                                                                                                                                                                                                                                           New proteins and nucleic acid molecules from Streptococcus useful as medicaments for treating or preventing a disease due to streptococcus bacteria, such as pneumonia, sepsis, o or ear infection
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CC sequence and the second primer is substantially complementary to the CC complement of the target sequence, and where the parts of the primers CC having substantial complementarity define the termini of the target CC sequence to be amplified, assay comprising contacting a test compound CC with the protein, and determining whether the test compound binds to the protein and a Streptococcus pneumoniae bacterium, where one or more CC genes encoding the proteins has been rendered inactive. The proteins, CC nucleic acid molecules, antibody and compositions are useful as CC medicaments for treating or preventing a disease or infection due to CC streptococcus bacteria, particularly S. pneumoniae, such as pneumonia, CC sepsis, otitis media or ear infection. They are also useful for CC vaccines, diagnostics and antibiotics. The methods are useful for CC identifying immunodominant proteins. The present sequence is one of CC the 2489 identified coding region from the genomic sequence.

CC Note: The sequence data for this patent did not form part CC in the printed specification, but was obtained in electronic CC format directly from WIPO at
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Pred. No. 7.7e-87;
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                           Query Match
                                                                                                                                                The present invention describes nucleic acids (I) encoding protein antigens (II) from Streptococcus pneumoniae. The protein antigens have bactericidal activity. The nucleic acids, encoding the protein antigens, may be used for the recombinant production of the proteins they encode. The protein antigens may then be used as vaccines for the prevention and treatment of Streptococcal infections in mammals (especially humans) which result in, e.g. meningitis, otitis media, bacteraemia and/or pneumonia. The present sequence encodes the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 200
P-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Streptococcus pneumoniae; BVH-3; BVH-11; BVH-28; antigen; vaccine; prophylaxis; therapy; infection; diagnosis; meningitis; bacteraemi otitis media; pneumonia; immunisation; bactericidal; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Streptococcal antigens useful for otitis media, bacteremia and/or
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Best Local Similarity
Matches 631; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Streptococcus pneumoniae; BVH-3; BVH-11; BVH-28; antigen; vaccine; prophylaxis; therapy; infection; diagnosis; meningitis; bacteraemia; otitis media; pneumonia; immunisation; bactericidal; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
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                                                                                                                                      TAAAGACGCTGATATTGTCAATGAAGTCAAGGGTGGTTATATCATCAAGGTCGATGGAAA
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                                                                                                                                                                                                                                                                                                                  GATAACAGACCAAGGCTATGTCACTTCACATGGCGACCACTATCATTATTACAATGGTAA
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                                                            ATATTATGTCTACCTGAAAGATGCAGCTCATGCTGATAATGTTCGAACTAAAGATGAAAT
                                                                                  ATACTATGTTTACCTTAAGGATGCTGCCCACGCGGATAACGTCCGTACAAAAGAGGGAAAT
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20-JUN-2000; 2000US-212683P
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                                                                                                                                                                                                                                                                                                                                                                                                                  pneumonia; streptococcal bacterial infection; gene;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Streptococcus pneumoniae BVH-3 version
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                                                                                                                                                                                                                                 /product= "BVH-3"
/note= "The gene :
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                                                                                                                                                                              "The gene is flanked by sequences vector SP64, no information on wh given in the specification"
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    TAATGTTGCTGTAGCAAGGTCTCAGGGACGATATACGACAAATGATGGTTATGTCTTTAA
                               TGCTGTTGCCTTGGCACGTTCGCAAGGACGCTATACTACAGATGATGGTTATATCTTTAA 516
                                                                                           CAATCGTCAAAAACAAGAACATGTCAAAGATAATGAGAAGGTTA-----ACTC 2282
                                                                                                                          CAATCGACAAAAACAAGAGCATAGTCAACATCGTGAAGGTGGAACTCCAAGAAACGATGG
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The invention describes an isolated polypeptide (I) with 70-90% (C) identity to Streptococcus pneumonia protein BVH-3, BVH-11, variants of EWH-3 or BWH-11, or chimeric sequences derived from them. A vaccine (II) CC comprising (I) is useful for therapeutic or prophylactic treatment of meningitis, otitis media, bacteraemia or pneumonia infection in an CC individual susceptible to these disorders. (II) is also useful for therapeutic or prophylactic treatment of any streptococcal bacterial CC infection (e.g., caused by Streptococcus pneumoniae, group A Streptococcus such as Streptococcus popennes, group B Streptococcus such as Streptococcus popennes, group B Streptococcus such as Streptococcus popennes, suberis, S. nocardia or CC staphylococcus aureus) in an individual susceptible to the infection. CC techniques. The Streptococcus polypeptides are useful in DNA immunisation CC test for S. pneumoniae infection. (III) is useful for designing DNA CC sample suspected of containing the presence of Streptococcus in a biological CC sused for detecting the presence of Streptococcus in a biological CC suspended of containing the bacteria. The DNA probes may also be used for detecting streptococcus in a biological CC states for Streptococcus infections. This sequence encodes the Streptococcus portion BNH-), used to create the antigenic contribation in the method of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New Streptococcus pneumoniae BVH-3 and BVH-11 variant and epitope-bearing polypeptides, useful as vaccine components for treating or preventing streptococcal infections such as otitis media, meningitis, and bacteraemia
peptides described in the method of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Example 3; Fig 2; 113pp; English
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Sequence 5048 BP; 1709 A; 907 C; 1104 G; 1328 T; 0 other;

Length

GATAACAGACCAAGGCTATGTCACTTCACATGGCGACCACTATCATTATTACAATGGTAA TTTGACTCCTGATGAGGTTAGCAAGCGTGAAGGAATCAATGCTGAGCAAATCGTCATCAA 156 TAAAGACGCTGATATTGTCAATGAAGTCAAGGGTGGTTATATCATCAAGGTCGATGGAAA AAAAGATGAGGATATTGTTAATGAGGTCAAGGGTGGATATGTTATCAAGGTAGATGGAAA 336 AGTTCCTTATGATGCCCTCTTTAGTGAAGAACTCTTGATGAAGGATCCAAACTATCAACT GGTTCCTTATGACGCTATCATCAGTGAAGAATTACTCATGAAAGATCCAAACTATAAGCT 276 AATTACAGATCAGGGCTATGTAACGTCACACGGTGACCACTATCATTACTATAATGGGAA CTTGACACCAGACCAGGTTAGCCAGAAAGAAGGAATTCAGGCTGAGCAAATTGTAATCAA TAAGGACAATAATCGTGTCTCTTATGTGGATGGCAGCCAGTCAAGTCAGAAAAGTGAAAA TAAGGAAAATAATCGTGTTTTCCTATATAGATGGAAAAACAAGCGACGCAAAAAAACGGAGAA ATACTATGTTTACCTTAAGGATGCTGCCCACGCGGATAACGTCCGTACAAAAGAGAGAAAT Conservative 16.1**%**; 65.3**%**; 0. Score 385.4; DB 24; Pred. No. 9.5e-87; Mismatches 276; Indels 60; Gaps 2174 2114 2054 216 1934 1994 96

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                       Computer-readable medium with recorded Streptococcus pneumoniae polynucleotide sequences - useful in diagnostic kits and assays pharmaceutical compositions and vaccines for Streptococcus
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               pneumoniae
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                                                                                                                 Dillon PJ,
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Query Match Best Local Similarity

16.1%;

Score 385.4; DB 19; Pred. No. 1.1e-86;

Length

Claim 1; Page 1157-1161; 1409pp; English.

The present invention describes a computer readable medium which has CC the nucleotide sequences SEQ ID NO:1 to 391 (AAV52134 to AAV52524) CC recorded on it, or a representative fragment or a sequence at least 95% CC identical to SEQ ID NO: 1 to 391. The nucleotide sequences depicted in SEQ ID NO: 1 to 391. The nucleotide sequences depicted in CC SEQ ID NO: 1 to 391 (AAV52134 to AAV52524) are genomic fragments from CC streptococcus pneumoniae. The present invention also describes an CC isolated nucleic acid molecule encoding a homologue of any of the CC nucleic acid molecule seconding a homologue of any of the CC nucleic acid molecule seconding a homologue of any of the CC nucleic acid molecule second by a process comprising: (a) screening CC a genomic DNA library using as a probe a target sequence defined by any CC of the sequences in SEQ ID NO: 1 to 391, identifying members of the library which contain sequences that hybridise to the target sequence and CC isolating the nucleic acid molecules from the members; or (b) isolating CC mRNA, DNA or cNA produced from an organism, amplifying nucleic acid colorules whose nucleotide sequence is homologous to amplification CC primers derived from the fragment of the S. pneumoniae genome to prime CC the amplification and isolating the amplified sequences. The computer creadable medium can be used in a computer-based system for identifying CC expression modulating fragments of the S. pneumoniae genome. Products CC from the present invention can be used in diagnosis kits and assays, and CC pharmaceutical compositions and vaccines for S. pneumoniae.

Sequence 6867 BP; 1896 A; 1325 C; 1212 G; 2433 T; 1 other;

Matches 6387 6567 6687 6219 6279 6327 6447 6507 6627 457 397 157 637 517 337 277 217 631; 37 97 ATCTGGTCGAGGAAATCTGTCAAATTCAAGAACCTATCGCCGACAAAATAGCGATAACAC GGTTCCTTATGACGCTATCATCAGTGAAGAATTACTCATGAAAGATCCAAACTATAAGCT AATTACAGATCAGGGCTATGTAACGTCACACGGTGACCACTATCATTACTATAATGGGAA GATAACAGACCAAGGCTATGTCACTTCACATGGCGACCACTATCATTATTACAATGGTAA TAAGGACAATAATCGTGTCTCTTATGTGGATGGCAGCCAGTCAAGTCAGAAAAGTGAAAA TAAGGAAAATAATCGTGTTTTCCTATATAGATGGAAAACAAGCGACGCCAAAAAAACGGAGAA TCACTACATTCCCAAAAGCGATTTATCTGCTAGTGAATTAGCAGCAGCTAAAGCACATCT ATACTATGTTTACCTTAAGGATGCTGCCCACGCGGATAACGTCCGTACAAAAGAGAGAAAT TAAAGACGCTGATATTGTCAATGAAGTCAAGGGTGGTTATATCATCAAGGTCGATGGAAA AAAAGATGAGGATATTGTTAATGAGGTCAAGGGTGGATATGTTATCAAGGTAGATGGAAA AGTTCCTTATGATGCCCCTCTTTAGTGAAGAACTCTTGATGAAGGATCCAAACTATCAACT CTTGACACCAGACCAGGTTAGCCAGAAAGAAGGAATTCAGGCTGAGCAAATTGTAATCAA TTTGACTCCTGATGAGGTTAGCAAGCGTGAAGGAATCAATGCTGAGCAAATCGTCATCAA CCATTACATTCCTAAGAATGAGTTATCAGCTAGCGAGTTGGCTGCTGCAGAAGCCTTCCT TCCAGCTGATATTATCGAAGATACGGGTAATGCTTATATCGTTCCTCATGGAGGTCACTA TGCTTCTGATATCATAGAGGATACTGGTGATGCTTATATCGTTCCTCATGGAGATCATTA 576 TAATGTTGCTGTAGCAAGGTCTCAGGGACGATATACGACAAATGATGGTTATGTCTTTAA TGCTGTTGCCTTGGCACGTTCGCAAGGACGCTATACTACAGATGATGGTTATATCTTTAA CAATCGTCAAAAACAAGAACATGTCAAAGATAATGAGAAGGTTA---CAATCGACAAAAACAAGAGCATAGTCAACATCGTGAAGGTGGAACTCCAAGAAACGATGG ATATTATGTCTACCTGAAAGATGCAGCTCATGCTGATAATGTTCGAACTAAAGATGAAAT Conservative 0 Mismatches 276; Indels -----ACTC 60; Gaps 6628 696 6160 6220 6100 636 516 6280 456 6328 6388 336 6448 276 6508 216 156 96 396 6568 N

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RESULT 35
AAV52488
ID SAV52
XX AAV52
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XX Strep
XX Strep
XX Compu
XX Strep
XX COMPU
XX Strep
XX WO981
PN GOMPU
PT PD PN WO981
PT PD PN WO981
PN WPI;
XX COMPU
PT PD PN WO981
PT PD PN WO981
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PT PN WO981
PN WO
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Computer-readable medium with recorded Streptococcus pneumoniae polynucleotide sequences - useful in diagnostic kits and assays, pharmaceutical compositions and vaccines for Streptococcus
Streptococcus pneumoniae. The present invention also describes an isolated nucleic acid molecule encoding a homologue of any of the fragments of the S.pneumoniae genome (SEQ ID NO:1 to 391) where the nucleic acid molecule is produced by a process comprising: (a) scr
                                                                                                                                 The present invention describes a computer readable medium which has the nucleotide sequences SEQ No:1 to 391 (AAV52134 to AAV52524) recorded on it, or a representative fragment or a sequence at least identical to SEQ ID NO: 1 to 391. The nucleotide sequences depicted identical to SEQ ID NO: 1 to 391. The nucleotide sequences depicted is SEQ ID NO: 1 to 391 (AAV52524) are genomic fragments from SEQ ID NO: 1 to 391 (AAV52134 to AAV52524) are genomic fragments from
                                                                                                                                                                                                                                                                                                                                                  Claim 1; Page 1369-1370; 1409pp;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    a genomic DNA library using as a probe a target sequence defined by any of the sequences in SEQ ID NO:1 to 391, identifying members of the library which contain sequences that hybridise to the target sequence an isolating the nucleic acid molecules from the members; or (b) isolating mcNA, DNA or cDNA produced from an organism, amplifying nucleic acid molecules whose nucleotide sequence is homologous to amplification primers derived from the fragment of the S. pneumoniae genome to prime readable medium can be used in a computer-based system for identifying fragments of the S. pneumoniae genome. Products from the present invention can be used in diagnosis kits and assays, and pharmaceutical compositions and vaccines for S. pneumoniae.
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GTTATCAGCTAGCGAGTTGGCTGCTGCAGAAGCCT
                                              CACGGGTGATGCTTATATCGTTCCTCACGGCGACCATTACCATTACATTCCTAAGAATGA
                                                                                                          CCAAGGACGTTATACAACGGATGATGGGTATATCTTCAATGCATCTGATATCATTGAGGA
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Streptococcus

pneumoniae

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Example 6; Fig 18; 106pp; English.
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                                                             CAATCGACAAAAAACAAGAGCATAGTCAACATCGTGAAGGTGGAACTCCAAGAAACGATGG
                                                                                                                                       ATACTATGTTTACCTTAAGGATGCTGCCCACGCGGATAACGTCCGTACAAAAGAGGGAAAT
                                                                                                                                                                                         TAAAGACGCTGATATTGTCAATGAAGTCAAGGGTGGTTATATCATCAAGGTCGATGGAAA
                                                                                                                                                                                                                 AAAAGATGAGGATATTGTTAATGAGGTCAAGGGTGGATATGTTATCAAGGTAGATGGAAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            antigens useful for vaccinating bacteremia and/or pneumonia -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       pneumonia;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          960 A; 398
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infection; diagnosis; meningitis; bacteraemia;
ia; immunisation; bactericidal; ds.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 347; DB Pred. No. 3.5e-0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        505 G;
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3.5e-77;
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The invention describes an isolated polypeptide (I) with 70-90% condensity to Streptococcus pneumonia protein BVH-3, BVH-11, variants of EVH-3 or BVH-11, or chimeric sequences derived from them. A vaccine (II) comprising (I) is useful for therapeutic or proptic or prophylactic comprising (I) is useful for therapeutic or proptic or prophylactic comprising (I) is useful for therapeutic or prophylactic or in an individual susceptible to these disorders. (II) is also useful for therapeutic or prophylactic treatment of any streptococcal bacterial confection (e.g., caused by Streptococcus pneumoniae, group A Streptococcus such as Streptococcus pneumoniae, group B Streptococcus such as Streptococcus pneumoniae, subserie, S. nocardia or CC staphylococcus aureus) in an individual susceptible to the infection. CC Apolymucleotide (III) encoding (I) is useful in DNA immunisation techniques. The Streptococcus polypeptides are useful in a diagnostic test for S. pneumoniae infection. (III) is useful in a diagnostic probes for use in detecting the presence of Streptococcus in a biological
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               á
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New Streptococcus pneumoniae BVH-3 and BVH-11 variant and epitope-bearing polypeptides, useful as vaccine components for treating or preventing streptococcal infections such as otitis media, meningitis, and bacteraemia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Streptococcus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Example 8; Fig 9; 113pp; English.
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Best Local
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WO200017370-A1
                            Streptococcus pneumoniae
                                                           Human C3-degrading protein; inhibitor; inflammation; or;
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                                                                                                            kDa human
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                                                                                                                                                                                                             DNA;
                                                                                                                                            entry)
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73.0%;
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                                                            in; 20
organ
                                                                                                            C3-degrading
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                                                                                                                                                                                                             ВP
                                                            kDa; immunostimulatory; rejection; xenotransplar
                                                                                                            protein
                                                              xenotransplantation;
                                                                                                                                                                                                                                                                                              663
                                                                                                            coding
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present sequence, isolated from Streptococcus pneumoniae, encodes a human C3-degrading protein (see AAY91938) of about 20 kba. This sequence may be part of a larger open reading frame (see AAA0857) which encodes an approximately 92 kba protein also having human C3-degrading activity. The DNA sequences can be used for producing an immune response to Streptococcus pneumoniae in a mammal. Antibodies against the proteins can be used to inhibit S. pneumoniae mediated C3 degradation. C3-mediated inflammation and rejection in xenotransplantation can be inhibited by expressing the nucleic acid sequences on the surface of an organ of an animal. In particular, the polypeptides are useful for stimulating the immune system and are effective to immunize or treat a mammalian subject against Streptococcus pneumoniae infection or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 20
P-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 504 BP;
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31-MAR-1999;
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DB; AAY91938.
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AMERICAN CYANAMID
                                                                                                                                                                                                                                                                                                                                                                                                               AGTCGAACAGCTAGAGGTGTTGCAGTGCCACACGGAGATCATTACCACTTCATCCCTTAC 952
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CCTTTGAGTCAACGACATGTAGAATCTGATGGCCTTGTCTTTGATCCAGCACAAATCACA
                                                                                                                                                     TCTTTGGTTAGTCAGCTGGTACGAAAAGTTGGGGAAGGATATGTATTCGAAGAAAAGGGC
                                                                                                                                                                                                                                                                                                                                               TCTCAAATGTCTGAAGTAGAACGAATCGCTCGTATTATTCCCCCTTCGTTATCGTTCA 1012
                                                                                                                                                                                                                                                                                                                                                                                           AGTCGAACCGCCAATGGTGTTGCTGTACCGCACGGAGACCATTATCACTTTATTCCTTAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                             CCCTTATCAGAACGCCATGTAGAATCTGATGGCCTTATTTTCGACCCAGCGCAAATCACA
                       AAGTTATCAAAACAAGAGAGTGTTTCACACA 1271
                                                                GTTCCTCGTTATATCCCCAGCCAAGGATCTTTCAGCAGAAACAGCAGCAGCAGCATTGATAGC
                                                                                    ATCTCTCGTTATGTCTTTGCGAAAGATTTACCATCTGAAACTGTTAAAAAATCTTGAAAGC 1240
                                                                                                                               AAATTGGTCAAAGAAGCTGTTCGAAAAGTAGGCGATGGTTATGTCTTTGAGGAGAATGGA 393
                                                                                                                                                                                                              AGTCCAGGCCGCAACCTGCACCAAATCTTAAAATAGACTCAA------ATTCT 1120
                                                                                                                                                                                                                                                            AACCATTGGGTACCAGATTCAAGACCAGACAACCAAGTCCACAATCGACTCCGGAACCT
                                                                                                                                                                                                                                                                                              AACCATTGGGTACCAGATTCAAGGCCAGAACAACCAAGTCCACAACCGACTCCGGAACCT
AAACTGGCCAAGCAGGAAAGTTTATCTCATA
                                                                                                                                                                                               TCACAACTGTCACCTTTGGAAGAAAAATTGGCTCGTATTATTCCCCCTTCGTTATCGTTCA
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99US-0283094
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Pred. No. 2.
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RESULT 39
AAV52391
ID AAV52391
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Best Local Similarity
Matches 493; Conserv
                                                                                                                                                                                                                                                                                                                   Sequence 1684 BP; 593 A; 292 C; 345 G; 453 T; 1 other;
                                                                                                                                                                                                                                                                                                                                                                           mRNA, DNA or cDNA produced from an organism, amplifying nucleic acid molecules whose nucleotide sequence is homologous to amplification primers derived from the fragment of the S. pneumoniae genome to prime the amplification and isolating the amplified sequences. The computer readable medium can be used in a computer-based system for identifying fragments of the S. pneumoniae genome of commercial importance, or expression modulating fragments of the S. pneumoniae genome. Products from the present invention can be used in diagnosis kits and assays, ar pharmaceutical compositions and vaccines for S. pneumoniae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQ ID NO:1 to 391 (AAV52134 to AAV52524) are genomic fragments from Streptococcus pneumoniae. The present invention also describes an isolated nucleic acid molecule encoding a homologue of any of the fragments of the S.pneumoniae genome (SEQ ID NO:1 to 391) where the nucleic acid molecule is produced by a process comprising: (a) screening a genomic DNA library using as a probe a target sequence defined by any of the sequences in SEQ ID NO:1 to 391, identifying members of the library which contain sequences that hybridise to the target sequence and isolating the nucleic acid molecules from the members; or (b) isolating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Computer-readable medium with recorded Streptococcus pneumoniae polynucleotide sequences - useful in diagnostic kits and assays, pharmaceutical compositions and vaccines for Streptococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Streptococcus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 1; Page 1284-1285;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (HUMA-) HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            present invention describes a computer readable medium which has nucleotide sequences SEQ ID NO:1 to 391 (AAVS2134 to AAVS2524) orded on it, or a representative fragment or a sequence at least 95% ntical to SEQ ID NO: 1 to 391. The nucleotide sequences depicted in
1689 ATAAGGAAAAAGTTGCAGCTCAAGCCTATACTAAAGAAAAAGGTATCCTACCTCCATCTC 1748
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SC,
                                                                                                                          ATGCATATGTAACGCCTCATATGGGCCATAGTCACTGGATTGGAAAAGATAGCCTTTCTG
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                                                              ATGCCTATGTAACTCCACATATGACCCATAGCCACTGGATTAAAAAAGATAGTTTGTCTG
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Rosen CA;
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                                                                                                                                                                                                                         Score 243.4; DB 1
Pred. No. 4.2e-51;
                                                                                                                                                                                            Mismatches
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RESULT 40
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24-NOV-2000;
07-MAR-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Streptococcus bacteria, particularly S. agalactiae and S. pyrogenes. Nucleic acids encoding (I) are used to detect Streptococcus in a biological sample. (I) is used to determine whether a compound binds t (I). A composition comprising (I) or a nucleic acid encoding (I), may used as a vaccine or diagnostic composition. The disease caused by Streptococcus that is prevented or treated may be meningitis. Nucleic acid encoding (I) may be used to recombinantly produce (I) and may be used in gene therapy. Antibodies to (I) are used for affinity chromosography, immunoassays, and distinguishing/identifying
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The invention relates to a protein (ABP25413-ABP30895) from group B streptococcus/GBS (Streptococcus agalactiae) or group A streptococcus/GAS (Streptococcus proteins) or group A streptococcus yogenes), comprising one of 5483 sequences (S1), given in the specification. The proteins have antibacterial and antiinflammatory activity. (I), nucleic acids encoding (I), ABN66044-ABN71556 and antibodies that bind (I) are used in the manufacture of medicaments for the treatment or prevention of infection or disease caused by
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         The sequence encodes Streptococcus pyogenes Group A Streptococci protein 36, GAS36. A recombinant cell producing GAS36, GAS36(2) or GBS36 is useful as a vaccine for vaccinating an animal, preferably a human against infection by a bacterial organism such as a streptococcal or staphylococcal bacteria, and for treating a disease caused by group A streptococci, group B streptococci or Staphylococcus aureus in an animal preferably a human. Vaccines and antibodies against the proteins of the invention are useful in prophylaxis and/or treatment of diseases such as necrotising fascilitis, scarlet fever, sepsis, impetigo, bacterial meningitis, otitis media, community-acquired pneumonia and many diseases
                                                                                                                                                                                       New polypeptides obtained from group A or B streptococci , especially Staphylococcus aureus homologous to Sp36 protein of Streptococcus pneumoniae useful as antibacterial vaccines -
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 meningitis, of newborns.
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Matches 402;
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               Group B Streptococcus; Streptococcus agalactiae; protein vaccine; screening; immunogen; detection; diagnosis; infe antibody; affibody; antibacterial; ds.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New Group B Streptococcus protein, useful as vaccine, for diagnosis of Streptococcal infections and for screening of antibodies or affibodies
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19-MAR-1999;
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 TGGTGCTGTTGGCACGTTCGCAAGGACGCTATACTACAGATGATGGTTATATCTT
                                AACTAAAGAAGCTAAAGAAAAAGGTTTAGCTCAAGTGGCCCATCTCAGTAAAGAAGAAGT
                                                                 TAGTCAACATCGTGAAG----
                                                                                                AGGTAGTAAGCGCAAAAACATTCGAACCAAACAACAATTGCTGAGCAAGTAGCCAAAGG
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Streptcoccus/GBS (Streptcoccus agalactiae) or group A streptcoccus/GBS (Streptcoccus) agalactiae) or group A streptcoccus/GAS (Streptcoccus/GAS (Streptcoccus) comprising one of 5483 sequences (S1), given in the specification. The proteins have antibacterial and antiinflammatory activity. (I), nucleic acids encoding (I), ABN66044-ABN71526 and antibodies that bind (I) are used in the manufacture of medicaments for the treatment or prevention of infection or disease caused by Streptcoccus bacteria, particularly S. agalactiae and S. pyrogenes. Nucleic acids encoding (I) are used to detect Streptcoccus in a composition comprising (I) or a nucleic acid encoding (I), may be used as a vaccine or diagnostic composition. The disease caused by Streptcoccus that is prevented or treated may be meningitis. Nucleic acid encoding (I) may be used to recombinantly produce (I) and may be used in gene therapy. Antibodies to (I) are used for affinity chromatography, immunoassays, and distinguishing/identifying
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24-NOV-2000;
07-MAR-2001;
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                                                                                                                                                                                                                                                                                                                            Claim 7; Page 3860-3861; 4525pp; English.
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       the treatment or prevention of infection or disease caused by Streptococcus bacteria, particularly S. agalactiae and S. pyrogenes. Nucleic acids encoding (I) are used to detect Streptococcus in a biological sample. (I) is used to determine whether a compound binds to (I). A composition comprising (I) or a nucleic acid encoding (I), may be used as a vaccine or diagnostic composition. The disease caused by Streptococcus that is prevented or treated may be meningitis. Nucleic acid encoding (I) may be used to recombinantly produce (I) and may be used in gene therapy. Antibodies to (I) are used for affinity chromatography, immunoassays, and distinguishing/identifying
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 2466 BP; 841
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The invention relates to a protein (ABP25413-ABP30895) from group B streptococcus/GBS (Streptococcus agalactiae) or group A streptococcus/GBS (Streptococcus agalactiae) or group A streptococcus/GBS (Streptococcus agalactiae) or group A streptococcus possible of S483 sequences (S1), given in the specification. The proteins have antibacterial and antiinflammatory activity. (I), nucleic acids encoding (I), ABN66044-ABN71526 and antibodies that bind (I) are used in the manufacture of medicaments for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Telford J,
Tettelin H;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            27-OCT-2000; 2000GB-0026333.
24-NOV-2000; 2000GB-0028727.
07-MAR-2001; 2001GB-0005640.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The invention relates to a protein (ABP25413-ABP30895) from
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P-PSDB; ABP29703.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            w Streptococcus protein for the treatment or prevention of infection disease caused by Streptococcus bacteria, such as meningitis, and r detecting a compound that binds to the protein -
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INST GENOMIC RES
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TGAAATCTTAGACGGTTACGTTATTAAAGTCAATGGCAACTATTATGTTTACCTCAAGCC
                              TGAGGTCAAGGGTGGATATGTTATCAAGGTAGATGGAAAATACTATGTTTACCTTAAGGA 357
                                                                                                                                      TACCTCACACGGTGACCATTATCATTTTACAATGGGAAAGTTCCTTATGATGCGATTAT
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                                                                                                                                                                                                                                                                                                                                                TTACCAGCTTGGTAAGCATCATATGGGTCTAGCAACAAAGGACAATCAGATTGCCTATAT
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                 in AAY91275 to AAY91343) isolated from Group B Streptococcus (GBS), als known as Streptococcus agalactiae. The GBS polynucleotides and polypeptides have antibacterial activity. Immunogenic compositions comprising GBS polynucleotides or polypeptides can be used as vaccines and for the treatment or prophylaxis of GBS infection. The polynucleotides and polypeptides can also be used in the detection of G and for screening DNA encoding bacterial cell envelope associated or secreted antigens in gram positive bacteria. AAA05873 to AAA05941 represent primers used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Group B Streptococcus; Streptococcus agalactiae; protein antigen; vaccine; screening; immunogen; detection; diagnosis; infection;
                                                                                                                                                                                                                                                                                                                                            Claim 4;
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Streptococcal infections a
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antibody; affibody; antibacterial;
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in AAY91275 to AAY91343) isolated fro
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                                        Streptococcus
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Location/Qualifiers 1..2469
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Pred. No. 6e-
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The sequence encodes Streptococcus agalactiae Group B Streptococci protein 36, GBS36. A recombinant cell producing GAS36, GAS36(2) or GBS36 is useful as a vaccine for vaccinating an animal, preferably a human against infection by a bacterial organism such as a streptococcal or staphylococcal bacteria, and for treating a disease caused by group A streptococci, group B streptococci or staphylococcus aureus in an animal preferably a human. Vaccines and antibodies against the proteins of the invention are useful in prophylaxis and/or treatment of diseases such as mecrotising fasciitis, scarlet fever, sepsis, impetigo, bacterial meningliis, otitis media, community-acquired pneumonia and many diseases of newborns. The proteins are also used as immunogens to stimulate the production of antibodies for use in passive immunotherapy, for use as diagnostic reagents and for use as reagents in other processes such as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New polypeptides obtained from group A or B Staphylococcus aureus homologous to Sp36 propneumoniae useful as antibacterial vaccines
                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          affinity chromatography.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 10; Page 53-54; 62pp; English
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                                        TGAGGTCAAGGGTGGATATGTTATCAAGGTAGATGGAAAATACTATGTTTACCTTAAGGA 357
                                                                                                                                               CAGTGAAGAATTACTCATGAAAGATCCAAACTATAAGCTAAAAGATGAGGATATTGTTAA
                                                                                                                                                                            TACCTCACACGGTGACCATTATCATTTTACAATGGGAAAGTTCCTTATGATGCGATTAT
                                                                                                                                                                                                    CACTTCACATGGCGACCACTATCATTATTACAATGGTAAGGTTCCTTATGACGCTATCAT
                                                                                                                                                                                                                                                        CAAGCGTGAAGGAATCAATGCTGAGCAAATCGTCATCAAGATAACAGACCAAGGCTATGT
                                                                                                                                                                                                                                                                                     2469 BP; 844 A; 477 C; 514 G;
               AGGTAGTAAGCGCAAAAACATTCGAACCAAACAACAATTGCTGAGCAAGTAGCCAAAGG
                                                                                                                                                                                                                              TGCTGAAGAAGGCATCTCTGCTGAACAGATCGTAGTCAAAATTACTGACCAAGGTTATGT
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                                                                                                                                                                                                                                                                                                                                                                                           Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                       8.8%;
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to Sp36 protein of Streptococcus
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                                                                                                                                                                                                                                                                                                                                                                                                     New Streptococcus protein for the treatment or prevention of inf
or disease caused by Streptococcus bacteria, such as meningitis,
for detecting a compound that binds to the protein -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         27-OCT-2000; 2000GB-0026333
24-NOV-2000; 2000GB-0028727
07-MAR-2001; 2001GB-0005640
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Streptococcus; GAS; GBS; grogroup A streptococcus; Streptantinflammatory; infection;
        the treatment or prevention of infection or disease caused by Streptococcus bacteria, particularly S. agalactiae and S. pyrogenes. Nucleic acids encoding (I) are used to detect Streptococcus in a biological sample. (I) is used to determine whether a compound binds (I). A composition comprising (I) or a nucleic acid encoding (I), maused as a vaccine or diagnostic composition. The disease caused by
                                                                                                                                                             The invention relates to a protein (ABP25413-ABP30895) from group B streptococcus/GBS (Streptococcus agalactiae) or group A streptococcus/GAS (Streptococcus sugalactiae) or group A streptococcus (S1), given in (Streptococcus pyogenes), comprising one of 5483 sequences (S1), given in the specification. The proteins have antibacterial and antiinflammatory activity. (I), nucleic acids encoding (I), ABN66044-ABN71526 and antibodies that bind (I) are used in the manufacture of medicaments for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Streptococcus sp
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INST GENOMIC RES
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Best Local Simi
Matches 400;
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Pred. No. 1.2e-
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Streptococcus pneumoniae; BVH-3; prophylaxis; therapy; infection;

BVH-11; BVH-28; antigen; vaccine; diagnosis; meningitis; bacteraemia;

Streptococcus

pneumoniae GBS

BVH-71

gene SEQ

ij

NO:80

(first

entry)

AAA65740

standard;

DNA;

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Query Match
Best Local S
Matches 399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present invention describes nucleic acids (I) encoding protein antigens (II) from Streptococcus pneumoniae. The protein antigens have bactericidal activity. The nucleic acids, encoding the protein antigens, may be used for the recombinant production of the proteins they encode. The protein antigens may then be used as vaccines for the prevention and treatment of Streptococcal infections in mammals (especially humans) which result in, e.g. meningitis, otitis media, bacteraemia and/or pneumonia. The present sequence encodes the S. pneumoniae GBS BVH-71 protein antigen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 2469 BP; 842 A; 481 C; 519 G; 627 T; 0 other;
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TGGTGCTGTTGGCCTTGGCACGTTCGCAAGGACGCTATACTACAGATGATGGTTATATCTT
                          AACTAAAGAAGCTAAAGAAAAAGGTTTAGCTCAAGTGGCCCATCTCAGTAAAGAAGAAGT
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Pred. No. 1.5e-42;
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WPI; 1999-540309/45.
P-PSDB; AAY27346, AAY27347, AAY27348, AAY27349, AAY27350, AAY27351,
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                            TTACCATTACATTCCTAAGAATGAGTTATCAGCTAGCGAGTTGGCTGCTGCAGAAGCCTT
                                                                                                               TAATGCTTCTGATATCATAGAGGATACTGGTGATGCTTATATATCGTTCCTCATGGAGATCA
                                                                                                                                                        TGCGGCAGTCAATGAAGCAAAAAGACAAGGACGCTATACTACAGACGATGGCTATATTTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                provides Group B Streptococcus (GBS) antigens and nucleic acids (AAX91103-X91111) encoding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Streptococcus antigens - useful as vaccine for prophylaxis or therapy of Streptococcus infections
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Matches 397
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Streptococcus pneumoniae; BVH-3; BVH-11; BVH-28; antigen; vaccine; prophylaxis; therapy; infection; diagnosis; meningitis; bacteraemia; otitis media; pneumonia; immunisation; bactericidal; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Streptococcal antigens useful for vaccinating against otitis media, bacteremia and/or pneumonia -
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                                          GACCTCACACGGTGACCATTATCATTTTTACAATGGGAAAGTTCCTTATGATGCGATTAT
                                                                               CACTTCACATGGCGACCACTATCATTATTACAATGGTAAGGTTCCTTATGACGCTATCAT
                                                                                                                                                                                                           AGATGGAAAACAAGCGACGCAAAAA-----ACGGAGAATTTGACTCCTGATGAGGTTAG
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nilarity 60.1%;
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| Search completed: November 13, 2003, 21:21:13<br>Job time : 726 secs | 726 C 726 | 634 C 634 | 666 CTATCATTATATTCCTAAAAAAGATTTGTCTCCAAGTGAGCTAGCT | 574 TTACCATTACATTCCTAAGAATGAGTTATCAGCTAGCGAGTTGGCTGCAGAAGCCCTT 633 | 606 TAGTCCGACAGATATCATTGATGATTTAGGAGACGCTTATTTAGTACCTCATGGTAATCA 665 | 514 TAATGCTTCTGATATCATAGAGGATACTGGTGATGATGATATATCGTTCCTCATGGAGATCA 573 | 546 TGCGGCAGTCAATGAAGCAAAAAAGACAAGGACGCTATACTACAGACGATGGCTATATTTT 605 | 454 TGGTGCTGTGCCTTGGCACGTTCGCAAGGACGCTATACTACAGATGATGATGTTATATCTT 513 | 486 AACTAAAGAAGCTAAAGAAAAAGGTTTAGCTCAAGTGGCCCATCTCAGTAAAGAAGAAGT 545 | 418 TAGTCAACATCGTGAAG | 426 AGGTAGTAAGCGCAAAAACATTCGAAACCAAACAAATTGCTGAGCAAGTAGCCAAAGG 485 | 358 TGCTGCCCACGCGGATAACGTCCGTACAAAAGAGGAAAATCAATC | 366 TGAAATCTTAGACGGTTACGTTATTAAAGTCAATGGCAACTATTATGTTTACCTCAAGCC 425 | 298 TGAGGTCAAGGGTGGATATGTTATCAAGGTAGATGGAAAATACTATGTTTACCTTAAGGA 357 | 306 TAGTGAAGAGTTGTTGATGACGGATCCTAATTACCATTTTAAACAATCAGACGTTATCAA 365 |
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Entamoeba histolytica
Entamoeba histolytica
                                                                                                                                                                                        Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville,
Tel: 301 838 0208
Fax: 301 838 3543
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ENTTS83TF Entamoeba histolytica (
genomic, genomic survey sequence.
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                                                                                                                                                                                                                                    Contact: Brendan J Loftus
                                                                                                                                                                                                                                                                                                                    BH153606.1 GI:15725323
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                                                                                                                                                                                   Email: bjloftus@tigr.org
                                                                                                                                                                                                                                           Unpublished
                                                                                                                                                                                                                                                           Loftus,B., Wang,Z., Van Aken,S. and Fraser,C. Determination of clone end sequences from Ent
                                                                                                                                                                                                                                                                          Eukaryota; Entamoebidae; Entamoeba
1 (bases 1 to 906)
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/clone_lib="Entamoeba histolytica Sheared DNA"
/note="Vector: pHOS1; Site_l: Bst_l: Constructed at The
Institute for Genomic Research (TIGR), Rockville, MD.
Genomic DNA isolated from broth cultures of E. histolytica
using a method described by Clark and Diamond (Clark,
C.G., and Diamond, L.S. (1993) Entamoeba histolytica: a
method for isolate identification. Exp. Parasitol.
77:450). The DNA was mechanically sheared to give a
tight size distribution (~2 kb). The v + i method used for
the library construction is described in detail in Smith,
                                                                                          /mol_type="genomic
/strain="HM1:IMSS"
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Sequencing: A Practical Approach, eds. M. Vaudin
Barell, Oxford University Press, 1999)."
293 c 66 g 398 t
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Eukaryota; Entamoebidae; 1 (bases 1 to 890) Loftus, B., Wang, Z., Van ! 890 bp DNA ENTPK48TF Entamoeba histolytica Sheared genomic, genomic survey sequence. Entamoeba histolytica histolytica GI:15302963 Aken, S. and Fraser, C. Entamoeba DNA Entamoeba histolytica

linear

GSS 27-AUG-2001

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BASE COUNT
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Clones are derived from 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Department of Bukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: Brendan J Loftus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Determination of HM1:IMSS sheared
ATATTAAATTTGCTTGGTTTGATGATCACACATACAAAGCTCCAAATGGCTATACCTTGG
                                                                                                                                                                            TTTACAATCGTGTGAAAGGGGAAAAACGAATTCCACTCGTTCGACTTCCATATATGGTTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /Clone_lib="Entamoeba histolytica Sheared DNA"
/note="Vector: pHOS1; Site 1: Bst I; Constructed at The
Institute for Genomic Research (TIGR), Rockville, MD.
Genomic DNA isolated from broth cultures of E. histolytic
using a method described by Clark and Diamond (Clark,
C.G., and Diamond, L.S. (1993) Entamoeba histolytica: a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         method for
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Pred. No. 0.00018;
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Leptospira interrogans serovar lai
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West China University of Med
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27 c
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/note="obtained through DNA subtraction using the
nonpathogenic strain Leptospira biflexa serovar Pat
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Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Loftus, B., Van Aken, S. and Fraser, C. Determination of clone end sequences HM1: IMSS sheared DNA library
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1 (bases 1 to 908)
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                                   TAAAGCAAATCCAACTGGAGATAGTGCAGCAGCTATTTACAATCGTGTGAAAAGGGGAAAA 1821
                                                                                                            TGCAGCTCAAGCCTATACTAAAGAAAAAGGTATCCTACCTCCATCTCCAGACGCAGATGT 1761
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /clone_lib="Entamoeba histolytica Sheared DNA"
/note="Vector: pHOS1; Site_1: Bst_I; Constructed at The
Institute for Genomic Research (TIGR), Rockville, MD.
Genomic DNA isolated from broth cultures of E. histolytica
using a method described by Clark and Diamond (Clark,
C.G., and Diamond, L.S. (1993) Entamoeba histolytica: a
method for isolate identification.
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/mol_type="genomic DNA"
/strain="HM1:IMSS"
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196; Conserv
                                                                                                                                                                                                                                                                               Campus, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enqui
humquery@sanger.ac.uk Unpublished
This sequence was generated from the SP6 end of BAC 150M6.
part of the Daniokey BAC Library created by R. Plasterk and
                                                                                                                                                                                                                                                                                                                            Submitted (13-MAR-2003) The Sanger Institute, Campus, Hinxton, Cambridgeshire, CB10 1SA, UK.
                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes; Cyprinidae; Danio.

1 (bases 1 to 829)
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Danio rerio
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                                                      Conservative
                                                                                                                          /tissue_type="Testis"
/note="vector pIndigoBAC-536"
103 c 32 g 434 t
                                                                                                                                                                   /mol_type="genomic DNA"
/db_xref="taxon:7955"
/clone="DKEY-150M6"
                                                                                                                                                                                                              /organism="Danio rerio'
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                                                   Score 66.4; DB 29;
Pred. No. 0.00097;
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Fax:
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1 (bases 1 to 843)

Loftus, B., Van Aken, S. and Fraser, C. Determination of clone end sequences
HM1: IMSS sheared DNA library
                                                                                                                                                                                                                                                                                                          Email: bjloftus@tigr.org Clones are derived from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Entamoeba histolytica
Entamoeba histolytica
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GSS.
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                                                                                                                                                                                                                                                                  Class: shotgun
                                                                                                                                                                                                                                                                                                                                                                           Department of Eukaryotic Genomics
The Institute for Genomic Research
                                                                                                                                                                                                                                                                                                                                                                                                       Contact: Brendan J Loftus
                                                                                                                                                                                                                                                                                                                                                                                                                  Unpublished
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                                                                                                                                                                                                                          quality sequence start: 39 quality sequence stop: 838 Location/Qualifiers
        /clone lib="Entamoeba histolytica Sheared DNA"
/note="Vector: pHOS1; Site 1: Bst I; Constructed at The
Institute for Genomic Research (TIGR), Rockville, MD.
Genomic DNA isolated from broth cultures of E. histolytica
using a method described by Clark and Diamond (Clark,
C.G., and Diamond, L.S. (1993) Entamoeba histolytica: a
method for isolate identification. Exp. Parasitol.
77:450.). The DNA was mechanically sheared to give a
tight size distribution (-2 kb). The v + i method used for
the library construction is described in detail in Smith,
H.O. and Venter, J.C. (Making small insert libraries for
                                                                                                                                                          /mol_type="genomic DN:
/strain="HM1:IMSS"
/db_xref="taxon:5759"
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Eukaryota; Entamoebid
                                                 genomic, genomic survey
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ATGATGAAGATGAAGATGAAGATGAAGATGAAGATGAAGACGACGAATATAATT
                             <u>ATGAAGAGCCAGTAGAGGAAACACCTGCTGAGCCAGAAGTCCCTCAAGTAGAGACTGAAA</u>
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Barell, Oxford University Press, 1999)
a 266 c 18 g 404 t
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High quality sequence stop: (
Location/Qualifiers
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The Institute for Genomic Research
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Contact: Brendan J Loftus
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                                CCTCATAAGGATCATTACCATAATATTAAATTTGCTTGGTTTGATGATCACACATACAAA 1954
 GAAGATGATGAAGATGATGAAGAAGAAGAAGATGATGAAGATGAAGATGAAGACGAT
                                                                                                    GTTCGACTTCCATATATGGTTGAGCATACAGTTGAGGTTAAAAAACGGTAATTTGATTATT 1894
                                                                                                                                      ACTGGAGATAGTGCAGCAGCTATTTACAATCGTGAAAGGGGAAAAACGAATTCCACTC 183
                                                                                                                                                                                                         TATACTAAAGAAAAAGGTATCCTACCTCCATCTCCAGACGCAGATGTTAAAGCAAATCCA 1774
                                                                                                                                                                                                                                                                            GATGATGAAGAAGAAGATGATGAAGATGAAGATGAAGACGATGAAGACGACGAA
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/note="Vector: pHOS1; Site_1: Bst 1; Constructed at The
Institute for Genomic Research (TIGR), Rockville, MD.
Genomic DNA isolated from broth cultures of E. histolytica
using a method described by Clark and Diamond (Clark,
C.G., and Diamond, L.S. (1993) Entamoeba histolytica: a
method for isolate identification. Exp. Parasitol.
77:450.). The DNA was mechanically sheared to give a
tight size distribution (-2 kb). The v + i method used for
the library construction is described in detail in Smith,
H.O. and Venter, J.C. (Making small insert libraries for
whole genome sebterum sequencing.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 whole genome shotgun sequencing projects. In Ger
Sequencing: A Practical Approach, eds. M. Vaudin
Barell, Oxford University Press, 1999)."
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/strain="HM1:IMSS"
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Pred. No. 0.0036;
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Loftus,B., Van Aken,S. and Fraser,C.
Determination of clone end sequences
HM1:IMSS sheared DNA library
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AZ551092 912 bp DNA linear GS ENTFJ22TF Entamoeba histolytica Sheared DNA Entamoeba
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Tel: 301 838 0208
Fax: 301 838 3543
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Department of Eukaryotic Genomics
The Institute for Genomic Research
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Entamoeba histolytica
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Email: bjloftus@tigr.org
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method for isolate identification. Exp. Parasitol. 77:450.). The DNA was mechanically sheared to give a right size distribution (~2 kb). The v + i method used for the library construction is described in detail in Smith, H.O. and Venter, J.C. (Making small insert libraries for whole genome shorgun sequencing projects. In Genome Sequencing: A Practical Approach, eds. M. Vaudin and B. Barell, Oxford University Press, 1999)."
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/clone lib="Entamoeba histolytica Sheared DNA"
/clone lib="Entamoeba histolytica Sheared DNA"
/note="Vector: pHOS1; Site 1: Bst I; Constructed at The
Institute for Genomic Research (TIGR), Rockville, MD.
Genomic DNA isolated from broth cultures of E. histolytica
using a method described by Clark and Diamond (Clark
C.G., and Diamond, L.S. (1993) Entamoeba histolytica: a
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strain="HM1:IMSS"
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Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville
                                                           Unpublished
Contact: Brendan J Loftus
                                                                                                      Eukaryota, Entamoebidae, Entamoeba.

(bases 1 to 849)

Loftus, B., Van Aken, S. and Fraser, C. Determination of clone end sequences

HM1:IMSS sheared DNA library
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Medical Center Dr., Rockville,
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Pred. No. 0.0082;
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MD 20850, USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Email: bjloftus@tigr.org
Clones are derived from the Entamoeba histolytica HM1:IMSS sheared
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      High quality sequence
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Fax: 301 838 3543
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DNA library
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GGTATCCTACCTCCATCTCCAGACGCAGATGTTAAAGCAAATCCAACTGGAGATAGTGCA 1789
                                                                                                                                                                                                                      GATGATGAAGATGAAGATGAAGATGAAGATGAAGATGAAGATGAAGATGAA
                                                                                                                                                                                                                                                        ATTGCTCAATTAGCTGATAAGTATACAACGTCAGATGGTTACATTTTTGATGAACATGAT
                                                                                                                                                                                                                                                                                                        AATAAGGGTCGTAATTCTGATTTCCAAGCCTTAGACAATTATTAGAACGCTTGAATGAT 1429
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                                           GGAAAAGATAGCCTTTCTGATAAGGAAAAAGTTGCAGCTCAAGCCTATACTAAAGAAAAA 1729
                                                                                                                               ATAATCAGTGATGAAGGAGATGCATATGTAACGCCTCATATGGGCCCATAGTCACTGGATT
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/note="Vector: pHOS1; Site 1: Bst I; Constructed at The
/note="Vector: pHOS1; Site 1: Bst I; Constructed at The
Institute for Genomic Research (TIGR), Rockville, MD.
Genomic DNA isolated from broth cultures of E. histolytica
using a method described by Clark and Diamond (Clark,
C.G., and Diamond, L.S. (1993) Entamoeba histolytica: a
method for isolate identification. Exp. Parasitol.
77:450.) The DNA was mechanically sheared to give a
tight size distribution (~2 kb). The v + i method used for
the library construction is described in detail in Smith,
H.O. and Venter, J.C. (Making small insert libraries for
whole genome shotgun sequencing projects In Genome
Sequencing: A Practical Approach, eds. M. Vaudin and B.
Barell, Oxford University Press, 1999)."
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'strain="HM1:IMSS"
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                                 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville,
Tel: 301 838 0208
Fax: 301 838 3543
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GSS
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ENTQV49TR Entamoeba histolytica
genomic, genomic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Class: shotgun
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Email: bjloftus@tigr.org
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: .Brendan J Loftus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Loftus, B., Wang, Z., Van Aken, S. and F
Determination of clone end sequences
HM1:IMSS sheared DNA library (2001)
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GCAGCTCAAGCCTATACTAAAGAAAAAGGTATCCTACCTCCATCTCCAGACGCAGATGTT 1762
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                                GATGATGATGAAGAAGAAGAAGATGATGATGAAGATGAAGACGATGAAGACGACGAA
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                                                                                                                                                               Conservative
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/note="Vector: pHOS1; Site_1: Bst I; Constructed at The
Institute for Genomic Research (TIGR), Rockville, MD.
Genomic DNA isolated from broth cultures of E. histolytica
using a method described by Clark and Diamond (Clark,
C.G., and Diamond, L.S. (1993) Entamoeba histolytica: a
method for isolate identification. Exp. Parasitol.
77:450.). The DNA was mechanically sheared to give a
tight size distribution (~2 kb). The v + i method used for
                                                                                                                                                                                                                                             the library construction is described in detail in Smith, H.O. and Venter, J.C. (Making small insert libraries for whole genome shotgun sending projects. In Genome Sequencing: A Practical Approach, eds. M. Vaudin and B. Barell, Oxford University Press, 1999)."

51 c 279 g 199 t
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'strain="HM1:IMSS"
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Sheared DNA Entamoeba histolytica
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1883 AATTTGATTATTCCTCATAAGGATCATTACCATAATATTAAATTTTGCTTGGTTTGATGAT 1942
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617 GAAGATGATGAAGATGAAGATGAAGATGAAGATGATGAAG 656
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Contact: Brendan J Loftus
Department of Eukaryotic Genomics
The Institute for Genomic Research
                                                    Unpublished
                                                                   1 (bases 1 to 900)

Loftus, B., Van Aken, S. and Fraser, C.

Determination of clone end sequences

HM1:IMSS sheared DNA library
                                                                                                                                                            Entamoeba histolytica
Entamoeba histolytica
                                                                                                                                                                                               GSS
                                                                                                                                                                                                                                                                     AZ549980 900 bp DNA ENTDD94TF Entamoeba histolytica Sheared
                                                                                                                                                                                                                  AZ549980
AZ549980.1 GI:11175122
                                                                                                                                             Eukaryota; Entamoebidae; Entamoeba
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/mol_type="genomic DNA"
/db_xref="taxon:7227"
/clone="BACRO8K10"
/clone lib="RPCI-98"
/note="end: TET3"
a 64 c 131 g 202 t 503 ot
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Best Local Sim
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Tel: 301 838 0208
Fax: 301 838 3543
Email: bjloftus@tigr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Clones are derived
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                                                                                                                                                                                                              ACGATGATGAAGACGATGAAGACGATGAAGACGATGAAGACGATGAAGACGATGAAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Genomic DNA isolated from broth cultures of E. histolytica using a method described by Clark and Diamond (Clark, C.G., and Diamond, L.S. (1993) Entamoeba histolytica: a method for isolate identification. Exp. Parasitol. 77:450.) The DNA was mechanically sheared to give a tight size distribution (~2 kb). The v + i method used for the library construction is described in detail in Smith, H.O. and Venter, J.C. (Making small insert libraries for whole genome shotgun sequencing projects. In Genome Sequencing: A Practical Approach, eds. M. Vaudin and B. Barell, Oxford University Press, 1999)."
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/note="Vector: pHOS1; Site_1: Bst I; Constructed &
Institute for Genomic Research (TIGR), Rockville,
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/strain="HM1:IMSS"
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The Institute for Genomic Research
9712 Medical Center Dr., Rockville,
Tel: 301 838 0208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Class: shotgun
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Contact: Brendan J Loftus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SSD
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AZ550256
AZ550256.1 GI:11175557
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Email: bjloftus@tigr.org
Clones are derived from the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Loftus, B., Van Aken, S. and Fraser, C. Determination of clone end sequences
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1 (bases 1 to 905)
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  TATGATAAAGCATATAATCTGTTAACTGAGGCTCATA-----AAGCCTTGTTTGNA 1369
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /clone_lib="Entamoeba histolytica Sheared DNA" /note="Vector: pHOS1; Site_l: Bst I; Constructed at The Institute for Genomic Research (TIGR), Rockville, MD. Genomic DNA isolated from broth cultures of E. histolytic using a method described by Clark and Diamond (Clark, C.G., and Diamond, I.S. (1993) Entamoeba histolytica: a
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Sequencing: A Practical Approach, eds. M. Vaudin an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Entamoeba histolytica"
/mol_type="genomic DNA"
/strain="HM1:IMSS"
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Parasite Genomics Group
The Institute for Genomic Research
9712 Medical Center Drive, Rockville,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Carlton,J.M., Daly,T.M., Long,C.A., Bergman,L.W., Fraser,C.M. and Carucci,D.J.
Plasmodium yoelii EST project at TIGR
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Plasmodium yoelii yoelii
Eukaryota, Alveolata; Apicomplexa; Haemosporida; Plasmodium.
1 (bases 1 to 645)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Unpublished
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Email: carlton@tigr.org
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Fax: 301-838-0208
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                                                                                                           /note="Vector: pAD-GAL4; At 20-25% parasitemia, blood collected from BALB/cByJ mice infected with Py17XL parasites, and leukocytes removed by passage over microcrystalline cellulose collumns. Total RNA was isolated using the guanidinium isothiocyanate method,
                                                        mRNA isolated using oligo(dT)-cellulose chromatography First strand cDNA synthesis was completed using a 50-ba primer and reverse transcriptase in the presence of
                     5-methyl dCTP. After second strand synthesis, uneven termini were treated with Pfu DNA polymerase and Ecol
adaptors ligated to the blunt ends.
                                                                                                                                                                                                                       /dev stage="Asexual blood stages"
/lab_host="E. coli XL-1 Blue"
/clone_lib="FyBS"
                                                                                                                                                                                                                                                                                                                                             mol_type="mRNA"
                                                                                                                                                                                                                                                                                                                                                                      organism="Plasmodium yoelii yoelii"
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Plasmodium yoelii yoelii cDNA clone PYCML60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           167
                                                                                                                                                                                  Email: cariton@tigr.org
Email: cariton@tigr.org
For clone info, please contact the
For clone info, please contact the
                                                                                                                                                                                                                                                                                  Parasite Genomics Group
The Institute for Genomic Research
9712 Medical Center Drive, Rockville,
                                                                                                                                                                                                                                                                                                                                                                                                         1 (bases 1 to 747)
Carlton, J.M., Daly, T.M., Long, C.A., Bergman, L.W.,
Fraser, C.M. and Carucci, D.J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BM162732.1 GI:17308413
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Plasmodium yoelii yoelii
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Eukaryota, Alveolata, Apicomplexa, Haemosporida, Plasmodium
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EST565255 PyBS Plasmodium yoelii
                                                                                                                                                  http://www.malaria.mr4.org/mr4pages/index.html
Seq primer: ADF.
                                                                                                                                                                                                                                                                      Tel: 301-530-9319
                                                                                                                                                                                                                                                                                                                                                                   Unpublished
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                                                                                                                                                                                                                                                                                                                                                     Contact: Jane Carlton
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                                                                            /organism="Plasmodium
/mol type="mRNA"
                  /db_xref="taxon:73239"
/clone="PYCKW24"
                                                        /strain="17XL"
                                                                                                                                Location/Qualifiers
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_stage="Asexual blood stages"
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                                                                                                                                                                                                            Malaria Research
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Contact: Brendan J Loftus
Department of Eukaryotic Genomics
The Institute for Genomic Research
                                                                                  1 (bases 1 to 816)
Loftus,B., Van Aken,S. and Fraser,C.
Determination of clone end sequences
HMI: MSS sheared DNA library
                                                                                                                                                                              Entamoeba histolytica
Entamoeba histolytica
Eukaryota; Entamoebidae; Entamoeba
                                                                                                                                                                                                                                                                                                                                          AZ535744 816 bp DNA linear GSS 03-NOV-2000 ENTCQ25TR Entamoeba histolytica Sheared DNA Entamoeba histolytica
                                                                                                                                                                                                                                                                                                  genomic, genomic AZ535744
                                                                      Unpublished
                                                                                                                                                                                                                                                                            AZ535744.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GAGGATGAAGATGAAGAAGATGACGATGATTCTAAAAAAGAAGATGGATCAAATGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GATGATGATGACGACGATGAAGATGACGATGAAGACGATGATGAAGACGACGATGAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAACAAGAGCATAGTCAACATCGTGAAGGTGGAACTCCAAGAAACGATGGTGCTGTTGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  5-methyl dCTP. After second strand synthesis, uneven termini were treated with Pfu DNA polymerase and EcoRI adaptors ligated to the blunt ends. The sample was cleaved with XhoI and separated on a Sephacryl S-500 column. Size-fractionated cDNA was precipitated and ligated to HybriZAP arms directionally using EcoRI-XhoI cleaved arms. After packaging, the phagemid vector (pAD-GAL4) was excised from the HybriZAP vector and plasmid DNA isolated."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /clone_lib="PyBS"
/note="Vector: pAD-GAL4; At 20-25% parasitemia, blc
collected from BALB/cByJ mice infected with Py17XL
parasites, and leukocytes removed by passage over
microcrystalline cellulose collumns. Total RNA was
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              isolated using the guanidinium isothiocyanate method, and mRNA isolated using oligo(dT)-cellulose chromatography. First strand cDNA synthesis was completed using a 50-base
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /lab_host="E. coli XL-1 Blue"
                                                                                                                                                                                                                                                                          GI:11092691
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Class: shotgun
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ACGATGATGAAGAAGACGATGATGAAGAAGACGATGATGAAGAAGACGATGATGAAGAAG
                                                GCTATACCTTGGAAGATTTGTTTGCGACGATTAAGTACTACGTAGAACACCCTGACGAAC
                                                                                                       ACGATGATGAAGAAGACGATGATGAAGAAGACGATGATGAAGAAGACGATGATGAAGAAG
                                                                                                                                                        ATCATTACCATAATATTAAATTTGCTTGGTTTGATGATCACACATACAAAGCTCCAAATG
                                                                                                                                                                                                            ACGATGATGAAGAAGACGATGATGAAGAAGACGATGATGAAGAAGACGATGATGAAGAAG
                                                                                                                                                                                                                                                               CATATATGGTTGAGCATACAGTTGAGGTTAAAAAACGGTAATTTGATTATTCCTCATAAGG
                                                                                                                                                                                                                                                                                                                   AATTTGAATTAGAAGACGATGATGAAGAAGACGATGATGAAGAAGAAGACGATGATGAAGAAG
                                                                                                                                                                                                                                                                                                                                                                       GTGCAGCAGCTATTTACAATCGTGAAAGGGGAAAAACGAATTCCACTCGTTCGACTTC 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAAAAGGTATCCTACCTCCATCTCCAGACGCAGATGTTAAAGCAAATCCAACTGGAGATA 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ACGATGAAGAAGACGATGAAGAAGACGATGAAGAAGACGATGAAGAAGACGATGAAGAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GGATTGGAAAAGATAGCCTTTCTGATAAGGAAAAAGTTGCAGCTCAAGCCTATACTAAAAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TTCGTATTGCTCAATTAGCTGATAAGTATACAACGTCAGATGGTTACATTTTTGATGAAC 1604
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /clone lib="Entamoeba histolytica Sheared DNA"
/note="Vector: pHOS1; Site 1: Bst I; Constructed at The
Institute for Genomic Research (TIGR), Rockville, MD.
Genomic DNA isolated from broth cultures of E. histolytica
using a method described by Clark and Diamond (Clark,
C.G., and Diamond, L.S. (1993) Entamoeba histolytica: a
method for isolate identification. Exp. Parasitol.
77:450,). The DNA was mechanically sheared to give a
tight size distribution (~2 kb). The v + i method used for
the library construction is described in detail in Smith,
H.O. and Venter, J.C. (Making small insert libraries for
whole genome shotgun sequencing projects. In Genome
Sequencing: A Practical Approach, eds. M. Vaudin and B.
Barell, Oxford University Press, 1999)."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              are derived from the Entamoeba histolytica HM1: IMSS sheared
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/strain="HM1:IMSS"
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Pred. No. 0.
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The Institute for Genomic Research
9712 Medical Center Drive, Rockvil
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Plasmodium yoelii yoelii
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Plasmodium yoeliata; Apicomplexa; Haemosporida;
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Fax: 301-838-0208
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                                                                                                                         with XhoI and separated on a Sephacryl S-500 column. Size-fractionated cDNA was precipitated and ligated to HybriZAP arms directionally using EcoRI-XhoI cleaved arms After packaging, the phagemid vector (pAD-GAL4) was excised from the HybriZAP vector and plasmid DNA
                                                                                                                                                                                                                               isolated using the guanidinium isothiocyanate method, and mRNA isolated using Oligo(GT)-cellulose chromatography. First strand cDNA synthesis was completed using a 50-base primer and reverse transcriptase in the presence of 5-methyl dCTP. After second strand synthesis, uneven termini were treated with Pfu DNA polymerase and ECORI adaptors ligated to the blunt ends. The sample was cleaved
                                                                                                                                                                                                                                                                                                                                                                          /clone_lib="PyBS"
/note="Vector: pAD-GAL4; At 20-25% parasitemia, blc
collected from BALB/cByJ mice infected with Py17XL
parasites, and leukocytes removed by passage over
microcrystalline cellulose collumns. Total RNA was
                                                                                                        isolated."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           organism="Plasmodium yoelii yoelii"
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lab_host="E. coli XL-1 Blue"
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mRNA sequence.
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Parasite Genomics Group
The Institute for Genomic Research
The Center Drive, Rockville,
                                                                                                                                                                                                                                                                                         http://www.malaria.mr4.org/mr4pages/index.html Seq primer: ADF.
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Fraser, C.M. and Carucci, D.J.
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parasites, and leukocytes removed by passage over microcrystalline cellulose collumns. Total RNA was isolated using the guandidnium isothiocyanate method, an mRNA isolated using oligo(dT) cellulose chromatography. First strand cDNA synthesis was completed using a 50-bai primer and reverse transcriptase in the presence of 5-methyl dCTP. After second strand synthesis. uneven
                                                                                                    /note="Vector: pAD-GAL4; At 20-25% parasitemia, blocollected from BALB/cByJ mice infected with Py17XL
                                                                                                                                                  /dev_stage="Asexual blood stages"
/lab_host="E. coli XL-1 Blue"
                                                                                                                                                                                                                          /organism="Plasmodium yoelii yoelii"
/mol type="mRNA"
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/clone="PYCJO90"
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                                        AAACAAGAGCATAGTCAACATCGTGAAGGTGGAACTCCAAGAAACGATGGTGCTGTTGC
                                                                                                                                  GACGATGATGATGACGACGACGATGAAGATTTTGAAGATATGGATGATGATGATGAT
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Pred. No.
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Contact: Jane Carlton
Parasite Genomics Group
The Institute for Genomic Research
9712 Medical Center Drive, Rockvill
                                                                                                                                                                                                                                                                                                                                                                                                                                             Plasmodium yoelii yoelii
Plasmodium yoelii yoelii
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                                                                                                                                                     For clone info, please contact the Malaria Research and Reference Reagent Resource Center, ATCC
                                                                                                                                                                                                                                                                                                                                Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BM168242.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            mRNA sequence.
                                                                                                                                 http://www.malaria.mr4.org/mr4pages/index.html
                                                                                                                                                                                         Email: carlton@tigr.org
                                                                                                                                                                                                               Fax: 301-838-0208
                                                                                                                                                                                                                                 Tel: 301-530-9319
                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Alveolata; Apicomplexa; Haemosporida;
                                                                                                                                                                                                                                                                                                                                                                                                           (bases 1 to 694)
                                                                                                              primer: ADF
                  /mol_type="mRNA"
/strain="17XL"
                                                      organism="Plasmodium"
                                                                                              Location/Qualifiers
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                                                                              . 694
_xref="taxon:73239"
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                                                        yoelii yoelii"
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PYCOX60 5' end,
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VERSION
KEYWORDS
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                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 20
                                                                                                                                                                                                                                                                                                      ACCESSION
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Parasite Genomics Group
The Institute for Genomic Research
9712 Medical Center Drive, Rockvil
                                                                                                        Carlton,J.M., Daly,T.M., Long,C.A., Fraser,C.M. and Carucci,D.J. Plasmodium yoelii EST project at TI
                                                                                                                                                                   Plasmodium yoelii yoelii
Plasmodium yoelii yoelii
Eukaryota, Alveolata; Apicomplexa; Haemosporida; Plasmodium.
1 (bases 1 to 717)
                                                                                                                                                                                                                                                                                                                                       HM160500 717 bp mRNA linear EST563023 PyBS Plasmodium yoelii yoelii cDNA clone
                                                                Contact: Jane Carlton
                                                                                        Unpublished
                                                                                                                                                                                                                                                                                  BM160500.1 GI:17306181
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/note="Vector: pAD-GAL4; At 20-25% parasitemia, blood /note="Vector: pAD-GAL4; At 20-25% parasitemia, blood collected from BALB/cByJ mice infected with Py17XL parasites, and leukocytes removed by passage over microcrystalline cellulose collumns. Total RNA was isolated using the guanidinium isothlocyanate method,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       dev_stage="Asexual blood stages"
|lab_host="E. coli XL-1 Blue"
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0.28;
                                                                                                                                                    Bergman,L.W.,
    MD 20850,
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Matches 169
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BM160500

COMMENT

TITLE

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167 CAAGGCTATGTCACTTCACATGGCGACCACTATCATTATTACAATGGTAAGGTTCCTTAT 226
                                                                                                                                                                                                                                                                                                                                                                                                                                          265 GACGATGATGACGATGACGATGACGACGATGATGATGATGATGATGACGATGATGAA
                        mRNA sequence.
BM162492
                                                                                  BM162492 756 bp mRNA linear EST 04-
EST565015 PyBS Plasmodium yoelii yoelii cDNA clone PYCKT28
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For clone info, please contact the Malaria Research and Reference
Reagent Resource Center, ATCC
http://www.malaria.mr4.org/mr4pages/index.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Seq primer: ADF.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GACGATGATGATGACGACGATGAAGATTTTGAAGATATGGATGATGATGATGAT
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/note="Vector: pAI
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lab_host="E. coli XL-1 Blue"
GI:17308173
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Best Local Similarity
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Carlton,J.M., Daly,T.M., Long,C.A., Bergman,L.W., Vaidya,A.B. Fraser,C.M. and Carucci,D.J.
Plasmodium yoelii EST project at TIGR
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The Institute for Genomic Research
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Plasmodium yoelii yoelii
Plasmodium yoelii yoelii
Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Unpublished
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GACGATGACGATGACGATGAAGACGATGATGAAGATGAAGATGAAGATGAAGATGAT 412
                                     GACGATGATGATGACGACGATGAAGATTTTGAAGATATGGATGATGATGATGAT
                                                                                                                      GATATTGTTAATGAGGTCAAGGGTGGATATGTTATCAAGGTAGATGGAAAATACTATGTT
                                                                                                                                                               GAAGATGACGATGAAGATGATGATGATGACGACGACGATGATGATGAGAATGAT 292
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                                                                                                                                                                                                                                                                                                                                 GATGATGATGACGACGATGAAGATGACGATGAAGACGATGATGAAGACGACGATGAC
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l: 301-530-9319
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/note="Vector: pAD-GAL4; At 20-25% parasitemia, blc collected from BALB/cByJ mice infected with Py17XL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          parasites, and leukocytes removed by passage over microcrystalline cellulose collumns. Total RNA was
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               isolated.
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/lab_host="E. coli XL-1 Blue"
/clone_lib="PyBS"
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/strain="17XL"
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Pred. No.
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Plasmodium yoelii yoelii
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For clone info, please contact the Malaria Research and Reference
Reagent Resource Center, ATCC
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The Institute for Genomic
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                                                             GATGATGATGACGACGATGAAGATGACGATGAAGACGATGATGAAGACGACGACGATGAC
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                                                                                                     GATGAGGTTAGCAAGCGTGAAGGAATCAATGCTGAGCAAATCGTCATCAAGATAACAGAC
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                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                             microcrystalline cellulose collumns. Total RNA was isolated using the guanidinium isothiocyanate method, and mRNA isolated using oligo(dT)-cellulose chromatography. First strand cDNA synthesis was completed using a 50-base primer and reverse transcriptase in the presence of 5-methyl dCTP. After second strand synthesis, uneven termini were treated with Pfu DNA polymerase and ECORI adaptors ligated to the blunt ends. The sample was cleaved with XhoI and separated on a Sephacryl S-500 column.
                                                                                                                                                                                                                                                                                   Size-fractionated cDNA was precipitated and ligated to HybriZAP arms directionally using EcoR-XhoI cleaved arms After packaging, the phagemid vector (pAD-GAL4) was excised from the HybriZAP vector and plasmid DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                collected from BALB/cByJ mice infected with Py17XL parasites, and leukocytes removed by passage over microcrystalline cellulose collumns. Total RNA was
                                                                                                                                                                                                                                                 isolated."
60 c
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/mol_type="mRNA"
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/note="Vector: pAD-GAL4; At 20-25% parasitemia,
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/lab_host="E. coli XL-1 Blue"
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Pred. No. 0.29
0; Mismatches
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yoelii yoelii cDNA clone
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The Institute for Genomic Research
9712 Medical Center Dr., Rockville,
Tel: 301 838 0208
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Entamoeba histolytica
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Clones are derived from
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                                                                                                                                                          /clone_lib="Entamoeba histolytica Sheared DNA"
/note="Vector: pHOS1; Site 1: Bst I; Constructed at The
Institute for Genomic Research (TIGR), Rockville, MD.
Genomic DNA isolated from broth cultures of E. histolytica
using a method described by Clark and Diamond (Clark,
C.G., and Diamond, L.S. (1993) Entamoeba histolytica: a
method for isolate identification. Exp. Parasitol.
77:450.). The DNA was mechanically sheared to give a
tight size distribution (-2 kb). The v + i method used for
the library construction is described in detail in Smith,
H.O. and Venter, J.C. (Making small insert libraries for
                                                                                whole genome shotgun sequencing projects. In Gen
Sequencing: A Practical Approach, eds. M. Vaudin
Barell, Oxford University Press, 1999)."
72 c 175 g 229 t
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/mol_type="genomic DNA"
/strain="HM1:IMSS"
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RESULT 24
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                                                                                                                                                                                                                                                                                                                                                                    Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville,
                                                                                                                                                                                                                                                                                                                                                                                                                                           Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Entamoebidae; Entamoeba.

1 (bases 1 to 823)

Loftus, B., Van Aken, S. and Fraser, C. Determination of clone end sequences
HM1:IMSS sheared DNA library
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                                                                                                                                                                                                                                                                                                                        Email: bjloftus@tigr.org
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                                                               /clone_lib="Entamoeba histolytica Sheared DNA"
/note="Vector: pHOS1; Site_1: Bst I; Constructed at
/notitute for Genomic Research (TIGR), Rockville, M
method for isolate identification.
                                                                                                                               /organism="Entamoeba histolytica"
/mol_type="genomic_DNA"
/strain="HM1:IMSS"
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Department of Eukaryotic Genomics
The Institute for Genomic Researc
                                                                                                                                                                                                                                                                                                                                            genomic, genomic survey sequence.
BH139532
BH1395321 GI:15098593
GSS.
                                                                                                         Tel: 301 838 0208
Fax: 301 838 3543
Email: bjloftus@tigr.org
                                                                                                                                                                                                                                 Loftus,B., Wang,Z., Van Aken,S. and Fraser,C. Determination of clone end sequences from Ent HM1: MSS sheared DNA library (2001)
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Entamoeba histolytica
Eukaryota; Entamoebidae; Entamoeba
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                                               Seq primer: M13-Forward
Class: shotgun
                                                                             DNA
                                                                                            Clones are derived from the
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quality sequence start: 4 quality sequence stop: 714 Location/Qualifiers
                                                                                                                                                        Medical Center Dr.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Genomic DNA isolated from broth cultures of E. histolytica using a method described by Clark and Diamond (Clark, C.G., and Diamond, L.S. (1993) Entamoeba histolytica: a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /clone_lib="Entamoeba histolytica Sheared DNA"
/note="Vector: pHOS1; Site_1: Bst I; Constructed a
/natitute_for Genomic_Research (TIGR), Rockville,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /mol_type="genomic
/strain="HM1:IMSS"
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REFERENCE AUTHORS TITLE JOURNAL COMMENT RESULT 26 BW141179/c ACCESSION VERSION SOURCE KEYWORDS DEFINITION ORGANISM BW141179 721 bp mRNA linear EST 03-NOV-2002 BW141179 Nori Satoh unpublished cDNA library, gastrula and neurula Ciona intestinalis cDNA clone rcign058f11 3', mRNA sequence. Unpublished Contact: Nori Satou,Y., Shin-i,T., Kohara,Y. and Satoh,N. Expressed genes in Ciona intestinalis (200) 1 (bases 1 to 721) Satou, Y., Shin-i, T. Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea; Enterogona; Phlebobranchia; Cionidae; Ciona. Ciona intestinalis BW141179.1 BW141179 Department of Zoology Ciona intestinalis GI:24498404 Satoh

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RESULT 27
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                                                                                                 bw144040 Nori Satoh unpublished cDNA library, gastrula and r Ciona intestinalis cDNA clone rcign067b16 3', mRNA sequence.
Eukaryota; Metazoa; Chordata; Urochordata; Phlebobranchia; Cionidae; Ciona.

1 (bases 1 to 656)
Satou, Y., Shin-i, T., Kohara, Y. and Satoh, N.
                                                 Ciona intestinalis
Ciona intestinalis
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Tel: 81-75-753-4081
Fax: 81-75-705-1113
                                                                                        BW144040.1 GI:24501265
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/tissue_type="whole body"
/dev_stage="gastrula and neurula"
/clone_lib="Wori Satoh unpublished
and neurula"
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/mol_type="mRNA"
/db_xref="taxon:7719"
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Query Match
Best Local Similarity
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Danio rerio (
BX139987
BX139987.1 (
GSS.
              Danio rerio
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi;
Cypriniformes; Cyprinidae; Danio.
1 (bases 1 to 844)
1 (bases 1 to Humphray, S.J.,
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                                                                                                                        Danio rerio (zebrafish)
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Email: satoh@ascidian.zool.kyoto-u.ac.jp.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Department of
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/mol_type="mRNA"
/db_xref="taxon:7719"
/clone="rcign067b16"
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/clone_lib="Nori Satoh unpublished cDNA library,
and neurula"
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AGENCOURT 14011375 NICHD XGC
IMAGE:6939285 5', mRNA sequen
CD099026
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (13.MAR-2003) The Sanger Institute, W Campus, Hinxton, Cambridgeshire, CB10 1SA, UK. humquery@sanger.ac.uk Unpublished This sequence was generated from the T7 end of part of the Daniokey BAC Library created by R. Keygene. Further details:

Keygene. Further details:
           Contact: Robert Strausberg, Email: cgapbs-r@mail.nih.go
                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
                                  Unpublished
                                                      NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anat
                                                                                                                              Xenopus laevis
                                                                                                                                                                  CD099026.1 GI:30752129
                                                                                           Kenopodinae; Kenopus.
                                                                                                                                            Kenopus laevis (African clawed frog)
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                                             Gene Index
Procurement: Drs. Donald Brown
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/note="vector pIndigoBAC-536"
49 c 81 g 308 t
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/db_xref="taxon:7955"
/clone="DKEY-99E7"
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Plasterk and N.V.
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                                                                                                     Pipidae;
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1 (bases 1 to 671)
Satou, Y., Shin-i, T., Koha
Expressed genes in Ciona
Unpublished
                                                                                                                                                                                                                                                BW273704 Nori Satoh unpublished cDNA library, gastrula and neurula Ciona intestinalis cDNA clone cign067b16 5', mRNA sequence.
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Phlebobranchia; Cionidae; Ciona.
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CDNA Library Arrayed by: The I.M.A.G.E. Consortium
CDNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: NCI-CGAP clone distribution info
                                                                                                                                                                                                                                                                                                                                                                                                                             CACCATGATGATGACCAACAAC 669
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Site 1: Sfi; Site 2: Sfi; 5' and 3' adaptors were used i
cloning as follows: 5' adaptor sequence:
5'-CACGGCCATTATGGCC-3' and 3' adaptor sequence:
5'-ATTCTAGAGGCCGAGCCGACATG-dT(30)BN-3' (where B = A,
C, or G and N = A, C, G, or T). Average insert size 1.6
(range 0.9-3.0 kb). 15/15 colonies contained inserts by
PCR. This library was enriched for full-length clones an
was constructed by Clontech Laboratories (Palo Alto, CA)
a 128 c 208 g 169 t
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/clone_lib="NICHD_XGC_Tad1"
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db_xref="taxon:8355"
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                                                                                    Entamoeba histolytica
Entamoeba histolytica
Eukaryota; Entamoebidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Kyoto University Sakyo-ku, Kyoto, Kyoto 606-8502, Japan Tel: 81-75-753-4081
                1 (bases 1 to 890)
Loftus, B., van Aken, S. and Fraser, C.
Determination of Clone end sequences
HM1:IMSS sheared DNA library
                                                                                                                                            GSS
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Email: satoh@ascidi
Unpublished
                                                                                                                                                               AZ530768.1 GI:11084894
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/tlssue_type="whole body"
/dev_stage="gastrula and neurula"
/clone_lib="Nori Satoh unpublished cDNA library,
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/mol_type="mRNA"
/db_xref="taxon:7719"
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High quality sequence stop: 822
Location/Qualifiers
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Fax: 301 838 3543
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The Institute for Genomic Research
9712 Medical Center Dr., Rockville,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Class: shotgun
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                                   ATGAAGACGATG
                                                                         CTGCTGCAGAAG
                                                                                                                                        TTCCTCATGGAGATCATTACCATTACATTCCTAAGAATGAGTTATCAGCTAGCGAGTTGG
                                                                                                                                                                                                                                                       GAACTCCAAGAAACGATGGTGCTGTTGCCTTGGCACGTTCGCAAGGACGCTATACTACAG 497
                                                                                                                                                                                                                                                                                                                                                              TCCGTACAAAAGAGGAAATCAATCGACAAAAACAAGAGCATAGTCAACATCGTGAAGGTG 437
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AACTTGAAGACGATTATCAACTAGATAATGAATTTGAAATAGAAGAAGAAATCTTGATA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATCATTATTACAATGGTAAGGTTCCTTATGACGCTATCATCAGTGAAGAATTACTCATGA
                                                                                                          ACGATGATGAAGACGATGATGAAGACGATGATGAAGATGAAGATGAAGACGATGATG
                                                                                                                                                                                ACGATGATGAAGACGATGATGAAGACGATGAAGACGATGATGAAGACGATGATGAAG
                                                                                                                                                                                                               ATGATGGTTATATCTTTAATGCTTCTGATATCATAGAGGATACTGGTGATGCTTATATCG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /clone lib="Entamoeba histolytica Sheared DNA"
/note="Vector: pHOS1; Site 1: Bst I; Constructed at The
Institute for Genomic Research (TIGR), Rockville, MD.
Genomic DNA isolated from broth cultures of E. histolytica
using a method described by Clark and Diamond (Clark,
C.G., and Diamond, L.S. (1993) Entamoeba histolytica: a
method for isolate identification. Exp. Parasitol.
77:450.) The DNA was mechanically sheared to give a
tight size distribution (-2 kb). The v + i method used for
the library construction is described in detail in Smith,
H.O. and Venter, J.C. (Making small insert libraries for
whole genome shotgun sequencing projects. In Genome
Sequencing: A Practical Approach, eds. M. Vaudin and B.
Barell, Oxford University Press, 1999)."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /mol_type="genomic DNA"
/strain="HM1:IMSS"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2.2%;
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Best Local Similarity
                                                                                                                                                                                                                                                                  Matches 146;
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  370
                                           284
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                                                                                                                                                                                                                   164 GACCAAGGCTATGTCACTTCACATGGCGACCACTATCATTATTACAATGGTAAGGTTCCT
                                                                                                                            224 TATGACGCTATCATCAGTGAAGAATTACTCATGAAAGATCCAAACTATAAGCTAAAAGAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: Jane Carlton
Parasite Genomics Group
The Institute for Genomic Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Plasmodium yoelii yoelii
Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
1 (Dases 1 to 677)
Carlton,J.M., Daly,T.M., Long,C.A., Bergman,L.W., Vaidya,A.E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BM161314
BM161314.1 GI:17306995
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   For clone info, please contact the Malaria Research and Reference Reagent Resource Center, ATCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Email: carlton@tigr.org
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Fax: 301-838-0208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Plasmodium yoelii
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                                         GAGGATATTGTTAATGAGGTCAAGGGTGGATATGTTATCAAGGTAGATGGAAAATACTAT 343
                                                                                                                                                                          GACGACGATGATGACGATGACGATGACGACGATGATGATGATGATGATGACGATGAT
GATGACGATGATGACGACGACGATGAAGATTTTGAAGATATGGATGATGATGAT
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                                                                                                                                                                                                                                                                                                                                                                              288
                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      primer and reverse transcriptase in the presence of 5-methyl dCTP. After second strand synthesis, uneven termini were treated with Pfu DNA polymerase and EcoRI adaptors ligated to the blunt ends. The sample was cleaved with XhoI and separated on a Sephacryl S-500 column.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Size-fractionated cDNA was precipitated and ligated to HybriZAP arms directionally using EcoRI-XhoI cleaved arms.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="Vector: pAD-GAL4; At 20-25% parasitemia, blc collected from BALB/cByJ mice infected with Py17XL parasites, and leukocytes removed by passage over microcrystalline cellulose collumns. Total RNA was
                                                                                                                                                                                                                                                                                                                                                                                                                   After packaging, the phagemid vector (pAD-GAL4) excised from the HybriZAP vector and plasmid DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    mRNA isolated using oligo(dT)-cellulose chromatography. First strand cDNA synthesis was completed using a 50-base
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                isolated using the guanidinium isothiocyanate method,
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/lab_host="E. coli XL-1 Blue"
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48.3%;
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Pred. No. 1
                                                                                                                                                                                                                                                               Mismatches 156;
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yoelii yoelii cDNA clone PYCKD34 5' end,
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BM169486
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Query Match 2.2%;
Best Local Similarity 48.3%;
Matches 146; Conservative
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Carlton, J.M., Daly, T.M., Long, C.A., Bergman, L.W., Vaidya, A.B.,
Fraser, C.M. and Carucci, D.J.
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Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: Jane Carlton
Parasite Genomics Group
The Institute for Genomic Research
9712 Medical Center Drive, Rockville, MD 20850, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                For clone info, please contact the Malaria Research and Reference Reagent Resource Center, ATCC
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BM169486
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Email: carlton@tigr.org
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Fax: 301-838-0208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Tel: 301-530-9319
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                                                                                                                              263
                                                                                                                                                                        primer and reverse transcriptase in the presence of 5-methyl dCTP. After second strand synthesis, uneven termini were treated with Pfu DNA polymerase and EcoRI adaptors ligated to the blunt ends. The sample was cleaved with XhoI and separated on a Sephacryl S-500 column. Size-fractionated cDNA was precipitated and ligated to HybriZAP arms directionally using EcoRI-XhoI cleaved arms. After packaging, the phagemid vector (pAD-GAL4) was excised from the HybriZAP vector and plasmid DNA
                                                                                                                                                                                                                                                                                                                                                                                                /dev stages"
/dev stages"
/lab_host="B. coli XL-1 Blue"
/clone_lib="PyBS"
/clone_lib="PyBS"
/note="Vector: pAD-GAL4; At 20-25% parasitemia, blood was collected from BALB/CByJ mice infected with Py17XL parasites, and leukocytes removed by passage over microcrystalline cellulose collumns. Total RNA was isolated using the guanidinium isothiocyanate method, and mRNA isolated using oligo(dT)-cellulose chromatography.
First strand cDNA synthesis was completed using a 50-base
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/strain="17XL"
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  Score 52.4; DI
Pred. No. 1;
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725; 0,

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and

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Gaps

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464 GC 465
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Department of Eukaryotic Genomics The Institute for Genomic Research 9712 Medical Center Dr., Rockville, Tel: 301 838 0208 Fax: 301 838 3543
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Entamoeba histolytica
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Class: shotgun
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Seq primer: M13-Reverse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DNA library
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Email: bjloftus@tigr.org
Clones are derived from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: Brendan J Loftus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Loftus,B., Van Aken,S. and Fraser,C. Determination of clone end sequences HM1:IMSS sheared DNA library
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Entamoebidae; Entamoeba.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AZ527885.1 GI:11080056
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                                                                                                                                                                                                                                                                                                                                                                                                                                quality sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                       quality sequence start: 15
              /clone_lib="Bntamoeba histolytica Sheared DNA"
/note="Vector: pHOS1; Site_1: Bst 1; Constructed at The
Institute for Genomic Research (TIGR), Rockville, MD.
Genomic DNA isolated from broth cultures of E. histolytica
using a method described by Clark and Diamond (Clark,
C.G., and Diamond, L.S. (1993) Entamoeba histolytica: a
method for isolate identification. Exp. Parasitol.
77:450.). The DNA was mechanically sheared to give a
tight size distribution (-2 kb). The v + i method used for
the library construction is described in detail in Smith,
H.O. and Venter, J.C. (Making small insert libraries for
whole genome shotgun sequencing
                                                                                                                                                                                                                                                                                                        /mol_type="genomic DNA"
/strain="HM1:IMSS"
                                                                                                                                                                                                                                                                                          db xref="taxon:5759"
                                                                                                                                                                                                                                                                                                                                                         organism="Entamoeba histolytica"
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AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                         Class: shotgun
High quality sequence start: 38
High quality sequence stop: 740
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Loftus,B., Wang,Z., Van Aken,S. and Fraser,
Determination of clone end sequences from E
HM1:IMSS sheared DNA library (2001)
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Entamoeba histolytica
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Email: bjloftus@tigr.org
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: Brendan J Loftus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Entamoebidae; Entamoeba 1 (bases 1 to 976)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Seq primer: M13-Forward
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Fax: 301 838 3543
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      301 838 0208
              /clone lib="Entamoeba histolytica Sheared DNA"
/note="Vector: pHOS1; Site 1: Bst 1; Constructed at The
Institute for Genomic Research (TIGR), Rockville, MD.
Genomic DNA isolated from broth cultures of E. histolytica
using a method described by Clark and Diamond (Clark,
C.G., and Diamond, L.S. (1993) Entamoeba histolytica: a
method for isolate identification. Exp. Parasitol.
77:450.). The DNA was mechanically sheared to give a
tight size distribution (-2 kb). The v + i method used for
the library construction is described in detail in Smith,
H.O. and Venter, J.C. (Making small insert libraries for
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Barell, Oxford University Press, 1999)."
116 c 181 g 216 t
                                                                                                                                                                                                                                                                                                             'mol_type="genomic DNA"
'strain="HM1:IMSS"
                                                                                                                                                                                                                                                                                                                                                              organism="Entamoeba
                                                                                                                                                                                                                                                                                                                                                                                                          ocation/Qualifiers
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Pred. No. 1
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Entamoeba

histolytica

linear

GSS 27-AUG-2001

JOURNAL COMMENT

FEATURES

source

projects. In

REFERENCE AUTHORS

TITLE

SOURCE KEYWORDS

ORGANISM

VERSION ACCESSION RESULT 34 AZ527885

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Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP). The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Osoegawa and Maron Mammoser in pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial BCORI digestion of Drosophila DNA provided by the BDGP from the isogenic strain y2; cn bw sp, the same strain used for the BDGP's pl and EST libraries: A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
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                                                                                                                                                                                                                                                                                                      Direct Submission
Submitted (02-JUN-1999) Genoscope -
BP 191 91006 EVRY cedex - FRANCE (E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CNS008CA 945 bp DNA linear GSS 03-JUN-1999 Drosophila melanogaster genome survey sequence TET3 end of BAC # BACR16N06 of RPCI-98 library from Drosophila melanogaster (fruit
                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygo
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Drosophila melanogaster (fruit fly)
Drosophila melanogaster
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Barell, Oxford University Press, 1999)."
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No. 1
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(E-mail : seqref@genoscope.cns.f)
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                                                                                                                                                                                                           Parasite Genomics Group
The Institute for Genomic Research
9712 Medical Center Drive, Rockvill
Tel: 301-550-9319
Fax: 301-838-0208
                                                                                                                                                                                                                                                                                                                                           Carlton, J.M., Daly, T.M., Long, Fraser, C.M. and Carucci, D.J. Plasmodium yoelii EST project
                                                                                                                                                                                                                                                                                                                                                                                                                                    Plasmodium yoelii yoelii
Plasmodium yoelii yoelii
                                                                                                                                                   For clone info, please contact the Malaria Research and Reference Reagent Resource Center, ATCC
                                                                                                                                                                                                                                                                                                        Contact: Jane Carlton
                                                                                                                                                                                                                                                                                                                              Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
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                                                                                                                                     http://www.malaria.mr4.org/mr4pages/index.html
                                                                                                                                                                                          Email: carlton@tigr.org
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                mRNA sequence.
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/note="end : TET3"
149 c 155 g
                         /mol_type="mRNA"
/strain="17XL"
                                                            /organism="Plasmodium
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/clone="BACR16N06"
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6; Mismatches 155;
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REFERENCE
AUTHORS
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                                                                                                                                                                                                      Entamoeba histolytica
Eukaryota; Entamoebidae; Entamoeba.
1 (bases 1 to 880)
                                                                                                                                                                                                                                                                                                                                AZ529191 880 bp DNA linear GSS 03-NOV-20 ENTBV68TR Entamoeba histolytica Sheared DNA Entamoeba histolytica genomic, genomic survey sequence.
                                  Fax:
                                                               Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville,
                                                                                                                                                                                                                                                                                                                 genomic, genomic AZ529191
                                                                                                                      Contact: Brendan J Loftus
                                                                                                                                      Unpublished
                                                                                                                                                        HM1:IMSS
                                                                                                                                                                       Loftus, B., Van Aken, S. and Fraser, C. Determination of clone end sequences
                                                                                                                                                                                                                                                            Entamoeba histolytica
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are derived from the Entamoeba histolytica HM1:IMSS sheared
            bjloftus@tigr.org
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /clone_lib="PyBS"
/note="Vector: pAD-GAL4; At 20-25% parasitemia, blc
collected from BALB/cByJ mice infected with Py17XL
parasites, and leukocytes removed by passage over
microcrystalline cellulose collumns. Total RNA was
                                                                                                                                                      sheared DNA library
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lab_host="E. coli XL-1 Blue"
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331 AGÁCGAAGÁTGATGAAGACGAÁGATGATGAÁGACGAAGATGATGAAGACGAAGATGATGA 272
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Class: shotgun
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AGCTAGCGAGTTGGCTGCAGAAGCCTTCCTATCTGGTCGAGGAAATCTGTCAAATT
                                                                                                              TGATGCTTATATCGTTCCTCATGGAGATCATTACCATTACATTCCTAAGAATGAGTTATC 603
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                                                              TGATGATGAAGACGAAGATGAAGACGAAGATGATGATGATGTAGTCCCATACGTATC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      method for isolate identification. Exp. Parasitol. 77:450.). The DNA was mechanically sheared to give a tight size distribution (-2 kb). The v+ i method used for the library construction is described in detail in Smith, H.O. and Venter, J.C. (Making small insert libraries for whole genome shotgun sequencing projects. In Genome Sequencing: A Practical Approach, eds. M. Vaudin and B. Barell, Oxford University Press, 1999)."
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RESULT 39
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This sequence is a single read and was generated as par scale clone-end sequencing project of the Tetraodon nig genome. For more information, please take a look at http://www.genoscope.cns.fr/Tetraodon.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Roest Crollius, H., Jaillon, O., Dasilva, C., Ozouf-Costaz, C., Fizames, C., Fischer, C., Bouneau, L., Billault, A., Quetier, F., Saurin, W., Bernot, A. and Weissenbach, J. Characterization and repeat analysis of the compact genome of freshwater pufferfish Tetraodon nigroviridis

Genome Res. 10 (7), 939-949 (2000)
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Direct Submission
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PUC-Ori"
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/db_xref="taxon:99883"
/clone="233A11"
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/mol_type="genomic DNA"
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AU088119 Sugano Malaria cDNA library
clone XPFn6549, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Email: jwatanab@manage.ims.u-tokyo.ac.jp
Suzuki,Y., Yoshitomo-Nakagdwa,K., Maruyama,K., Suyama,A. and Sug
S. Construction and characterization of a full length-enriched
a 5'-end-enriched_DNA_library Gene 200 (1-2), 149-156 (1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The University of Tokyo, Department of Parasitology 4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japa Tel: 81-3-5449-5378
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/clone_lib="Sugano Malaria cDNA
37 c 86 g 163 t
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/clone="XPFn6549"
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/mol type="mRNA"
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Seg primer: SP6
Class: BAC ends
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Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa;
Echinoidea; Euechinoidea; Echinacea; Echinoida;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Email: acameron@caltech.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pasadena California 91125, USA
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California Institute of Technology
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CGTTCCTCATGGAGATCATTACCATTACATTCCTAAGAATGA 597
                                                                                                                                                                       sea urchin genome project: Sequence scan, virtual map,
                                               AGATGATGGTTATATCTTTAATGCTTCTGATATCATAGAGGATACTGGTGATGCTTATAT 555
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(626) 793-3047
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DH10B"
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urchin, sperm genomic BAC library"
/note="Organ: sperm; Vector: BACe3.6; BAC Clones in E
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/mol_type="genomic DNA"
/mol_type="genomic DNA"
/db xref="taxon: 1668"
/clone="Plate=1031 Col=10 Row=I"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (08-SEP-2000) Genoscope - Centre National de Sequencage,
2 rue Gaston Cremieux, CP 5706, 91057 EVRY cedex, FRANCE. (E-mail:
5 seqref@genoscope.cns.fr - Web: www.genoscope.cns.fr)
This GSS is part of a random genomic sequencing program of thirteen
yeast species: Saccharomyces bayanus var. uvarum, Saccharomyces
exiguus, Saccharomyces servazzii, Zygosaccharomyces rouxii,
Saccharomyces kluyveri, Kluyveromyces thermotolerans, Kluyveromyces
lactis var. lactis, Kluyveromyces marxianus var. marxianus, Pichia
angusta, Debaryomyces hansenii var. hansenii, Pichia sorbitophila,
Candida tropicalis and Yarrowia lipolytica. Genomic inserts of 3 to
5 kb were prepared and both extremities were sequenced. See
keywords for description of this sequence and for the sequence of
the other extremity of this insert.
1153 GGAAGGATATGTATTCGAAGAAAAGGGCATCTCTCGTTATGTCTTTTGCGAAAGATTTACC 1212
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Genomic exploration of the hemiascomycetous yeasts: 1. A set o
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Bolotin-Fukuhara, M., Bon, E., Brottier, P., Casaregola, S.,
de-Montigny, J., Dujon, B., Durrens, P., Lepingle, A., Llorente, B.,
Malpertuy, A., Neuveglise, C., Ozier-Kalogeropoulos, O.,
Dotier, S.,
Malpertuy, A., Neuveglise, C., Ozier-Kalogeropoulos, O.,
Dotier, S.,
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T3 end of clone AX0AA039F08 of libsof Pichia farinosa, genomic survey
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/db_xref="taxon:4920"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Parasite Genomics Group
The Institute for Genomic Research
9712 Medical Center Drive, Rockvil
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Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Unpublished
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Fraser,C.M. and Carucci,D.J.
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primer and reverse transcriptase in the presence of 5-methyl dCTP. After second strand synthesis, uneven termini were treated with Pfu DNA polymerase and EcoRI adaptors ligated to the blunt ends. The sample was cleaved with XhoI and separated on a Sephacryl S-500 column. Size-fractionated cDNA was precipitated and ligated to HybriZAP arms directionally using EcoRI-XhoI cleaved arms. After packaging, the phagemid vector (pAD-GAL4) was excised from the HybriZAP vector and plasmid DNA
                                                                                                                                                                                                                                                 /dev_stage="Asexual blood stages"
/lab_host="E. coli XL-1 Blue"
/clone_lib="PyBS"
/clone_stage="Vector: pAD-GAL4; At 20-25% parasitemia, blood was collected from BALB/cByJ mice infected with Py17XL parasites, and leukocytes removed by passage over microcrystalline cellulose collumns. Total RNA was isolated using the guantidinium isothiocyanate method, and mRNA isolated using oligo(dT)-cellulose chromatography.
First strand cDNA synthesis was completed using a 50-base
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                                                                                                                                                      Email: estawatson.wustl.edu
Library was constructed by Debopam Chakrabarti DNA
Washington University Genome Sequencing Center For
obtaining a clone please contact: L. David Sibley
(sibley@borcim.wustl.edu), Washington University
Seq primer: -40UP from Gibco
High quality sequence stop: 421.
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                                                                                                                                                                                                                                                                                      Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                         WashU Plasmodium EST Project
Washington University School of Medicine
                                                                                                                                                                                                                                                                                                                                                                              Contact: L. David Sibley
                                                                                                                                                                                                                                                                                                                                                                                               Unpublished
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                                                                                                                                         quality sequence stop: Location/Qualifiers
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/mole="Vector: pBluescript SK plus; Site_1: EcoRI; Site_2:
/note="Vector: pBluescript SK plus; Site_1: EcoRI; Site_2:
                                                                                                     organism="Plasmodium"
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JOURNAL COMMENT
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                                                                                                                                                  Carlton, J.M., Daly, T.M., Long, C.A., Fraser, C.M. and Carucci, D.J. Plasmodium yoelii EST project at TIO
                                                                                                                                                                                                                               Plasmodium yoelii yoelii
Plasmodium yoelii yoelii
Bukaryota, Alveolata; Apicomplexa; Haemosporida; Plasmodium.
1 (bases 1 to 707)
                                                  Parasite Genomics Group
The Institute for Genomic Research
                                                                                                       Contact: Jane Carlton
                                                                                                                               Unpublished
                                                                                                                                                                                                                                                                                                                                                                  BM164483.1 GI:17310164
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ACCTTGGAAGATTTGTTTGCGACGATTAAGTACTACGTAGAACACCCTGACGAACGTCCA 2029
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AGTTTAATACCTACATATTCAAAAGAAAAGTTGAACAGCATGAAATTAACAAAATGGAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            261
Medical Center Drive, Rockville, 301-530-9319
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Total RNA samples were isolated from mixed stage saponin(0.1%)-lysed P. falciparum 3D7 infected erythrocytes by the acidic guanidinium-phenol chloroform method. The poly A+ RNA was isolated by the polyAT-Tract mRNA isolation system (Promega, WI) using streptavidin Magnesphere particles. Directional cDNA libraries were constructed by oligo d(T) priming of poly(A)+ RNA (5mg) into EcoRI and XhoI sites of 1 ZapII vector using the Zap CDNA synthesis kit (Stragene, CA). The average size of the CDNA inserts in the library was between 1.0 and 1.5kb. Clones were mass excised using the ExAssist helper phage (Stratagene), the phagemids were precipptated with PEG 8000 and extracted with phenol/chloroform. Phagemid DNA was electroporated into DH10B cells."
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Pred. No.
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yoelii yoelii cDNA clone
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Best Local Similarity
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2288 CTTCAAATTATGGATAACAATAGTATCATGGCAGAAAGGCAGAAAAATTACTTGCGTTGTTA 2347
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Seq primer: ADF.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Email: carlton@tigr.org
                                                                                                                                                                                                                                                       GACGATGAAAAAGAAGATGAACTAGACGATGAAAAAGAAGAAGAAGAAGAAGAAGAACTA 344
                                                                                                                 GATTCTAGTCTGAAAGCCAATGCAACAGAAACTCTAGCTGGTTTACGAAATAATTTGACT 2287
                                                                                                                                                              GACGATGAAAAAGAAGATGAACTAGACGATGAAAAAGAAGATGAACTAGACGATGAAAAA 284
                                                                                                                                                                                                        GCTTGGTTTGATGATCACACATACAAAGCTCCAAATGGCTATACCTTGGAAGATTTGTTT 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GATGAAATAGAAGATGAACTAGACGATGAACTAGACGATGAAATAGAACGATGAAATAGAA 584
                                                                      GAAGATGAAAAAGAAGATGAAAAAGAAGATGAACTAGACGATGAAAAAAGAAGATGAACTA 224
                                                                                                                                                                                                                                                                                                  TTCANAGCGGATGAAGAGCCAGTAGAGGAAACACCTGCTGAGCCAGAAGTCCCCTCAAGTA 2167
                                                                                                                                                                                                                                                                                                                                                    GAAGATGAACTAGACGATGAAAAAGAAGATGAACTAGACGATGAAAAAGAAGATGAAAAA 404
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5-methyl dCTP. After second strand synthesis, uneven termini were treated with Ptu DNA polymerase and EcoRI adaptors ligated to the blunt ends. The sample was cleaved with XhoI and separated on a Sephacryl S-500 column. Size-fractionated cDNA was precipitated and ligated to HybriZAP arms directionally using EcoRI-XhoI cleaved arms. After packaging, the phagemid vector (pAD-GAL4) was excised from the HybriZAP vector and plasmid DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              collected from BALB/cByJ mice infected with Py17XL parasites, and leukocytes removed by passage over microcrystalline cellulose collumns. Total RNA was isolated using the guanidinium isothiocyanate method,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             isolated."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      mRNA isolated using oligo(dT)-cellulose chromatography. First strand cDNA synthesis was completed using a 50-base
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/lab_host="E. coli XL-1 Blue"
/clone lib="PyBs"
/note="Vector: pAD-GAL4; At 20-25% parasitemia,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /mol_type="mRNA"
/strain="17XL"
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167 CAAGGCTATGTCACTTCACATGGCGACCACTATCATTATTACAATGGTAAGGTTCCTTAT 226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Reagent Resource Center, ATCC http://www.malaria.mr4.org/mr4pages/index.html Seg primer: ADF.
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Carlton,J.M., Daly,T.M., Long,C.A., Bergman,L.W., Fraser,C.M. and Carucci,D.J.
Plasmodium yoelii EST project at TIGR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: Jane Carlton
Parasite Genomics Group
The Institute for Genomic Research
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Fax: 301-838-0208
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Bukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium
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EST573189 PyBS Plasmodium yoelii yoelii cDNA clone PYCQJ49
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                                                                                                                                                         Similarity
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                                                                                   GATGAGGTTAGCAAGCGTGAAGGAATCAATGCTGAGCAAATCGTCATCAAGATAACAGAC 166
                                         GATGATGATGACGACGATGAAGATGACGATGAAGACGATGATGAAGACGACGATGAC
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                                                                                                                                                                                                                                               256
                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                mRNA isolated using oligo(dT)-cellulose chromatography. First strand cDNA synthesis was completed using a 50-base primer and reverse transcriptase in the presence of 5-methyl dCTP. After second strand synthesis, uneven termini were treated with Pfu DNA polymerase and EcoRI adaptors ligated to the blunt ends. The sample was cleaved with XhoI and separated on a Sephacryl S-500 column. Size-fractionated cDNA was precipitated and ligated to HybriZAP arms directionally using EcoRI-xhoI cleaved arms. After packaging, the phagemid vector (pAD-GAL4) was excised from the HybriZAP vector and plasmid DNA account.
                                                                                                                                                                                                                                          isolated."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="Vector: pAD-GAL4; At 20-25% parasitemia, blood was collected from BALB/cByJ mice infected with Py17XL parasites, and leukocytes removed by passage over microcrystalline cellulose collumns. Total RNA was isolated using the guanddinium isothiocyanate method, and
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/lab_host="E. coli XL-1 Blue"
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Carlton,J.M., Daly,T.M., Long,C.A., Bergman,L.W., Fraser,C.M. and Carucci,D.J.
Plasmodium yoelii EST project at TIGR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Email: carlton@tigr.org
For clone info, please contact the Malaria Research
Reagent Resource Center, ATCC
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The Institute for Genomic |
9712 Medical Center Drive,
Tel: 301-530-9319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Unpublished
Contact: Ja
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Plasmodium yoelii yoelii
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isolated using the guanidinium isothiocyanate method, and mRNA isolated using oligo (dT)-cellulose chromatography. First strand cDNA synthesis was completed using a 50-base primer and reverse transcriptase in the presence of 5-methyl dCTP. After second strand synthesis, uneven termini were treated with Pfu DNA polymerase and EcoRI adaptors ligated to the blunt ends. The sample was cleaved with XhoI and separated on a Sephacryl S-500 column. Size-fractionated cDNA was precipitated and ligated to HybriZAP arms directionally using EcoRI-XhoI cleaved arms. After packaging, the phagemid vector (pAD-GAL4) was excised from the HybriZAP vector and plasmid DNA
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/lab host="E. coll XL-1 Blue"
/clone libs"PyBS"
/note="Vector: pAD-GAL4; At 20-25% parasitemia, blocollected from BALB/CByJ mice infected with Py17XL parasites, and leukoyytes removed by passage over microcrystalline cellulose collumns. Total RNA was
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'strain="17XL"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BJ073162
629 bp mRNA linear EST 11-DEC-BJ073162 NIBB Mochii normalized Xenopus tailbud library Xenopus laevis cDNA clone XL109b17 5', mRNA sequence.
                                                                                                                                                                                                                                                              Center For Genetic Resource Information
National Institute of Genetics
1111 Yata, Mishima, Shizuoka 411-8540, Japan
                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea;
                                                                                                                                                                                                                                                                                                            Contact: Tadasu Shin-i
                                                                                                                                                                                                                                                                                                                         Unpublished
                                                                                                                                                                                                                                                                                                                                       Expressed genes in X. laevis embryo
                                                                                                                                                                                                                                                                                                                                                                  Kitayama,A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                        Xenopus laevis (African clawed frog)
Xenopus laevis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BJ073162.1 GI:17503351
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Location/Qualifiers
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                                                        /tissue_type="whole embryo"
/dev stage="stage 25"
/clome_lib="NIBB Mochii normalized
library"
109 c 165 g 148 t
                                                                                                                                           /mol_type="mRNA"
/db_xref="taxon:8355"
                                                                                                                                  clone="XL109b17"
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Pred. No. 4;
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Score 49.4; D
Pred. No. 4.5;
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JOURNAL COMMENT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Parasite Genomics Group
The Institute for Genomic
9712 Medical Center Drive,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Unpublished Contact: Jane Carlton
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Plasmodium yoelii yoelii
Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium
1 (bases 1 to 687)
Carlton,J.M., Daly,T.M., Long,C.A., Bergman,L.W., Vaidya,A.E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EST572188 PyBS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Email: carlton@tigr.org
For clone info, please contact the Malaria Research
Reagent Resource Center, ATCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Fraser, C.M. and Carucci, D.J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            mRNA sequence
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/note="Wector: pAD-GAL4; At 20-25% parasitemia, blood was collected from BALB/CByJ mice infected with Py17XL parasites, and leukocytes removed by passage over microcrystalline cellulose collumns. Total RNA was isolated using the guanidinium isothiocyanate method, and mRNA isolated using oligo(dT)-cellulose chromatography. First strand cDNA synthesis was completed using a 50-base primer and reverse transcriptase in the presence of 5-methyl dCTP. After second strand synthesis, uneven termini were treated with Pfu DNA polymerase and EcoRI adaptors ligated to the blunt ends. The sample was cleaved with XhoI and separated on a Sephacryl S-500 column. Size-fractionated cDNA was precipitated and ligated to
                                                                                                                                                                                                                                                         /dev_stage="Asexual blood stages"
/lab_host="E. coli XL-1 Blue"
/clome_lbb="PyBS"
/note="Vector: pAD-GAL4; At 20-25
                                                                                                                                                                                                                                                                                                                                            db_xref="taxon:73239"
clone="PYCPU72"
                                                                                                                                                                                                                                                                                                                                                                                                              T OH
                                                                                                                                                                                                                                                                                                                                                                                                                           organism="Plasmodium"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ocation/Qualifiers
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AUTHORS
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                                                                                                                                                       http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=CSOCAP005AF01NP1&cluster=5744.r.
Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ Invitroden Corporation
Faraday Avenue Genoscope sequence ID : CSOCAP005AF01NP1.
                                                                                                                                                                                                                                           Email: segref@genoscope.cns.fr. Web: www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 5744.r
more information about this cluster, see
                                                                                                                                                                                                                                                                                                             Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3-PRIME, mRNA sequence.
BX415231
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BX415231 Homo
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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EST.
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1 (bases 1 to 1044)
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/tissue_type="THYMUS"
/clone_lib="Homo sapiens THYMUS"
/note="Vector: pCMVSPORT_6; 1st strand cDNA was
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2206
                                                         /clone="CS0CAP005YK01"
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/db_xref="taxon:9606"
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a 130 c 89 g 513 t 189 others
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6: /cgn2_6/ptodata/2/ina/backfiles1.seq:*
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4 US-09-620-312D-668
Sequence 187, App sequence 215, App sequence 217, App sequence 217, App sequence 1027, App sequence 1027, App sequence 1027, App sequence 1191, App sequence 119, App sequence 1191, App sequence 2010, App sequence 2011, App
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|--|--|--|---|---|---|---|---|---|--|---|--|--|--|---|---|--|---|--|
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| 1381 TAATTCTGATTTCCAAGCCTTAGACAATTATTAGAACGCTTGAATGATGATCGACTAA 1440 | 1321 TGATAMAGCATATAATCTGTTAACTGAGGCTCATAAAGCCTTGTTTGNAAATAAGGGTCG 13     | 1201 TOTAL CACACACTITANCI GUI AMANAMAMAMATIGI I GUI CUI CUI CUI CACACACTITITI I 10 I I I I I I I I I I I I I I I I I | 1261 TGTTTTAACACACTTTTAAAACTGTTAAAAAATCTTGAAAGCAAGTTATCAAAACAAGAATTTTTA 122 | 1141  | 1081 CCCGCAACCTGCACAAATCTTAAAATAGACTCCAAATTCTTCTTTGGTTAGTCAGCTGGT 1 | 1021 GGTACCAGATTCAAGGCCAGAACAACCAAGTCCACAACCGACTCCGGAACCTAGTCCAGG | 961 GTCTGAATTGGAAGAACGAATCGCTCGTATTATTCCCCTTCGTTATCGTTCAAACCATTG 1020<br> | 901 AGCTAGAGGTGTTGCAGTGCCACACGGAGATCATTACCACTTCATCCCTTACTCTAAAT 960<br> | / 841 TCAACGACATGTAGAATCTGATGGCCTTGTCTTTGATCCAGCACAAATCACAAGTCGAAC 900<br> | 781 AGCAAGTCAAAGTAATGACATTGATAGTCTCTTGAAACAGCTCTACAAACTGCCTTTGAG 840<br>            | 721 TGTAAGCAATCCAGGAACTACAAATACTAACACAAGCAACAACAGCAACACTAACAGTCA 780<br>                   | , 661 TTCAAGAACCTATCGCCGACAAAATAGCGATAACACTTCAAGAACAAACTGGGTACCTTC 720 | 601  | 7 S41 TGGTGATGCTTATATCGTTCCTCATGGAGATCATTACCATTACATTCCTAAGAATGAGTT 600  | 481<br>481  | / 421 TCAACATCGTGAAGGTGGAACTCCAAGAAACGATGGTGCTGTTGCCTTGGCACGTTCGCA 480                                       | 7 361 TGCCCACGCGGATAACGTCCGTACAAAAGAGGAAATCAATC | 301 GGTCAAGGGTGGATATGTTATCAAGGTAGATGGAAAATACTATGTTTACCTTAAGGATGC 3 |

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RESULT 2
US-09-536-784-55
   Sequence 55, Application US/09536784
Patent No. 6573082
GENERAL INFORMATION:
APPLICANT: Choi et. al.
TITLE OF INVENTION: Streptoco
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TELEPHONE: (301) 309-8504
TELEPAX: (301) 309-8512
INFORMATION FOR SEQ ID NO: 55:
SEQUENCE CHARACTERISTICS:
LENGTH: 2389 base pairs
TYPE: nucleic acid.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches 2389;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
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COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.2
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/536,784
FILING DATE: 30-0ct-1997
CLASSIFICATION: CUNknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/961,083
APPLICATION NUMBER: 08/961,083
FILING DATE: OCT-30-1997
ATTORNEY/AGENT INFORMATION:
NAME: Michelle S. Marks
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRANDEDNESS: double TOPOLOGY: linear SEQUENCE DESCRIPTION: SEQ ID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES: 452
CORRESPONDENCE ADDRESS;
CORRESPONDENCE ADDRESSES
ADDRESSEE: Human Genome Sciences,
STREET: 9410 Key West Avenue
CITY: Rockville
STATE: Maryland
COUNTRY: USA
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                                                                 TCAACATCGTGAAGGTGGAACTCCAAGAAACGATGGTGCTGTTGCCTTGGCACGTTCGCA
                                                                                                                                       GGTCAAGGGTGGATATGTTATCAAGGTAGATGGAAAATACTATGTTTTACCTTAAGGATGC
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       AGGACGCTATACTACAGATGATGGTTATATCTTTAATGCTTCTGATATCATAGAGGATAC
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| 1561 AGCTGATAAGTATACAACGTCAGATGGTTACATTTTTGATGAACATGATATAATCAGTGA 1620 | 1501 ACTTGGCAAACCAAATTCTCAAATTGAGTATACTGAAGACGAAGTTCGTATTGCTCAAIT 1560<br>                           | 1441 TAAAGAAAAATTGGTAGATGATTTATTGGCATTCCTAGCACCAATTACCCATCCAGAGCG 1500                                      | 1381 TAATTCTGATTTCCAAGCCTTAGACAAATTATTAGAACGCTTGAATGATGAATCGACTAA 1440<br>                  | 1321 TGATAAAGCATATAATCTGTTAACTGAGGCTCATAAAGCCTTGTTTGNAAATAAGGGTCG 1380     | 1261 TGTTTCACACACTTTAACTGCTAAAAAAGAAATGTTGCTCCTCGTGACCAAGAATTTTA 1320<br> | 1201 GAAAGATTTACCATCTGAAACTGTTAAAAATCTTGAAAGCAAGTTATCAAAACAAGAGAG 1260<br> | 1141 ACGAAAAGTTGGGGAAGGATATGTATTCGAAGAAAAGGGCATCTCTCGTTATGTCTTTGC 1200 | 1081 CCCGCAACCTGCACCAAATCTTAAAATAGACTCAAATTCTTCTTTGGTTAGTCAGCTGGT 1140 | 1021 GGTACCAGATTCAAGGCCAGAACCAACCAAGTCCACAACCGACTCCGGAACCTAGTCCAGG 1080 | 961 GTCTGAATTGGAAGAACGAATCGCTCGTATTATTCCCCTTCGTTATCGTTCAAACCATTG 1020<br> | 901 AGCTAGAGGTGTTGCAGTGCCACACGGAGATCATTACCACTTCATCCCTTACTCTCAAAT 960 | 841 TCAACGACATGTAGAATCTGATGGCCTTGTCTTTGATCCAGCACAAATCACAAGTCGAAC 900 | 781 AGCAAGTCAAAGTAATGACATTGATAGTCTCTTGAAACAGCTCTACAAACTGCCTTTGAG 840 | 721 TGTAAGCAATCCAGGAACTACAAATACTAACACAAGCAACAACAGCAACACTAACAGTCA 780<br> | 661 TTCAAGAACCTATCGCCGACAAAATAGCGATAACACTTCAAGAACAAACTGGGTACCTTC 720 | 601 ATCAGCTAGCGAGTTGGCTGCAGAAGCCTTCCTATCTGGTCGAGGAAATCTGTCAAA 660 | 541 TGGTGATGCTTATATCGTTCCTCATGGAGATCATTACCATTACATTCCTAAGAATGAGTT 600 541 TGGTGATGCTTATATCGTTCCTCATGGAGATCATTACATTACATTCCTAAGAATGAGTT 600 | AGGACGCTATACTACAGATGATGGTTATATCTTTAATGCTTCTGATATCATAGAGGATAC |
| ; SOFTWARE: PatentIn Ver   | ; CURRENT FILING DATE: 1 PRIOR APPLICATION NUMBE ; PRIOR FILING DATE: 1996 ; NUMBER OF SEO ID NOS: 1 | ; TITLE OF INVENTION: Pneu; TITLE OF INVENTION: Mot. ; FILE REFERENCE: 469201-44; CURRENT APPLICATION NUMBE | GENERAL INFORMATION: APPLICANT: Johnson, Les APPLICANT: Adamou, Joh TITLE OF INVENTION: Vac | RESULT 3 US-09-468-656A-9 ; Sequence 9, Application U ; Patent No. 6582706 | 2341  |  | 2221   | 2161<br>2221   | 2101<br>2161  | 2041<br>2101  |  | 1921<br>1981   | 1861   | 1801   | 1741<br>1801   |   | Db 1621 TGAAGGAGATGCAY   | Oy 1621 TGAAGGAGATGCA:                                       |

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US-09-468-656A-9
; Sequence 9, Application US/09468656A

Patent No. 6582706
; GENERAL INFORMATION:
; APPLICANT: Johnson, Leslie S.
APPLICANT: Johnson, John E.
TITLE OF INVENTION: Vaccine Compositions Comprising Streptococcus
; TITLE OF INVENTION: Motifs
; US/09/468,656A
; CURRENT APPLICATION NUMBER: US/09/468,656A
; PRIOR FILLING DATE: 1998-12-02
; PRIOR FILLING DATE: 1998-12-01
; NUMBER OF SEQ ID NOS: 14
; SEO ID NO 9

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TYPB: DNA
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NAME/KEY: misc_feature
LOCATION: (1)...(2451)
OTHER INFORMATION: n = a
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       TCAACGACATGTAGAATCTGATGGCCTTGTCTTTGATCCAGCACAAATCACAAGTCGAAC
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             TCCATCTCCAGACGCAGATGTTAAAGCAAATCCAACTGGAGATAGTGCAGCAGCTATTTA
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| Query Match 100.0%; Score 2388; DB 4; Length 8195; Best Local Similarity 100.0%; Pred. No. 0; Matches 2388; Conservative 0; Mismatches 1; Indels 0; Gaps 0; | nucleic acid<br>NESS: doub<br>(: linear | TELEFAX: (301) 309-8512 ; INFORMATION FOR SEQ ID NO: 94: ; SEQUENCE CHARACTERISTICS: ; LENGTH: 8195 base pairs |       | AT :   |  | COMPUTER: HP Vectra 486/33 OPERATING SYSTEM: MSDOS version 6.2 SOFTWARE: ASCII Text CHERENT APPLICATION DATA. | COUNTRY: USA ZIP: 20850 COMPUTER READABLE FORM: MEDITUM TYPE: District 2 50 inch 1 AM- | ADDRESSEE: Human Genome Sciences, Inc. STREET: 9410 Key West Avenue CITY: Rockville STATE: Marvland | ; APPLICANT: Charles Kunsch ; APPLICANT: Charles Kunsch ; TITLE OF INVENTION: Streptococcus pneumoniae Polynucleotides and Sequences ; NUMBER OF SEQUENCES: 391 . COMPACTOR OF SEQUENCES: 391 | US-08-961-527-94 US-08-961-527-94 ; Sequence 94, Application US/08961527 ; Patent No. 6420135 ; CENERAL INCOMPTON. | Db 2400 GTTGTTAAAAGGAAGTAATCCTTCATCTGTAAGTAAGGAAAAAATAAAC 2448 | Db 2340 TTTGÁCTCTTCAÁATTÁTGGÁTÁACAÁTÁGTÁTCÁTGGCÁGÁÁÁÁGCÁGÁÁÁÁÁTTÁCTTGC 2399  Qy 2341 GTTGTTAAAGGAAGGAACCTTCATCTGTAAGGAAAAAAAA | QY 2281 TITGACTCTCAAATTATGGATAACAATAGTATCATGGCAGAAGCAGAAAATTACTTGC 2340   | 2221 AGTAACGGATTCTAGTCTGAAAGCCAATGCAACAGAAACTCTAGCTGGTTTACGAAATAA | QY 2161 TCAAGTAGAGACTGAAAAAGTAGAAGCCCCAACTCAAAGAAGCAGAAGTTTTGCTTGC  | Qy       2101       TAAGAACTTCAAAGCGGATGAAGACCCAGTAGAGGAAACACCTGCTGAGCCAGAAGTCCC       2160  | Db 2100 TGGATGGGCAATGCCAGTGAGCATGTGTTAGGCAAGAAAGA | 2040  |
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| 4073 GGTACCAGATTCAAGGCCAGAACAACCAAGTCCACAACCGACTCCGGAACCTAGTCCAGG 4132  |   | 901 AGCTAGAGGTGTTGCAGTGCCACACGGAGATCATTACCACTTCATCCCTTACTCTCAAAT 960<br>                                       |       | 781 AGCAAGTCAAAGTAATGACATTGATAGTCTCTTGAAACAGCTCTACAAACTGCCTTTGAG.840<br> | 721 TGTAAGCAATCCAGGAACTACAAATACTAACACAAGCAACAACACAGCAACACTAACAGTCA 780<br> | 661 TTCAAGAACCTATCGCCGACAAAATAGCGATAACACTTCAAGAACAAACTGGGTACCTTC 720<br>                                      | 601 ATCAGCTAGCGAGTTGGCTGCAGAAĞCCCTTCCTATCTGGTCGAGGAAATCTGTCAAA 660<br>                 | 541 TGGTGATGCTTATATCGTTCCTCATGGAGATCATTACCATTACATTCCTAAGAATGAGTT 600<br>                            | 481 AGGACGCTATACTACAGATGATGGTTATATCTTTAATGCTTCTGATATCATAGAGGATAC 540  | 421 TCAACATCGTGAAGGTGGAACTCCAAGAAACGATGGTGCTGTTGCCTTGGCACGTTCGCA 480   | 361 TGCCCACGCGGATAACGTCCGTACAAAAGAGGAAATCAATC                  | 301 GGTCAAGGGTGGATATGTTATCAAGGTAGATGGAAAATACTATGTTTACCTTAAGGATGC 360<br>  | 241 TGARGARIT ROLCA IGARRORI CORRECTA LA RAGO LA MARRORI IGARGATA I EL ENTIGNE SOCIETA EL PERSONA DE LA CORRECTA DEL CORRECTA DE LA CORRECTA DEL CORRECTA DE LA CORRECTA DEL CORRECTA | TCACATGGCGACCACTATCATTATACAATGGTAAGGTTCCTTATGACGCTATCATCAG        | 3173 GCGTGAÁGGÁATCAÁTGCTGAGCAÁATCGTCATCAAGATAACAGACCAÁGGCTATGTCAC 3232 181 TTCACATGGCGACCACTATCATTATTACTATGAGTTAGGTTACCTTATGACGCTATCATCAG 240 | 3113 TATAGATGGAAAACAAGCGACGAAAAAACGGAGAATTTGACTCCTGATGAGGTTAGCAA 3172 121 GCGTGAAGGAATCAATGCTGAGCAAATCGTCATCAAGATAACAGACCAAGGCTATGTCAC 180 |   | 1 TTCTTACGAGTTGGGACTGTATCAAGCTAGAACGGTTAAGGAAAATAATCGTGTTTCCTA 60 |

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TAAGAACTTCAAAGCGGATGAAGAGCCAGTAGAGGGAAACACCTGCTGAGCCAGAAGTCCC
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APPLICANT: Johnson, Leslie S.
APPLICANT: Johnson, John E.
TITLE OF INVENTION: Vaccine Compositions Comprising Streptococcus
TITLE OF INVENTION: Pneumoniae Group A and B Having Selected Structural
TITLE OF INVENTION: Motifs
FILE REFERENCE: 469201-444
CURRENT APPLICATION NUMBER: US/09/468,656A
CURRENT APPLICATION NUMBER: 60/113,048
PRIOR APPLICATION NUMBER: 60/113,048
PRIOR APPLICATION NUMBER: 509112-21
NUMBER OF SEQ ID NOS: 14
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 11
LENGTH: 2531
TYPE: DNA
ORGANISM: Streptococcus pneumoniae
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Best Local
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TAGTCAACATCGTGAAGGTGGAACTCCAAGAAACGATGGTGCTGTTGCCCTTGGCACGTTC
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| B 6 B   | \$ \$ \$   | D Q  | D Q  | g Q  | B 8  | B 64  | 용양   | B &   | B 8  | 8 8  | B 8   | gb - 65   | 유 성  | B 8  | B 8  | Db Db  |
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| APPLICANT: Johnson, Leslie S. APPLICANT: Adamou, John E. FITTLE OF INVENTION: Vaccine Compositions Comprising Streptococcus TITLE OF INVENTION: Pneumoniae Group A and B Having Selected Structural TITLE OF INVENTION: Motifs FILE REFERENCE: 469201-444 | RESULT 6 US-09-468-656A-5 ; Sequence 5, Application US/09468656A ; Patent No. 6582706 ; Patent No. 6582706 | QY 2311 TATCATGGCAGAAGCAGAAAATTACTTGCGTTGTTAAAAGGAAGTAA 2358 | Db 2349 CAAAGACTCTCACAGGATTAAAAAATTACTATTTGGCACCCAGGACAACAATAC 2408        | 2191 ACTCAAAGAAGCAGAAGTTTTGCTTGCGAAAGTAACGGATTCTAGTCTGAAAGCCAATGC          | 2131 KGAGGANACCCTGCTGAGCCAGAAGTCCCTCAAGTNGAGACTGAAAAGTAGAAGCCCA            | 2122 ADMOCKAGA  | 2098 MARA IAMAGHALI ILMAMAGCUGA IUM.                                   | 2038 TUATIGGATUGGGUCHATIGCCHGIGAGUATIGTTAGGUCHAGHANGACCHCHGIGHAGATUC      | 1978 AGATTTUTTTGCGACGATTAAGIACTACGAAACACCCIGACGAACGTCCACATTCTAA      | 1918 MITAMATITY CITY OF THE ACCUMULATION OF TH | 1616 TATTA A TETTOCOTTO CONTROL CONTROL A ACCOUNTANT CONTROL CANADA CANTACCATAA  1869 ATATACTGTAGAAGTCAAAAACGGTAGTTTAATCATACCTCATTATGACCATTACCATAA  1818 TATTACTGTAGAAGTCAAAAACGGTAGTTTAATCATACCTCATTATGACCATTACCATAA | 1.78 11. CARA ICU TO IGANANG GERMANANGARII CARCIC CELICONCII CONTRA INCATICA I I CARCICONI I CARCIA | 1738 ACCICCACIC CAGACGARAILIANAGCARAICCARAICGARAIAGGARAGGARAGGARAGCTAT   | 16/8 TAGCCTTCTGATAGGAAAAAGTTGCAGCCTAAGCCTATACTAAAGAGAAAGGTTTGAC 1689 TAGTTTGTCTGAAGCTGAGAGAGAGGCCCAGGCTTATGCTRAAGAGAAAGGTTTGAC | 1629 TGATGAGGGGATACCATATGTAACTCCACATATGACCACTAAACAAAAAAAA            | 1558<br>1569   |

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CURRENT FILING DATE: 1999-12-02
PRIOR APPLICATION NUMBER: 60/113,048
PRIOR FILING DATE: 1998-12-21
NUMBER OF SEO ID NOS: 14
SOFTWARE: Patentin Ver. 2.1
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| 58 CTATATAGATGGANAACAAGCGACGCAAAANACGGAGAATTTGACTCCTGATGAGGTTAG<br>        | 1 TTCTTACGAGTTGGGACTGTATCAAGCTAGAACGGTTAAGGAAAATAATCGTGTTTC 57 | Quer<br>Best<br>Mato | nuclei<br>DNESS:<br>Y: li | (301) 309<br>R SEQ ID<br>RACTERIST                                    | TRATION<br>ENCE/DO<br>MUNICAT   | APPLICATION NUMBER:  FILING DATE:  ATTORNEY/AGENT INFORMATION:  NAME: Brocke & Anders | APPLICATION NUMBER: US/08/961,083 FILING DATE: CLASSIFICATION: 435 PRIOR APPLICATION DATE: | R: HP Vectra 486/33 NG SYSTEM: MSDOS version 6. E: ASCII Text PPLICATION DATA: | OUNTRY: USA IP: 20850 PUTER READABLE FORM: EDIUM TYPE: Diskette      |   | APPLICANT: Choi et. al.  APPLICANT: Choi et. al.  TITLE OF INVENTION: Streptococcus pneumoniae Antigens and Vaccines  NUMBER OF SEQUENCES: 452  CORPRESEDONDENCE ADDRESS: | יפש   | Db 2178 TGAATCTGATG 2188                             | Db 2118 CCAAGACAGTAAACCTGATGAAGATAAGGAACATGATGAAGTAAGT                  | 6 CAGTGAAGATCCAAATAAGAACTTCAAAGCGGATGAAGAGCCAGTAGAGGAAACACCTGC | Oy 2026 TCCACATTCTAATGATGGGGCATGTGCAGGTAGGCAAGAAAGA  | 1998 GTATACTCTTGAGGATCTTTTGGCGACTGTCAAGTACTATGTCGAACATCCAAACGAACG | Db 1938 CCATTACCATAACATCAAATTTGAGTGGTTTGACGAAGGCCTTTATGAGGCACCTAAGGG 1997  1966 CTATACCTTGGAAGATTTGTTTGCGACGATTAAGTACTACGTAGAACACCCCTGACGAACG 2025 |
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; Sequence 65, Application
; Patent No. 6573082
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INFORMATION FOR SEQ ID NO: 65: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REGISTRATION NUMBER: 41,9
REFERENCE/DOCKET NUMBER: 1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 309-8504
TELEFAX: (301) 309-8512
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/961,083
FILING DATE: OCT-30-1997
ATTORNEY/AGENT INFORMATION:
NAME: Michelle S. Marks
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COMPUTER READABLE FORM:

MEDIUM TYPE Diskette, 3.50 inch,

COMPUTER: HP Vectra 486/33

OPERATING SYSTEM: MSDOS version 6.

SOPTWARE: ASCII Text

CURRENT APPLICATION DATA:
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TITLE OF INVENTION: Streptococcus pneumoniae Antigens and
NUMBER OF SEQUENCES: 452
CORRESPONDENCE ADDRESS:
ADDRESSEE: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
CITY: Rockville
STATE: Maryland
COUNTRY: USA
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FILING DATE: 30-Oct-1997
CLASSIFICATION: «Unknown»
                                                                          TGCAGCTCATGCGGATAATATTCGGACAAAAGAAGAGATTAAACGTCAGAAGCAGGAACG
                                                                                                              TGAAATCAAGGGTGGTTATGTCATTAAGGTAAACGGTAAATACTATGTNTACCTTAAGGA
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Pred. No. 7.3e-262;
0; Mismatches 645;
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                                   TACCCATCCAGAGCGACTTGGCAAACCAAATTCTCAAATTGAGTATACTGAAGACGAAGT 1545
                                                                                                                             TGATGAATCGACTAATAAAGAAAAATTGGTAGATGATTTATTGGCATTCCTAGCACCAAT 1485
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                   TGAGCCAGAAGTCCCTCAAGTAGAGA
                                                     TTACAATCTTCAATATACTGTAGAAGTCAAAAACGGTAGTTTAATCATACCTCATTATGA
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TGAGGAAGAACCCCTCGAGAAGAGA
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US-08-961-527-243

(Sequence 243, Application US/08961527

Patent No. 6420135

(Patent No. 6420135

(CORESPONDENCE ADDRESS:

ADDRESSEE: Human Genome Sciences, Inc.

(CORTY: Rockville

STATE: Maryland

(COUNTRY: USA

ZIP: 20850

(COMPUTER READABLE FORM:

(COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage

(COMPUTER: HP Vectra 486/33

OPERATING SYSTEM: MSDOS version 6.2

SOFTWARE: ASCII Text

(CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/961,527

FILING DATE:

CLASSIFICATION: 424

PRIOR APPLICATION NUMBER:

EILING DATE:

EILING DATE:

APPLICATION NUMBER:

EILING DATE:

APTORNEY/AGENT INFORMATION:

Sequences

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Best Local Simi
Matches 1005;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Brookes, A. REGISTRATION NUMBER: 36,373
REFERENCE/DOCKET NUMBER: PB:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 309-8504
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
LENGTH: 2359 base pairs
TYPE: nucleic acid
STRANDENNESS: double
TOPOLOGY: linear
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                                                                      GATTGTCAGAGAACCACAATCTGACTGT
                                                                                                                                                                                                                                   GTTATCAGCTAGCGAGTIGGCTGCTGCAGAAGCCTTCCTATCTGGTCGAGGAAATCTGTC
                                                                                                                                                                                                                                                                                   CACGGGTGATGCTTATATCGTTCCTCACGGCGACCATTACCATTACATTCCTAAGAATGA
                                                                                                                                                                                                                                                                                                                  TACTGGTGATGCTTATATCGTTCCTCATGGAGATCATTACCATTACATTCCTAAGAATGA 597
                                                                                                                                                                                                                                                                                                                                                                               GCAAGGACGCTATACTACAGATGATGGTTATATCTTTAATGCTTCTGATATCATAGAGGA
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TCATCAAAATCAAGGGGAAAACATTTCAAGCCTTTTACGTGAATTGTATGCTAAACCCTT 1733
                                                                                                                                                                          AAATTCAAGAACCTATCGCCGACAAAATAGCGATAACACTTCAAGAACAAACTGGGTACC 717
                                                                                                                                                                                                               GTTATCAGCTAGCGAGTTAGCTGCTGCAGAAGCCTATTGGAATGG
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                                                                                                     TTCTGTAAGCAATCCAGGAACTACAAATACTAACACAAGCAACAACAGCAACACTAACAG
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Pred. No. 5.6e-170;
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                                                                                                                                                                                                                                                                                                                                                                                       Patent No. 6159469
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 181,
           APPLICATION NUMBER: U
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                    ZIP: 20850
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb
COMPUTER: HP Vectra 486/3
OPERATING SYSTEM: MSDOS Version 6.2
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                     APPLICANT: Choi et.
TITLE OF INVENTION:
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                               STREET: 9410 Key West Avenue CITY: Rockville
                                                                                                                                                                                                                           COUNTRY:
                                                                                                                                                                                                                                                  STATE:
                                                                                                                                                                                                                                                                                                    ADDRESSEE:
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TELEFAX: (301) 309-8512
INFORMATION FOR SEQ ID NO: 18
SEQUENCE CHARACTERISTICS:
LENGTH: 1342 base pairs
TYPE: nucleic acid
STRANDENNESS: double
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 309-8504
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ACAGCTCTACAAACTGCCTTTGAGTCAACGACATGTAGAATCTGATGGCCTTTGTCTTTTGA
                                                     AGCAAAAGGATCAACTAGCAAGCCAGCAAATAAATCTGAAAATCTCCAGAGTCTTTTGAA
                                                                                   CAACAACAGCAACACTAACAGTCAAGCAAGTCAAAGTAATGACATTGATAGTCTCTTGAA
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                                                                                                                                                                                                                       ATCTGGTCGAGGAAATCTGTCAAATTCAAGAACCTATCGCCGACAAAATAGCGATAACAC
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US-09-536-784-181
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PATENT NO. 6573082
GENERAL INFORMATION:
APPLICANT: Choi et. al.
TITLE OF INVENTION: Streptococcus pneumoniae
NUMBER OF SEQUENCES: 452
                                                                                                                                                                                                                                    Query Match
Best Local :
                                                                                                                                                                                                                     Matches
                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX: (301) 309-8512
INFORMATION FOR SEQ ID NO: 181:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                 : Local Sim
                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READBBLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4M
COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.2
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/536,784
FILING DATE: 30-Oct-1997
CLASSIFICATION - CURROWN>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/961,083
FILING DATE: OCT-30-1997
ATTORNEY/AGENT INFORMATION:
NAME: Michelle S. Marks
REGISTRATION NUMBER: 41,971
REFERENCE/DOCKET NUMBER: PB340P3
TELECOMMUNICATION INFORMATION:
TELEPHONE: (2013) 309-8504
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CITY: Rockville
STATE: Maryland
                                                                                         TTTGACTCCTGATGAGGTTAGCAAGCGTGAAGGAATCAATGCTGAGCAAATCGTCATCAA 156
                                                                     CTTGACACCAGACCAGGTTAGCCAGAAAGAAGAATTCAGGCTGAGCAAATTGTAATCAA 147
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 AATTACAGATCAGGGCTATGTAACGTCACACGGTGACCACTATCATTACTATAATGGGAA
                        GATAACAGACCAAGGCTATGTCACTTCACATGGCGACCACTATCATTATTACAATGGTAA 216
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                                                                                                                                                                                                                                                                                                                                                             TYPE: nucleic acid
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West Avenue
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                                                                                                                                                                                                                   Score 385.4; DB 4;
Pred. No. 3.2e-96;
0; Mismatches 276;
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                                                                                                                                                                                                                                                    Length 1342;
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RESULT 12
US-09-468-656A-7
; Sequence 7, Application US/09468656A
; Patent No. 6582706
; GENERAL INFORMATION:
APPLICANT: Johnson, Leslie S.
APPLICANT: Adamou, John E.
TITLE OF INVENTION: Vaccine Compositions Comprising Streptococcus
TITLE OF INVENTION: Pneumoniae Group A and B Having Selected Stru
TITLE OF INVENTION: Motifs
FILE REFERENCE: 469201-444
CURRENT APPLICATION NUMBER: US/09/468,656A
CURRENT FILING DATE: 1999-12-02
PRIOR APPLICATION NUMBER: 60/113,048
PRIOR FILING DATE: 1998-12-21
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; SOFTWARE: PatentIn Ver. 2.
; SEQ ID NO 7
; LENGTH: 1455
; TYPE: DNA
; ORGANISM: Streptococcus p
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Best Local Similarity
Matches 631; Conserv
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     CCACTTCATCCCTTACTCTCAAATGTCTGAATTGGAAGAACGAATCGCTCGTATTATTCC
                                     CCCTGCTAAGATTATCAGTCGTACACCAAATGGAGTTGCGATTCCGCATGGCGACCATTA
                                                             TCCAGCACAAATCACAAGTCGAACAGCTAGAGGTGTTGCAGTGCCACACGGAGATCATTA
                                                                                                            GGAACTCTATGATTCACCTAGCGCCCAACGTTACAGTGAATCAGATGGCCTGGTCTTTGA
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Pred. No. 3.3e-96;
0; Mismatches 276;
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US-08-961-527-192/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: (301) 309-851:
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
APPLICANT: Charles Kunsch
TITLE OF INVENTION: Strep:
NUMBER OF SEQUENCES: 391
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Brookes, A. Anders
REGISTRATION NUMBER: 36,373'
REFERENCE/DOCKET NUMBER: PB:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 309-8504
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE: ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION: 424
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION DATA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: Diskette, 3.50 inch, 1.4Mb
COMPUTER: HP Vectta 486/33
OPERATING SYSTEM: MSDOS version 6
                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEPHONE: (301) 309-8512
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STRANDEDNESS: doub
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STATE: Maryland
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                                                                                                                                                                                                                        CTTGACACCAGACCAGGTTAGCCAGAAAGAAGGAATTCAGGCTGAGCAAATTGTAATCAA
   TAAAGACGCTGATATTGTCAATGAAGTCAAGGGTGGTTATATCATCAAGGTCGATGGAAA
                            AAAAGATGAGGATATTGTTAATGAGGTCAAGGGTGGATATGTTATCAAGGTAGATGGAAA
                                                                                                                                                AATTACAGATCAGGGCTATGTAACGTCACACGGTGACCACTATCATTACTATAATGGGAA
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                                                                           AGTTCCTTATGATGCCCTCTTTAGTGAAGAACTCTTGATGAAGGATCCAAACTATCAACT
                                                                                                         GGTTCCTTATGACGCTATCATCAGTGAAGAATTACTCATGAAAGATCCAAACTATAAGCT
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                                                                                                                                                                                                                                                                                                                                                                                    Score 385.4; DB 4;
Pred. No. 7.4e-96;
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US-08-961-527-355
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                                                                                                                                                                                                                                                                                                                                                Sequence 355, Application US/08961527 Patent No. 6420135
                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
COMPUTER: HP Vectra 486,
OPERATING SYSTEM: MSDOS
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/(
FILING DATE:
                                                                                                                                                                                                                                                                       APPLICANT: Charles I
TITLE OF INVENTION:
NUMBER OF SEQUENCES:
                                                                                                         ZIP: 20850
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette,
                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
ADDRESSEE: Human Gen
                                                                                                                                                                                  STREET: 9410 Key
CITY: Rockville
STATE: Maryland
                                                                                                                                                               COUNTRY:
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RESULT 15
US-08-961-527-258
; Sequence 258, Application
; Patent No. 6420135
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US-08-961-527-355
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REGISTRATION NUMBER: 36,373
REFERENCE/DOCKET NUMBER: PB340P1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 309-8504
TELEPAC: (301) 309-8512
INFORMATION FOR SEQ ID NO: 355:
SEQUENCE CHARACTERISTICS:
LENGTH: 973 base pairs
TYPE: nucleic acid
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LIOR APPLICATION DATA:
APPLICATION NUMBER:
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Pred. No. 3.4e-95;
0; Mismatches 131
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Brookes, A. Anders
REGISTRATION NUMBER: 36,373
REFERENCE/DOCKET NUMBER: 'PB340P1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 309-8504
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE:
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: ASCII Text CURRENT APPLICATION DATA:
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MEDIUM TYPE: Diskette, 3.50 inch
COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version
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CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: nucleic acid
STRANDEDNESS: double
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CITY: Rockville
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GTAACGCTAGCGACCATGTTCAAAGAAACAAAAATGGTCAAGCTGATACCAATCAAACGG
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Pred. No. 4.4e:
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US-08-743-637B-34/c
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                                        TELEFAX: (414)277-5591
INFORMATION FOR SEQ ID NO: 3
SEQUENCE CHARACTERISTICS:
LENGTH: 841 base pairs
TYPE: nucleic acid
STRANDENNESC: 4-----1
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: PC-DOS/MS-DOS
                                                                                                                                    NAME: BAKER, Jean C.
REGISTRATION NUMBER: 35,433
REFERENCE/DOCKET NUMBER: 85
TELECOMMUNICATION INFORMATION:
TELEPHONE: (414) 277-5000
                                                                                                                                                                                                                           APPLICATION NUMBER: US 08/526,840 FILING DATE: 11-SEP-1995 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                    OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version
CURRENT APPLICATION DATA:
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STATE: WISCONSI
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                TOPOLOGY:
                                 STRANDEDNESS:
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TYPE:
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PROBES AND AMPLIFICATION PRIMERS TO RAPIDLY DETECT AND
IDENTIFY COMMON BACTERIAL PATHOCENS AND ASSOCIATED
ANTIBIOTIC RESISTANCE GENES FROM CLINICAL SPECIMENS ...
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RESULT 17
US-08-526-840B-34/c
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                               TELEPAX: (414)
INFORMATION FOR SEQ ID NO: 34
SEQUENCE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
TENGTH: 841 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Patent No. 6001
GENERAL INFORM
APPLICANT:
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TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
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                                                                                                                     NAME: BAKER, Jean C.
REGISTRATION NUMBER: 35,433
REFERENCE/DOCKET NUMBER: 85
TELECOMMUNICATION INFORMATION:
TELEPHONE: (414) 277-5000
                                                                                                                                                                                                                CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 0
FILING DATE: 12-SEP-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: Patentin Release #1.0, CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US/0 FILING DATE: 11-SEP-1995
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CITY: Milwaukee
             STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Wisconsin
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AMPLIFICATION PRIMERS TO RAPIDLY DETECT AND IDENTIFY
COMMON BACTERIAL PATHOCENS AND ANTIBIOTIC RESISTANCE
FROM CLINICAL SPECIMENS FOR ROUTINE DIAGNOSIS IN ...
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Pred. No. 3e-20;
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RESULT 18
US-08-232-463-14/c
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Sequence 14, App
--- No. 56703
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Best Local Similarity
                                                                                                           APPLICATION NUMBER: EP 91 114
FILING DATE: 26-AUG-1991
ATTORNEY, AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 3047
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
APPLICANT: DORNER
                                              INFORMATION FOR SEQ ID NO:
            SEQUENCE CHARACTERISTICS:
LENGTH: 7218 base pair
                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: SCHEIFLINGER, F.
APPLICANT: FALKNER, F.G.
TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
NUMBER OF SEQUENCES: 52
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ORIGINAL SOURCE:
ORGANISM: Str
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                               PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                               TELEFAX:
                                                                                           TELEPHONE:
                                                                                                                                                                                                                                                                               CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY:
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                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER:
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1800 Diagonal Road
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Pred. No. 3e-20;
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; ORGANISM: Staphylococcus epidermidis
US-09-134-001C-2243
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Best Local Similarity
Workshes 13; Conserve
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                                                                                                                        *Query Match
Best Local Similarity
Matches 187; Conserv
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APPLICANT: LYNN DOUGETTE-Stamm et al
APPLICANT: LYNN DOUGETTE-STAMM et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
TITLE OF INVENTION: EPIDERWIDIS FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: GTC-007
                                                                                                                                                                                                                                SEQ ID NO 2243
LENGTH: 11091
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 2243, Application US/09134001C Patent No. 6380370
                                                                                                                                                                                                                                                                           CURRENT APPLICATION NUMBER: US/09/134,001C CURRENT FILING DATE: 1998-08-13 PRIOR APPLICATION NUMBER: US 60/064,964 PRIOR FILING DATE: 1997-11-08 PRIOR APPLICATION NUMBER: US 60/055,779 PRIOR FILING DATE: 1997-08-14
                                                                                                                                                                                                                                                                NUMBER OF SEQ ID NOS: 5674
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AAATAGTTTAGATCAAATCAATAACTTCAGACCAGATTTTAGTAAAAAAACGTAATGCAGT
                                                            AAAAGCCAAAAATGATGTAAATCAATCTCAAACTAATCAGCAAGTTGAAAATGCTGAGCA
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Pred. No. 1.5
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Pred. No. 0.00072;
0; Mismatches 205;
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                                                                                                              Matches
                                                                                                                                        Query Match
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NAME: OSMAN Ph.D., Richard A
REGISTRATION NUMBER: 36,627
REFERENCE/DOCKET NUMBER: UCB96-
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415)343-4341
                                                                                                                                                                                                                                      TELEFAX: (415)343-4342
INFORMATION FOR SEQ ID NO: :
SEQUENCE CHARACTERISTICS:
LENGTH: 2277 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL
                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
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TITLE OF INVENTION: Human Tel
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                    MOLECULE TYPE:
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                                                                                                                                                                                             TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
                                                                                                                            Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE:
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER:
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268 Bush Street, Suite 3200
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29.7%; Prec
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                                                                                                                          Score 45.2; DB Pred. No. 0.018;
                                                                                                           Mismatches 131;
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US-08-676-974-2
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Sequence 2, Application US/08676974 Patent No. 5770422
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INFORMATION FOR SEQ ID NO:
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LENGTH: 2277 base pairs
Type: nucleic acid
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
CURRENT APPLICATION DATA:
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NAME: Osman Ph.D., Richard A
REGISTRATION NUMBER: 36,627
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CORRESPONDENCE ADDRESS:
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CITY: San Francisco
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                                              459 CTGTTGCCTTGGCACGTTCGCAAGGACGCTATACTACAGATGATGGTTATATCTTTAATG 518
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77; Conserv
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                                                                                                CNGTNCARATHCARAARMGNGCNGTNAARMGNCCNGCNGCNAARWSNWSNGAYCAYW 850
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ER: UCB96-055
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RESULT 23
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US-09-098-487-2
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APPLICANT: COLLIN
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
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LENGTH: 2277 base pairs
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NAME: OSMAN Ph.D., Richard A
REGISTRATION UMBER: 36,627
REFERENCE/DOCKET NUMBER: UCB96-055
TELECOMMUNICATION INFORMATION:
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STRANDEDNESS: double
TOPOLOGY: linear
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CITY: San Francisco
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CLASSIFICATION:
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(415)343-4342
OR SEQ ID NO: 2:
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APPLICANT: DAUBERSIES, PIERRE
APPLICANT: DAUBERSIES, PIERRE
APPLICANT: DAUBERSIES, PIERRE
APPLICANTON: MALARIAL PRE-ERYTHROCYTIC STITILE OF INVENTION: MALARIAL PRE-ERYTHROCYTIC STITILE OF INVENTION INVERER: US/08/973,462B
CURRENT APPLICATION NUMBER: US/08/973,462B
CURRENT FILING DATE: 1998-06-06-0894
EARLIER APPLICATION NUMBER: PCT/FR96/00894
EARLIER APPLICATION NUMBER: FR 95/07007
EARLIER FILING DATE: 1995-06-13
NUMBER OF SEQ ID NOS: 29
RESULT 24
US-08-973-462-1
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Best Local Similarity
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ORGANISM: P. falciparum
FEATURE:
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LOCATION: (1)
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                                                                                                                     TGGAAAAGATAGCCTTTCTGATAAGGAAAAAGTTGCAG 1706
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                                                                                 GGATGTTGATGTTCCTGCTATGAAAGATCAATTTTTAG
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                                                                                                                                                             TTCAAGTACTGAAGGTGTTCAAGAAACTGTAACTGAACATGTAGAACAAAATGTATATGT
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Sequence 1, Application US/08973462B
Patent No. 6191270
GENERAL IMFORMATION:
APPLICANT: DRUILHE, PIERRE
APPLICANT: DAUBERSIES, PIERRE
TITLE OF INVENTION: MALARIAL PRE-ERYTHROCYTIC ST/FILE REFERENCE: 0660-0125-0 PCT
CURRENT APPLICATION NUMBER: US/08/973,462B
CURRENT FILING DATE: 1998-02-06
EARLIER APPLICATION NUMBER: PCT/FR96/00894
EARLIER APPLICATION NUMBER: PCT/FR96/00894

STAGE

POLYPEPTIDE MOLECULES

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LENGTH: 696
TYPE: DNA
ORGANISM: Homo sapiens
US-09-461-697-193
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US-09-461-697-193
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; ORGANISM: P. falciparum
US-08-973-462-1
                                                                              NUMBER OF SEQ ID NOS: 466
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 193
                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 193, Application US/09461697 Patent No. 6277974
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LENGTH: 6152
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                                                                                                                                   APPLICANT: Puranam, Kasturi
APPLICANT: Katz, Lawrence C.
TITLE OF INVENTION: COMPOSITIONS AND METHODS
TITLE OF INVENTION: AND TREATING CONDITIONS,
TITLE OF INVENTION: CELL DEATH
FILE REFERENCE: 10001-005-999
CURRENT APPLICATION NUMBER: US/09/461,697
CURRENT FILING DATE: 1999-12-14
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EARLIER FILING DATE: 1995-06-13
NUMBER OF SEQ ID NOS: 29
SOFTWARE: Patentin Ver. 2.0
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APPLICANT: Thomas, Mary Beth
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Puranam, Kasturi
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APPLICANT: COGENT NEUROSCIENCE, Inc.
APPLICANT: Barney, Shawn
APPLICANT: Barney, Shawn
APPLICANT: Portbury, Stuart D.
APPLICANT: Portbury, Stuart D.
APPLICANT: Portbury, Stuart D.
APPLICANT: Portbury, Stuart D.
APPLICANT: Lawrence C.
TITLE OF INVENTION: COMPOSITIONS AND METHODS
TITLE OF INVENTION: CELL DEATH
FILE REFERENCE: 10001-005-999
CURRENT APPLICATION UMBER: US/09/461,697
CURRENT FILING DATE: 1999-12-14
NUMBER OF SEQ ID NOS: 466
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 191
LENGTH: 699
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; ORGANISM: Homo sapiens
US-09-461-697-191
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                                                                                                                                                                                                                    RESULT 27
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                                                                                                                                             Sequence 189, Application US/09461697 Patent No. 6277974 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Patent No. 6277974
GENERAL INFORMATION:
APPLICANT: COGENT NEUROSCIENCE, Inc.
APPLICANT: Lo, Donald C.
APPLICANT: Barney, Shawn
APPLICANT: Thomas, Mary Beth
APPLICANT: Portbury, Stuart D.
APPLICANT: Portbury, Stuart D.
APPLICANT: Puranam, Kasturi
APPLICANT: Katz, Lawrence C.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 191,
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Pred. No. 0.13;
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Pred. No. 0.13;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
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FILE REFERENCE: 10001-005-999
CURRENT APPLICATION NUMBER: US/09/461,697
CURRENT FILING DATE: 1999-12-14
NUMBER OF SEQ ID NOS: 466
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 189
LENGTH: 717
TYPE: DNA
ORGANISM: Homo sapiens
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                                                                                                                                                                                                                                                                                   ; TYPE: DNA; Homo sapiens US-09-461-697-187
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                                                                                                                                                                                                    Query Match
Best Local Similarity
Matches 88; Conserv
                                                                                                                                                                                                                                                                                                                                        FILE REFERENCE: 10001-005-999
CURRENT APPLICATION NUMBER: US/09/461,697
CURRENT FILLING DATE: 1999-12-14
NUMBER OF SEQ ID NOS: 466
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 187
LENGTH: 774
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Best Local Similarity
Matches 88; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: PORTBURY, Stuart D.
APPLICANT: Puranam, Kasturi
APPLICANT: Puranam, Kasturi
APPLICANT: Puranam, Kasturi
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSING
TITLE OF INVENTION: AND TREATING CONDITIONS, DISORDERS, OR I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Barney, Shawn
APPLICANT: Thomas, Mary Beth
APPLICANT: Portbury, Stuart D.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION: AND TREATING CONDITIONS, DISORDERS, OR DISEASES INVOLVING TITLE OF INVENTION: CELL DEATH
    2162 CAAGTAGAGACTGAAAAAGTAGAAGCCCAACTCAAAGAAGCAGAAG 2207
                                                                              2102 AAGAACTTCAAAGCGGATGAAGAGCCAGTAGAGGAAACACCTGCTGAGCCAGAAGTCCCT
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                                                                                                                       GGATGGGGCAATGCCAGTGAGCATGTGTTAGGCAAGAAGACCACAGTGAAGATCCAAAT 2101
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Sequence 185, Application US/09461697
Patent No. 6277974
GENERAL INFORMATION:
APPLICANT: COGENT NEUROSCIENCE, Inc.
APPLICANT: Lo. Donald C.
APPLICANT: Barney, Shawn
APPLICANT: Thomas, Mary Beth
APPLICANT: Portbury, Stuart D.
APPLICANT: Puranam, Kasturi
APPLICANT: Puranam, Kasturi
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US-09-220-132-155
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                                                                                                                        US-09-220-132-155
                                                                                                                                                                       SOFTWARE: Fast
SEQ ID NO 155
FENGTH: 1280
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                                        Query Match
Best Local S
Matches 88
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LENGTH: 819
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Best Local
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TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSING
TITLE OF INVENTION: AND TREATING CONDITIONS, DISORDERS, OR I
TITLE OF INVENTION: CELL DEATH
FILE REFERENCE: 10001-005-99
CURRENT FILING DATE: 1999-12-14
NUMBER OF SEQ ID NOS: 466
                                                                                                                                                                                                                                                      CURRENT APPLICATION NUMBER: US/09/220,132
CURRENT FILING DATE: 1998-12-23
PRIOR APPLICATION NUMBER: US 60/079,303
PRIOR FILING DATE: 1998-03-25
PRIOR APPLICATION NUMBER: US 60/068,821
PRIOR FILING DATE: 1997-12-24
                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Shyjan, Andrew W.
TITLE OF INVENTION: METHODS AND COMPOSITONS FOR THE IDENTIFICATION AND ASSESSMENT
TITLE OF INVENTION: OF PROSTATE CANCER THERAPIES AND THE DIAGNOSIS OF PROSTATE CAN
FILE REFERENCE: 07334-074001
                                                                                                                                                                                                                   NUMBER OF SEQ ID NOS: 191
SOFTWARE: FastSEQ for Windows Version 4.0
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                                                                                                                                      ORGANISM: Homo sapiens
                                                                                                                                                              TYPE: DNA
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                                        Local Similarity
les 88; Conserv
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  2042 GGATGGGGCAATGCCAGTGAGCATGTGTTTAGGCAAGAAGAAGACCACAGTGAAGATCCAAAT
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                                          Conservative
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53.0%;
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                                      Score 41.2; DB Pred. No. 0.17; O; Mismatches
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APPLICANT: PURPAIN, Kasturi
APPLICANT: RETE, LAWTENGE C.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR
TITLE OF INVENTION: CELL DEATH
FILE REFERENCE: 10001-005-999
CURRENT APPLICATION NUMBER: US/09/461,697
CURRENT FILING DATE: 1999-12-14
NUMBER OF SEQ ID NOS: 466
SOFTWARE: FASTSEQ for Windows Version 4.0
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US-09-461-697-184
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            SEQ ID NO 21
LENGTH: 5340
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APPLICANT:
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                                                                                                                                                                                                                                                                                                               Sequence 21, Application US/09627122
Patent No. 6472521
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                                                     FILLE REFERENCE: 02481.16/6
FILE REFERENCE: 02481.16/6
CURRENT APPLICATION NUMBER: US/09/627,122
CURRENT FILING DATE: 2000-07-27
MIMHER OF SEQ ID NOS: 23
                                                                                                                                                    APPLICANT: Schwerdel, Marc
TITLE OF INVENTION: OLIGONUCLECTIDES
TITLE OF INVENTION: EXPRESSION
                                                                                                                                                                                                APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 1669
TYPE: DNA
ORGANISM: Homo sapiens
TYPE: DNA
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Local Similarity 53.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2102 AAGAACTTCAAAGCGGATGAAGAGCCAGTAGAGGAAACACCTGCTGAGCCAGAAGTCCCT
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Unger, Eberhard
Gothe, Gislinde
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Thomas, Mary Beth
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Greiner,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 1669;
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US-09-601-198-56/c
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Patent No. 653...
Patent INFORMATION:
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Best Local Similarity
Matches 95; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Cassell, Gail H.
APPLICANT: Chen, Ellson Y.
APPLICANT: Glass, Jennifer S.
APPLICANT: Glass, John I.
APPLICANT: Glass, John I.
APPLICANT: Heiner, Cheryl R.
APPLICANT: Lefkowitz, Ellioc
TITLE OF INVENTION: NUCLEIC ACID PROBES AND METHOD FOR DETECTING UREAPLASMA
TITLE OF INVENTION: UREALYTICUM
FILE REFERENCE: UAB-13452/22
CURRENT APPLICATION NUMBER: US/09/601,198
CURRENT FILING DATE: 2000-12-08
CURRENT FILING DATE: 2000-12-08
CURRENT FILING DATE: 2000-12-08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION NUMBER: 60/073,189
PRIOR FILING DATE: 1998-01-30
NUMBER OF SEQ ID NOS: 181.
SOPTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: DNA
ORGANISM: Ureaplasma urealyticum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 14066
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                                                                                                                                                                                                  2199
2549 TAATTACTGAAACTGGAAATCCGGTTTTAAAAGTTATTCAAACTCAAAATGATACTA 2493
                                                                                                                                                                                                                                                                              2139 CACCTGCTGAGCCAGAAGTCCCTCAAGTAGAGACTGAAAAAGTAGAAGCCCAACTCAAAG 2198
                                                                                                                                                                                                                                                                                                                                                          2079 AAGACCACAGTGAAGATCCAAATAAGAACTTCAAAGCGGATGAAGAGCCAGTAGAGGAAA 2138
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                                 CAGAAGCAGAAAAATTACTTGCGTTGTTAAAAAGGAAGTAATCCTTCATCTGTAAGTA 2375
                                                                              AACCATTAAAAACTCACACTAATTTATCTGTATCGATTAATGATAAAGAAAATATAAGTT 2550
                                                                                                                                                                                                AAGCAGAAGTTTTGCTTGCGAAAGTAACGGATTCTAGTCTGAAAGCCAATGCAACAGAAA
                                                                                                                 CTCTAGCTGGTTTACGAAATAATTTGACTCTTCAAATTATGGATAACAATAGTATCATGG 2318
                                                                                                                                                                                                                                         AAGATGATAATGATGTTTTAAATAACATTGATGCAACTGTTAAATTTTAAAGATGAACATA 2730
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Pred. No. 0.41;
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CURRENT APPLICATION NUMBER: US/09/134,001C
CURRENT FILING DATE: 1998-08-13
PRIOR APPLICATION NUMBER: US 60/064,964
PRIOR FILING DATE: 1997-11-08
PRIOR APPLICATION NUMBER: US 60/055,779
PRIOR APPLICATION NUMBER: US 60/055,779
PRIOR FILING DATE: 1997-08-14
NUMBER OF SEQ ID NOS: 5674
SEQ ID NO 925
LENGTH: 1704
TYPE: DNA
                                                        ; SEQ ID NO 2472
; LENGTH: 792
; TYPE: DNA
; ORGANISM: Acinetobacter baumannii
US-09-328-352-2472
                                                                                                                                                                                                                                                                                                US-09-328-352-2472
US-09-328-352-2472
Equence 2472, Application US/09328352
Patent No. 6562958
GENERAL INFORMATION:
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Query Match
Best Local Similarity
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                                                                                                                                                        APPLICANT: GARY L. Breton et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID
TITLE OF INVENTION: BAUWANNII FOR DIAGNOSTICS AN
FILE REFERENCE: GTC99-03PA
CURRENT APPLICATION NUMBER: US/09/328,352
CURRENT FILING DATE: 1999-06-04
NUMBER OF SEQ ID NOS: 8252
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40.2;
No. 0
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US-09-134-001C-1027/c; Sequence 1027, Application; Patent No. 6380370
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US-09-134-001C-322
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GENERAL INFORMATION:
APPLICANT: LYNN DOUGETTE-Stamm et al
APPLICANT: LYNN DOUGETTE-STAMM et al
TITLE OF INVENTION: UCLEIC ACID AND AMINO
TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNO
FILE REFERENCE: GTC-007
CURRENT APPLICATION UNMBER: US/09/134,001C
CURRENT FILING DATE: 1998-08-13
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Best Local Similarity
Matches 112; Conserv
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LENGTH: 30549
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION NUMBER: US 60/055,779
PRIOR FILING DATE: 1997-08-14
NUMBER OF SEQ ID NOS: 5674
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION NUMBER: US/09/134,001C CURRENT FILING DATE: 1998-08-13 PRIOR APPLICATION NUMBER: US 60/064,964 PRIOR FILING DATE: 1997-11-08
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                                                                                                                                                                                                                                                                                                                                                                                                                                         AATAAAATTATTGAAAACGCTCAACCTAGTGTACAACAAGTGTCTGATGAGAAATCTAAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AGTCGACTAAAATTGCGCTTTATCTGGATGATACTTATCCGGAACATGCACTTTTACGCC 271
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AATCGACTAATAAAGAAAAATTGGTAGATGATTATTGGCATTCCTAGCACCAATTACCC 1490
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAGAACTTGATTACGTTGCACATAATTTGATTCCTGGATTTCACCGTGCTTTTGCACAAC
                                                                                                                                                                                                                                                                                                                GCCTTAGACAAATTATTAGAACGCTTGAATGATGAATCGACTAATAAAGAAAA 1449
                                                                                                                                                                                                                                                                                                                                                                                                CTGTTAACTGAGGCTCATAAAGCCTTGTTTGNAAATAAGGGTCGTAATTCTGATTTCCAA 1396
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Pred. No. 1.
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                                                            AMINO ACID SEQUENCES RELATING DIAGNOSTICS AND THERAPEUTICS
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US-09-134-001C-1028
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; LENGTH: 297
; TYPE: DNA
; ORGANISM: Staphylococcus epidermidis
US-09-134-001C-1027
                                                                                                                                                                                                                                                                                                                                                    ; LENGTH: 1716
; TYPE: DNA
; ORGANISM: Staphylococcus
US-09-134-001C-1028
                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION NUMBER: US 60/055,779
PRIOR FILING DATE: 1997-08-14
NUMBER OF SEQ ID NOS: 5674
SEQ ID NO 1028
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 1028, Application US/09134001C Patent No. 6380370
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Lynn Doucette-Stamm et al
TITLE OF INVENTION: NUCLEIC ACID AND
TITLE OF INVENTION: EPIDERMIDIS FOR
FILE REFERENCE: GTC-007
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PRIOR FILING DATE: 1997-11-08
PRIOR APPLICATION NUMBER: US 60/055,779
PRIOR FILING DATE: 1997-08-14
NUMBER OF SEQ ID NOS: 5674
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR FILING DATE: 1997-11-08
                                                                                                                                                                                                                                                                                                   Match 1.7%;
Local Similarity 48.5%;
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Local Similarity 48.5%;
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1502
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                                                                                                                                                                                                                                               1704 CAGCTCAAGCCTATACTAAAGAAAAAGGTATCCTACCTCCATCTCCAGACGCAGATGTTA 1763
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                                                                                                       GAATTCCACTCGTTCGACTTCCATATATGGTTGAGCATACAGTTGAGGTTAAAAAACGGTA
                                                                                                                                          ATTTGATTATTCCTCATAAGGATCATTACCATAATATTAAATTTGCT 1930
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ATCAAAATGCTGAACAAGGTAATACTGGCGGTACAGATAAAGATGCT 1548
                               ATTTGATTATTCCTCATAAGGATCATTACCATAATATTAAATTTGCT 1930
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Pred. No. 0.49,
0; Mismatches
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Pred. No. 0.2;
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PATENT OF INVENTION: Complete Genome Sequence
Patent No. 6503729
TITLE OF INVENTION: jannaschii
FILE REFERENCE: PB275
CURRENT APPLICATION NUMBER: US/08/916,421B
CURRENT FILING DATE: 1997-08-22
PRIOR APPLICATION NUMBER: US 60/024,428
PRIOR FILING DATE: 1996-08-22
NUMBER OF SEQ ID NOS: 3
SOFTWARE: PatentIn version 3.1
SOFTWARE: PatentIn version 3.1
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US-08-916-421B-1/c
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US-09-601-198-3
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Best Local :
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CURRENT FILING DATE: 2000-12-08
PRIOR APPLICATION NUMBER: 60/073,189
PRIOR FILING DATE: 1998-01-30
NUMBER OF SEQ ID NOS: 181
                                                                                                                                                                                                                                                                                                              APPLICANT: Bult et al.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Cassell, Gail
APPLICANT: Chen, Ellson
APPLICANT: Glass, Jennif
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                      LENGTH: 1
TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: DNA ORGANISM: Ureaplasma urealyticum
ORGANISM: Methanococcus jannaschii
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                                           1664976
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GAAATTTTAGGGGAAGTTAATTT 446
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Glass, Jennifer S. Glass, John I.
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LOCATION: (31200... n e OTHER INFORMATION: n e OTHER ENFORMATION: n e NAME/KEY: misc_feature (312993).()
                         OCATION: (312993)..(312993)
OTHER INFORMATION: n equals
                                                                                                    LOCATION: (309398)..(309398)
OTHER INFORMATION: n equals
NAME/KEY: misc_feature
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OTHER INFORMATION: n equals
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OTHER INFORMATION: n equals
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OTHER INFORMATION: n equals
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OTHER INFORMATION: n equals
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OTHER INFORMATION: n equals
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OCATION: (2342
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OTHER INFORMATION: (1310988)..(1310988)
OTHER INFORMATION: n equals a,
NAME/KEY: misc feature NAME/KEY: misc feature LOCATION: (559167). (5) LOCATION: (1096846)..(1096846)
OTHER INFORMATION: n equals a,
NAME/KEY: misc\_feature NAME/KEY: misc\_feature LOCATION: (1470091)..(1470091) OTHER INFORMATION: n equals a, NAME/KEY: misc\_feature LOCATION: (1349491)..(1349491) LOCATION: (1119881)..(1119881)
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FILE REFERENCE: 62.US3.CIP
CURRENT APPLICATION NUMBER: US/09/671,317
CURRENT FILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: US 09/536,178
PRIOR FILING DATE: 2000-03-23
PRIOR APPLICATION NUMBER: PCT/IB00/00403
PRIOR APPLICATION NUMBER: US 60/126,269
PRIOR APPLICATION NUMBER: US 60/126,269
PRIOR APPLICATION NUMBER: US 60/126,269
PRIOR FILING DATE: 1999-03-25
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US-09-671-317-14/c
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                                                       SEQ ID NO 14
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Best Local
                                                                                                                                                                                                                                                                                               TITLE OF INVENTION: BIALLELIC MARKERS RELATED TO GENES INVOLVED IN DRUG METABOLISM FILE REFERENCE: 62.US3.CIP
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                                                                                      PRIOR FILING DATE: 1
                 LENGTH: 92
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LOCATION: (1664854)..(1664855)
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ORGANISM: Homo Sapiens
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                                                                                                             APPLICATION NUMBER: US 60/131,961 FILING DATE: 1999-04-30
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LENGTH: 1839
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                                                                                                                                     Matches 105;
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Best Local Similarity
Matches 83; Conserv
                                                                                                                                                        Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Patent No.
                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION NUMBER: US/09/134,001C CURRENT FILING DATE: 1998-08-13 PRIOR APPLICATION NUMBER: US 60/064,964 PRIOR FILING DATE: 1997-11-08 PRIOR APPLICATION NUMBER: US 60/055,779 PRIOR FILING DATE: 1997-08-14 NUMBER OF SEQ ID NOS: 5674
                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Lynn Dougette-Stamm et al TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS FILE REFERENCE: GTC-007
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY: misc_feature
LOCATION: 674..679,881..882,892..893
OTHER INFORMATION: n=a, g, c or t
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LOCATION: 481.500
OTHER INFORMATION: 12-454-363.misl,
NAME/KEY: misc_binding
LOCATION: 502.521
OTHER INFORMATION: 12-454-363.mis2,
                                                                                                                                                                                                                                                           TYPE: DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OTHER INFORMATION: upstream amplification primer NAME/KEY: primer bind LOCATION: 634..652 OTHER INFORMATION: downstream amplification primer,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LOCATION: 501
OTHER INFORMATION: 12-454-363 : polymorphic base A or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: allele
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LOCATION: 139..158
1573 TACAACGTCAGATGGTTACATTTTTGATGAACATGATATAATCAGTGATGAAGGAGATGC 1632
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                                                                                               AAATTCTCAAATTGAGTATACTGAAGACGAAGTTCGTATTGCTCAATTAGCTGATAAGTA 1572
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                                                                                                                                 Score 39; DB 4;
Pred. No. 0.84;
0; Mismatches 11
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US-08-360-606B-29
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; ORGANISM: Sac
US-08-360-606B-29
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Matches
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ZIP: 60606
EXIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: IBM PC compatible
TAMOTTER: TEM PC-DOS/MS-DOS
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GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: (312)913-000 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                 HYPOTHETICAL:
                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
LENGTH: 1856 base pairs
TYPE: nucleic acid
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SOFTWARE: MS Word 7.0
CURRENT APPLICATION DATA:
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TITLE OF INVENTION: Methods and Reagents for
TITLE OF INVENTION: Detecting Fungal Pathogens in
TITLE OF INVENTION: Biological Sample
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEPHONE: (312) 913-0002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Berghoff, Paul H. REGISTRATION NUMBER: 30,243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US/08/360, FILING DATE: December 21, 1994 CLASSIFICATION: 435
                                                                                                                                                                                                                                      Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                     STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE:
                                    1396
                                                                                                                                                                                 1276 ААСТЭСТАЛАЛАЛАЛАЛАТЭТТЭСТССТСЭТЭЛССАЛЭЛАТТТТАТЭЛТЛАЛАЭСЛТАТАЛ 1335
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5919617
                                                                                                                                                                                                                                      Similarity
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AGATGTTTTAAAAAGATTCCCACAAGGTAATGGTATATTATATGATTTTAGAATTTTTAGA
                                AGCCTTAGACAAATTATTAGAACGCTTGAATGATGAATCGACTAATAAAGAAAAATTGGT 1455
                                                                      CCCATTAATTCATGAACATATTCAATTTGCTCATTGTTATAAAGATCAAGCTGGTTGGCA
                                                                                                        TCTGTTAACTGAGGCTCATAAAGCCTTGTTTGNAAATAAGGGTCGTAATTCTGATTTCCA 1395
                                                                                                                                            AACTGCTCCTAAAGAGAATTATTTTTGGTTTAAAAAGAATTACCTGAAAATGAAACTTT
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f: U.S.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  E: McDonnell Boehnen Hulbert & Berghoff
300 S. Wacker Drive Suite 3200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Jnanendra K. Bhattacharjee
Richard C. Garrad
Paul L. Skatrud
                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                    linear
                                                                                                                                                                                                                                                                                                              Saccharomyces cerevisiae
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                                                                                                                                                                                                                                                                                                                                                                                     single
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                                                                                                                                                                                                                                                       DB 2;
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US-08-861-464-13/c
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                                                                     Query Match
Best Local Similarity
                                                            Matches
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                                                                                                                                                                                                                                                                                                            TELEFAX: 781-861-9540
INFORMATION FOR SEQ ID NO:
                                                                                                                                NAME/KEY:
LOCATION:
FEATURE:
NAME/KEY:
LOCATION:
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APPLICANT: Austriaco Jr., Nicanor
APPLICANT: Kennedy. Brisn
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FILING DATE: 15-AUG-
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 1
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MEDIUM TYPE: Floppy
COMPUTER: IBM PC com
                                                                                                                                                                                                         FEATURE:
                                                                                                                                                                                                                          MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS
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PRIOR APPLICATION DATA:
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APPLICATION NUMBER: 1
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                                                                                                                                                                                                                                                                                                                                                                      NAME: Granahan, Patricia
REGISTRATION NUMBER: 32,
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE: 22
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                    STRANDEDNESS:
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                                                                                                                                                                                                                                                                                  ENGTH:
1152 GAAGAAGAAGAGGAGGAGGAAGAAGAAGAAGAAGTAGAAGTAGAAGTAGAA 1093
                           2090 GAAGATCCAAATAAGAACTTCAAAGCGGATGAAGAGCCAGTAGAGGAAACACCTGCTGAG 2149
                                                            91;
                                                                                                                                                                                                                                                                 : 2150 base pairs nucleic acid
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VENTION: Genes Determining Cellular Senescence
                                                            Conservative
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563..1987
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                                                                                                                                                                                                                                                                                                                                             781-861-6240
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                                                                        1.6%;
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                                                         Score 38.8; DE Pred. No. 1; 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Version #1.30
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US-08-396-001-13
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US-08-396-001-13/c
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Guarente, Leonard P.
APPLICANT: Austriaco Jr., Nicanor
APPLICANT: Claus, James
APPLICANT: Cole, Francesca
APPLICANT: Kennedy, Brian
TITLE OF INVENTION: Genes Determining
TITLE OF INVENTION: Yeast
                                                                                                                                                                                                                                                                                                                                                 FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELECOMMUNICATION INFORMATION: TELEPHONE: 617-861-6240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 2150 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Granahan, Patricia
REGISTRATION NUMBER: 32,227
REFERENCE/DOCKET NUMBER: MI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: FILING DATE: 28-FEE CLASSIFICATION: 435
                                                                                                                                                                                                                                      Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CITY: Lexington
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                                                                                                                                                                                 2090 GAAGATCCAAATAAGAACTTCAAAGCGGATGAAGACCAGTAGAGGAAACACCTGCTGAG 2149
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o. 5919618
                                                                                                                                                                                                                     91;
                                                                                                                                                                                                                                      Similarity
                                 TTGCTTGCGAAAGTAACGGATTCTAGTCTGAAAGCCCAATGCAACAGAAACTCTAGCTG
                                                                       GTAGAAGTAGATGGTGAAGTGGAAGAAGTACTAGATTTAGTGGCAGAAGAAGCACTAGAT 1033
                                                                                                       CCAGAAGTCCCTCAAGTAGAGACTGAAAAAGTAGAAGCCCAACTCAAAGAAGCAGGAGGTT
                                                                                                                                             GAAGAAGAAGAAGAGGAGGAAGGAAGAAGAAGAAGTAGAAGTAGAAGTAGAA
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                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         28-FEB-1995
N: .435
                                                                                                                                                                                                                                                                                                                                                                DNA (genomic)
                                                                                                                                                                                                                                      51.1%;
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                                                                                                                                                                                                                 Score 38.8; DE Pred. No. 1; 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MIT-6408A2
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US-09-323-433A-13/c
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CURRENT FILING DATE: 199-06-01
PRIOR APPLICATION NUMBER: US 08/396,001
PRIOR FILING DATE: 1995-02-28
PRIOR APPLICATION NUMBER: PCT/US94/09351
PRIOR TILING DATE: 1994-08-15
PRIOR APPLICATION NUMBER: US 08/107,408
PRIOR FILING DATE: 1993-08-16
PRIOR FILING DATE: 1993-08-16
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SEQ ID NO 13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity Matches 91; Conserv
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APPLICANT:
APPLICANT:
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NUMBER OF SEQ ID NOS:
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NAME/KEY: CDS
LOCATION: (563)...(1987)
OTHER INFORMATION: SAG1
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TYPE: DNA
ORGANISM: Saccharomyces cerevisiae
                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
COMPUTER: TEADABLE FORM:
MEDIUM TYPE: Diskette, 3.
COMPUTER: IBM compatible
OPERATING SYSTEM: MS-DOS
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APPLICANT: VECHT, Uri
                                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                               STREET:
                                                                                                                                                                                    COUNTRY: The Netherlands
                                                                                                                                                                                                                                                                                                                                         ADDRESSEE:
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                                                                                                                                                                                                                                                                PH Lelystad
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Cole, Francesca
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Claus, James J.
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                                                                                                                                                                                                                                                                                                   Edelhertweg
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51.1%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                             DNA Sequences which code for Virulence Characteristics of Streptococcus suis and parts thereof, polype antibodies derived therefrom and the use thereof for the diagn protection against infection by S. suis in mammals, including protection against infection by S. suis in mammals, including protection against infection by S. suis in mammals, including protection against infection by S. suis in mammals, including protection against infection by S. suis in mammals, including protection against infection by S. suis in mammals, including protection against infection by S. suis in mammals, including protection against infection by S. suis in mammals, including protection against infection by S. suis in mammals, including protection against infection by S. suis in mammals, including protection against infection by S. suis in mammals, including protection against infection by S. suis in mammals, including protection against infection by S. suis in mammals, including protection against infection by S. suis in mammals, including protection against infection by S. suis in mammals, including protection against infection by S. suis in mammals, including protection against infection by S. suis in mammals, including protection against infection by S. suis in mammals, including protection against infection by S. suis in mammals, including protection against infection by S. suis in mammals, including protection against the suit 
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                                                                            3.50 inch,
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           v.6.0
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SOFTWARE: WordPerfect v. 6.0 CURRENT APPLICATION DATA:

APPLICATION NUMBER: FILING DATE: 20-SE

20-SEP-1993

US/08/119,125A

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                                                                                                                          Query Match
Best Local Similarity
Matches 140; Conserv
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NFORMATION FOR SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                  LOCATION: FEATURE: NAME/KEY:
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APPLICATION NUMBER: PCT/I
FILING DATE: 19-MAR-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: NL 9100510
FILING DATE: 21-MAR-1991
ATTORNEY/AGENT INFORMATION:
NAME: Handal, Anthony H.
                                                                                                                                                                                                                                       FEATURE:
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NAME/KEY:
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ORIGINAL SOURCE:
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NAME/KEY:
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NAME/KEY:
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NAME/KEY:
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REGISTRATION NUMBER: 262
REFERENCE/DOCKET NUMBER:
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                               2111
 3601
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Nucleic acid with corresponding amino acids
DEDNESS: single stranded
GATGAGAAGGAATCAGCTAAGAATGCAGTGGAAGAGGCGGCTAAGGTAGCAACAGCCGCT 3660
                            APAGCGGATGAAGAGCCAGTAGAGGAAACACCTGCTGAGCCAGAAGTCCCTCAAGTAGAG
                                                             ATTGCCAAAGAAGCAGAATCAGCTAAGAAAGCGATTGACGACAATCCAAACTTGACTCCA
                                                                                          AATGCCAGTGAGCATGTGTTAGGCAAGAAAGACCACAGTGAAGATCCAAATAAGAACTTC 2110
                                                                                                                           Conservative
                                                                                                                                                                                                  dyad symmetry regions from bp 6631 to 6644
                                                                                                                                                                                                                                                                                                                                                              start of repetitive units R1-R11 bp 2869, 3097, 3292, 3520, 4087, 4381, 5065, 5293, 5521:
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                                                                                                                                                                                                                                                  dyad symmetry regions from bp 6554 to 6566 and
                                                                                                                                                                                                                                                                                                    start of repetitive Asn-Pro-Asn-Leu sequences bp 2932, 3160, 3355, 3583, 4150, 4444, 4672, 4900 5128, 5356, 5584:
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bp 176 to 181
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                                                                                                                                                                                                                                                                                                                                                                                                                                signal peptide
bp 361 to 498
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    genomic DNA
                                                                                                                                       1.6%;
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                                                                                                                          0;
                                                                                                                      Score 38.6; DB 1;
Pred. No. 2.1;
0; Mismatches 169;
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                                                                                                                                                       DB 1; Length 6744;
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GAGAANTITGACTCCTCATGAGGTTAGCAAGCGTGAAGGAATGAATGCTGACCAAATCGT
GAGAANTITGACTCCTCATGAGGTTAGCAAGCGTGAAGGAATGCAATGCTGAGATGCAAAATTAA 5970

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                                                                                                                                 US-08-446-855A-1
                                                             Query Match
Best Local Similarity
Matches 131; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 1, Applic
Patent No. 5849573
                                                                                                                                                                                                                                                INFORMATION FOR SEQ ID NO:
                                                                                                                                               TOPOLOGY: 15
MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: PatentIn Rel CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ZIP: 22201-4714
COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                                                                               ATTORNEY/AGENT INFORMATION:
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CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM PC
OPERATING SYSTEM:
SOFTWARE: PatentI
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CTTY: Arlington
TTTY: Arlington
                                                                                                                                                                                                                                                  TELEPHONE: 703-816-4100
                                                                                                                                                                                                                                                                                                                              NAME: Mitchard, Leo
REGISTRATION NUMBER:
                                                                                                                                                                             STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US/0 FILING DATE: 06-Jul-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDIUM TYPE:
                                                                                                                                                                                                                                                                                                               REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE:
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                                                                                                                                                                                        : 8920 base pairs
                            AACGGTTAAGGAAAATAATCGTGTTTCCTATATAGATGGAAAACAAGCGACGCAAAAAAC 90
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AATAGGGAATAATAAAAATATGGATATGTATTTATCTAAGGAAAAAAGTATATCTAATAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Virginia
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1100 No. 5849573th Glebe Road, 8th Floor
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O'Sullivan, William J
NENTION: Nucleotide sequence encoding carbamoyl
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                                                                Conservative
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                                                                                                                                                                SS: single
linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                              IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                            Leonard
                                                                            1.6%;
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                                                             Score 38.6; DB 2;
Pred. No. 2.4;
0; Mismatches 154;
                                                                                            Length 8920;
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RESULT 50
US-08-169-927-1
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US-09-150-741-1
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               GENERAL INFORMATION:
APPLICANT: Carl, M:
APPLICANT: Dobson,
APPLICANT: Ching, V
                                                                                        Patent No. 5783441
                                                                                                        Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 1, Application US/09150741 Patent No. 6183996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION: Nucleotide Sequence Encoding Carbamoyl Phosphate Patent No. 6183996
TITLE OF INVENTION: Synthetase II
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EARLIER FILING DATE: 1993-12-02
EARLIER APPLICATION NUMBER: 08/446,855
EARLIER FILING DATE: 1995-07-06
NUMBER OF SEQ ID NOS: 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION NUMBER: US/09/150,741
CURRENT FILING DATE: 1998-99-10
EARLIER APPLICATION NUMBER: PL6380
EARLIER FILING DATE: 1992-12-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: PatentIn Ver. 2.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Stewart et al.
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TYPE: DNA
ORGANISM: Plasmodium falciparum
 APPLICANT:
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                                                                                                            Application US/08169927
                                                                                                                                                                                                                                       TAAGCTAAAAGATGAGGATATTGTTAATGAGGTCAAGGGTGGATA, 315
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             Dobson, Michael E.
Ching, Wei Mei
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                                                    Carl, Mitchell
Gregory A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 8920;
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PUBLICATION INFORMATION:
AUTHORS: Carl, M.
AUTHORS: Dosson, M. E.
AUTHORS: Ching, W. M.
AUTHORS: Dasch, G. A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX: (301) 295-102
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE: D
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: i
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                   FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 0
FILING DATE: 08/09/91
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                       FEATURE:
NAME/KEY:
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NAME/KEY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM:
STRAIN: B
                                                                           TITLE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: FILING DATE:
                             JOURNAL:
                                                                                                                                                                                                                                        LOCATION:
                                                                                                                                                                                                                                                                                                                                  LOCATION:
                                                                                                                                                                                                                                                                                                                                                    NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Spevack, A. David REGISTRATION NUMBER: 24,743
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: PatentIn Release #1.0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
RELEVANT RESIDUES IN SEQ ID NO:
                                                                                                                                                                                          LOCATION:
                                                                                                                                                                                                                                                                                     LOCATION:
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                1990
                          Characterization of the gene encoding the protective S-layer protein of Rickettsia prowazekii; presence of a truncated identical homolog in rickettsia typhi proc. Natl. Acad. Sci. U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ₹
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391..5226
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5270..5306
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363..368
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Sequence 34, Appl Sequence 2179, Appl Sequence 2019, Appli Sequence 20619, Appli Sequence 20619, Appli Sequence 1597, Ap Sequence 1597, Ap Sequence 1988, A Sequence 2722, Apsequence 2722, Apsequence 2722, Apsequence 2723, App Sequence 2534, App Sequence 19974, App Sequence 19974, App Sequence 187, Appli Sequence 187, Appli Sequence 1884, App Sequence 1884, App Sequence 2184, App Sequence 2185, App Sequence 2184, App Sequence 2185, App Sequence 2187, App Sequence 2188, App Sequence 21894, App Seque
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| Query Ma<br>Best Loc<br>Matches                                    | REGISTRATION NUMBER: 30,3/3 REFERENCE, DOCKET NUMBER: PB340P2 REFERENCE, DOCKET NUMBER: PB340P2 RELEPHONE: (301) 309-8504 TELEPHONE: (301) 309-8512 INFORMATION FOR SEQ ID NO: 55: SEQUENCE CHARACTERISTICS: LENGTH: 2389 base pairs TYPE: nucleic acid STRANDEDNESS: double COPOLOGY: linear SEQUENCE DESCRIPTION: SEQ ID NO: 55: US-09-765-272-55 | COMPUTER: Nº VECLEA 100/33  OPERATING SYSTEM: MSDOS Version 6.2  SOFTWARE: ASCII Text CURRENT APPLICATION DATA:  APPLICATION NUMBER: US/09/765,272  FILING DATE: 22-Jan-2001  CLASSIFICATION: <unknown> PRIOR APPLICATION UNMBER: 08/961,083  FILING DATE: <unknown> APPLICATION NUMBER: 08/961,083  FILING DATE: <unknown> ATTORNEY/AGENT INFORMATION: NAME: Brookes, A. Ander: NAME: Brookes, A. Ander: NAME: Brookes, A. Ander: NAME: Brookes, A. Ander: NAME: Brookes, A. Ander:</unknown></unknown></unknown> | LICANT: Choi et<br>LICANT: Choi et<br>LICANT: CHOINCE<br>BER OF SEQUENCE<br>RESPONDENCE ADI<br>ADDRESSEE: HU<br>STREET: 9410<br>CITY: Rockvil<br>STATE: Maryla<br>COUNTRY: USA<br>ZIP: 20850<br>PUTER READABLE<br>MEDIUM TYPE: | ALIGNMENTS  RESULT 1 US-09-765-272-55 Sequence 55, Application US/09765272 Patent No. US20020061545A1 GENERAL INFORMATION:            | c 90 39.2 1.6 462 9 US-09-864-761-3829 Sequence 3829, Ap c 91 39.2 1.6 1074 9 US-09-861-451A-49 Sequence 49, Appl 92 39.2 1.6 1495 12 US-10-032-865-6091 Sequence 6091, Ap 93 39.2 1.6 6944 14 US-10-172-086-111 Sequence 111, Appl 94 39 1.6 477 9 US-09-864-761-5436 Sequence 5436, Ap 95 39 1.6 2050 14 US-10-086-510-1 Sequence 1, Appli c 96 38.8 1.6 277 9 US-09-294-093B-1831 Sequence 1831, Ap 100 38.8 1.6 505 10 US-09-917-800A-314 Sequence 18737, Ap 100 38.8 1.6 510 9 US-09-864-761-18737 Sequence 13, Appl 38.8 1.6 510 9 US-09-864-761-18737 Sequence 13, Appl 38.8 1.6 510 9 US-09-826-752-13 Sequence 13, Appl 510 US-09-826-752-13 Sequence 13, Appl 510 US-09-826-752-13 Sequence 302235, |
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Sequence 3, Application US/09884465A
Publication No. US20030077293A1
GENERAL INFORMATION:
APPLICANT: Shire Biochem, Inc.
APPLICANT: Hamel, Josee
APPLICANT: Brodeur, Bernard
APPLICANT: Martin, Denis
APPLICANT: Martin, Denis
APPLICANT: Charland, Nathalie
APPLICANT: Ouellet, Catherine
TITLE OF INVENTION: Streptcoccus Antigens
FILE REFERENCE: 055190-0044
CURRENT FILING DATE: 2001-06-20
PRIOR APPLICATION NUMBER: 60/212,683
PRIOR FILING DATE: 2000-06-20
PRIOR FILING DATE: 2000-06-20
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SOFTWARE: PatentIn version 3.1

SEQ ID NO 3

LENCTH: 2523

TYPE: DNA

ORGANISM: Streptococcus pneumoniae
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GAAAGCCAATGCAACAGAAACTCTAGCTGGTTTACGAAATAATTTGACTCTTCAAATTAT
                                                                                                                     AGTAGAAGCCCAACTCAAAGAAGCAGAAGTTTTGCTTGCGAAAGTAACGGATTCTAGTCT
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                                                 CAAGTCCAATGCCAAAGAGACTCTCACAGGATTAAAAAATAATTTACTATTTGGCACCCA
                                                                                                GGTTGAAGAAAACTGAGAGAGGCTGAAGATTTACTTGGAAAAATCCAGGATCCAATTAT
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US-09-884-465A-4

Sequence 4, Application US/09884465A

Publication No. US20030077293A1

GENERAL INFORMATION:
APPLICANT: Shire Blochem, Inc.
APPLICANT: Hamel, Josee
APPLICANT: Hamel, Josee
APPLICANT: Martin, Denis
APPLICANT: Martin, Denis
APPLICANT: Obellet, Catherine
TITLE OF INVENTION: Streptococcus Antigens
FILE REFERENCE: 055190-004

CURRENT FILING DATE: 2001-06-20

PRIOR APPLICATION NUMBER: 60/212,683
PRIOR FILING DATE: 2000-06-20

NUMBER OF SEQ ID NOS: 384

SOFTWARE: Patentin version 3.1

SEQ ID NO 4

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| Db 1004 CGCCAGAGGTGTAGCTGTCCCTCATGGTAACCATTACCACTTTATCCCCTTATGAACAAAT 1063 | OY 901 AGCTAGAGGTGTTGCAGTGCCACACGGAGATCATTACCACTTCATCCCTTACTCTCAAAT 960 | Qy 841 TCAACGACATGTAGAATCTGATGGCCTTGTCTTTGATCCAGCACAAATCACAAGTCGAAC 900 | Oy 781 AGCAAGTCAAAGTAATGACATTGATAGTCTCTTGAAACAGCTCTACAAACTGCCTTTGAG 840 | 721<br>824 | Qy 661 TTCAAGAACCTATCGCCGACAAAATAGCGATAACACTTCAAGAACAAACTGGGTACCTTC 720  | OY 601 ATCAGCTAGCGAGTTGGCTGCAGAAGCCTTCCTATCTGGTCGAGGAAATCTGTCAAA 660 | Qy 541 TGGTGATGCTTATATCGTTCCTCATGGAGATCATTACCATTACATTCCTAAGAATGAGTT 600 | OY 481 AGGACGCTATACTACAGATGATGGTTATATCTTTAATGCTTCTGATATACATAGAGGATAC 540 | OY 421 TCAACATCGTGAAGGTGGAACTCCAAGAAACGATGGTGCTGTTGCCTTTGGCACGTTCGCA 480 | Qy 361 TGCCCACGCGGATAACGTCCGTACAAAAGAGGAAATCAATC                  | OY 301 GGTCAAGGGTGGATATGTTATCAAGGTAGATGGAAAATACTATGTTTACCTTAAGGATGC 360 | Qy 241 TGAAGAATTACTCATGAAAGATCCAAACTATAAGCTAAAAGATGAGGATATTGTTAATGA 300   | Qy 181 TTCACATGGCGACCACTATCATTATTACAATGGTAAGGTTCCTTATGACGCTATCATCAG 240 | QY 121 GCGTGAAGGAATCAATGCTGAGCAAATCGTCATCAAGATAACAGACCAAGGCTATGTCAC 180 | QY 61 TATAGATGGAAACAAGCGACGCAAAAAAACGGAGAATTTGACTCCTGATGAGGTTAGCAA 120   | Qy 1 TTCTTACGAGTTGGGACTGTATCAAGCTAGAACGGTTAAGGAAAATAATCGTGTTTCCTA 60 | Query Match 57.5%; Score 1374.2; DB 11; Length 2647; Best Local Similarity 73.9%; Pred. No. 0; Matches 1819; Conservative 0; Mismatches 539; Indels 102; Gaps 2; | ; LENGTH: 2647<br>; TYPE: DNA<br>; ORGANISM: Streptococcus pneumoniae<br>US-09-884-465A-4 |
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|  | F &   |   | ס שם  |            | 0 dg 4   |  |   |  |  |   |   |   |   |   |  |  |  |   |
| 029 ACATTCTAATGATGGATGGGGCAATGCCAGTGAGCATGTGTTAGGCAAGAAAGA                 | 1969 TACCTTGGAAGATTTGTTTGCGACGATTAAGTACTACGTAGAACACCCTGACGAACGTCC 2028  |   | 1964 CAATCTTCAATATACTGTAGAAGTCAAAAACGGTAGTTTAATCATAACCTCATTATGACCA 2023 |            | 1/27 AGGIAICLIACCICCAIC ICCAGACGCAGAIGI MANGCAMAILCCAACIGGAGAIAGIGC 1/88 | 669 TGGAAAAGATAGCCTTCTCATAAGGAAAAAGTTGCAAGCCAAGCCTATACTAAAGAAAA      | 609 TATATCAGTGATGAGGAGATGCATATGTAACGCCTCATATGGGCCATAGTCACTGGAT          | 49 TATTGCTCAATTAGCTGATAACTATACAACGTCAGATGGTAACATTTTTGATGAACATGA 4        | BY CHAILCAGAGCGACTIGGCAAATCCICAAATTGGGTATATTGGAGAGGGAAGTTGGGTTGG         | 429 TGAATICGACTAATAAAAAAATIGGTAGATTATTAGCAATTACTGCATTAGCACCAATTAC | AAAIAAGGTIGTAATTCIGATTICCAAGCCTTAGACAAATTAGAAGGCTTGAATGA   HIII         | 100 CONCENTITION AND CONTRACT CONTRACT CARROCCIDE IN ANA CONTRACT | 249 AAAACAAGAGGIGITICACACACATTTAACTGCTAAAAAAAAAA                        | 189 TEATSTCTTTGCGAAAGCTAAGCTGTTAAAAATCTTGAAAGCAAGC                      | 22 IASI CROCLEGIA COMANGILI GEOGRAPOGALA GIALI GANGANANA GEOGLA CITOCO (CITOCO) (CIT | CCCCARCCICCACAATCITAMAATCITAMAACCAACCAATCAATCAATCAATTGATGAGAAATTGGT  | 021 GGTACCAGATTCAAGGCCAGAACCAAGTCCACAACCGACTCCGGAACCTAGTCCAGG  | 961 GTCTGAATTGGAAGAACGAATCGCTCGTATATTCCCCTTCGTTATCGTTCAAACCATTG                           |

| Oy 238 CAGTGAAGAATTACTCATGAAAGATCCAAACTATAAGCTAAAAGATGAGGATATTGTTAA    | 178  | Qy 118 CAAGCGTGAAGGAATCAATGCTGAGCAAATCGTCATGAAGATAACAGACCAAGGCTATGT    | Qy 58 CTATATAGATGGAAAAACAAGCGAAAAAAACGGAGAATTTGACTCCTGATGAGGTTAG        | Oy 1 TTCTTACGAGTTGGGACTGTATCAAGCTAGAAAGGTTAAGGAAAATAATCGTGTTTC | Query Match 42.0%; Score 1003.8; DB 11; Length Best Local Similarity 66.0%; Pred. No. 4.1e-229; Matches 1623; Conservative 0; Mismatches 693; Indels : |   | FILING DATE: 1999-03-19<br>R OF SEQ ID NOS: 388<br>ARE: PatentIn Ver. 2.1<br>NO 206 | FILING DATE: 2001-01-26 PLICATION NUMBER: GB 9816 LING DATE: 1998-03-27 PLICATION NUMBER: US 60/1 | Hansbro, Philip M<br>NVENTION: Proteins<br>ENCE: PWC/P21129WO<br>DITCATION NIMBER: US/O | ion No. US20030091577A1 INFORMATION: WI: Microbial Technics L         | RESULT 4<br>US-09-769-787-206<br>: Sequence 206. Application US/09769787 | Qy 2299 GGATAACAATAGTATCATGGCAGAAGCAGAAAATTACTTGCGTTGTTAAAAGGAAGTAA  | Qy 2239 GAAAGCCAATGCAACAGAAACTCTAGCTGGTTTACGAAATAATTTGACTCTTCAAATTAT | Qy 2179 AGTAGAAGCCCAACTCAAAGAAGCAGAAGTTTTGCTTGCGAAAGTAACGGATTCTAGTCT | Qy 2126CAGTAGAGGAAACACCTGCTGAGCCAGAAGTCCCTCAAGTAGAGACTGAAAA          | Qy       2126                                    | Qy 2089 TGAAGATCCAAATAAGAACTTCAAAGCGGATGAAGAG                        | Db 2144 GCATTCAGATAATGGTTTTGGTAACGCTAGCGACCATGTTCAAAGAAACAAAAATGGTCA |
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| ATATTGTTAA 297 . Qy  |  | JAAGGCTATGT 177  | 117   | 57   | 2481; Qy<br>144; Gaps 6; Db  | Qy<br>da  | סy<br>da  | Qy<br>Db  | Qy<br>Db  | Qy<br>da  | Qy<br>Db   | NAAGGAAGTAA 2358 Oy<br>  | TTCAAATTAT 2298 Qy<br>        Oy<br>TTGGCACCCA 2503 Db               | ATTCTAGTCT 2238  | 9AGACTGAAAA 2178   | CAAAACCAAC 2323 Db                               | 2125 Qy<br>3AAAAACCTGA 2263 Db                                       | NAAAATGGTCA 2203 Db  |
| 1306 TGACCAAGAATTTTATGATAAAGCATATAATCTGTTAACTGAGGCTCATAAAGCCTTGTT 1365 | 1246 ATCAAAACAAGAGAGTGTTTCACACACTTTAACTGCTAAAAAAGAAAATGTTGCTCCTCG 1305 | 1218 TCGTTATATCCCAGCCAAGGATCTTTCAGCAGAAACAGCAGCAGGCATTGATAGCAAACT 1277 | 1186 TCGTTATGTCTTTGCGAAAGATTTTACCATCTGAAACTTAAAAATCTTTGAAAAGCAAGTT 1245 | 1078 AGGCCGCAACCTGCACCAAATCTTAAAATAGACTAA                      | 18 TTGGGTACCAGATTCAAGGCCAGAACCAAGTCCACAACCGACTC  | 958 AATGTCTGAATTGGAAGAACGAATCGCTCGTATTATTCCCCTTCGTTATCGTTCAAACCA 1017<br> | 898 AACAGCTAGAGGTGTTGCAGTGCCACAGGGAGATCATTACCACTTCATCCCTTACTCTCA 957                | 838 GAGTCAACGACATGTAGAATCTGATGGCCTTGTCTTTGATCCAGCACAAATCACAAGTCG 897                              | 778 TCAAGCAAGTCAAAGTAATGACATTGATAGTCTCTTGAAACAGCTCTACAAACTGCCTTT 837                    | 718 TTCTGTAAGCAATCCAGGAACTACAAATACTAACACAAGCAACAACAGCAACACCTAACAG 777 | 658 AAATTCAAGAACCTATCGCCGACAAAATAGCGATAACACTTCAAGAACAAACTGGGTACC 717     | 598 GTTATCAGCTAGCGAGTTGGCTGCTGCAGAAGCCTTCCTATCTGGTCGAGGAAATCTGTC 657 | 538 TACTGGTGATGCTTATATCGTTCCTCATGGAGATCATTACCATTACATTCCTAAGAATGA 597 | 478 GCAAGGACGCTATACTACAGATGATGGTFATATCTTTAATGCTTCTGATATCATAGAGGA 537 | 418 TAGTCAACATCGTGAAGGTGGAACTCCAAGAAACGATGGTGCTGTTGCCTTGGCACGTTC 477 | 358 TGCTGCCCACGCGGATAACGTCCGTACAAAAGAGGAAATCAATC | 298 TGAGGTCAAGGGTGGATATGTTATCAAGGTAGATGGAAAATACTATGTTTACCTTAAGGA 357 |  |

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GGACAACAATACTATTATGGCAGAAGCTGAAAAACTATTGGCTTTATTAAAGGAGAGTAA
                               GGATAACAATAGTATCATGGCAGAAGCAGAAAAATTACTTGCGTTGTTAAAAGGAAGTAA 2358
                                                                                             CAAGTCCAATGCCAAAGAGACTCTCACAGGATTAAAAAATAATTTACTATTTGGCACCCA
                                                                                                                                  GAAAGCCAATGCAACAGAAACTCTAGCTGGTTTACGAAATAATTTGACTCTTCAAATTAT
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RESULT 5
US-09-765-272-65
; Sequence 65, Application US/09765272
; Patent No. US20020061345A1
; GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
Matches 1481; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX: (301) 309-8512
INFORMATION FOR SEQ ID NO: 65:
SEQUENCE CHARACTERISTICS:
LENGTH: 2290 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: 08/961,083 FILING DATE: <Unknown> ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/765,272
FILING DATE: 22-Jan-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch,
COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.
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ADDRESSEE: Human Genome Sciences,
STREET: 9410 Key West Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REFERENCE/DOCKET NUMBER: TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Choi et. al.
TITLE OF INVENTION: Streptococcus
NUMBER OF SEQUENCES: 452
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STATE: Maryland
COUNTRY: USA
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                      TGAGGTCAAGGGTGGATATGTTATCAAGGTAGATGGAAAATACTATGTTTACCTTAAGGA
                                                                                                 CAGTGAAGAATTACTCATGAAAGATCCAAACTATAAGCTAAAAGATGAGGATATTGTTAA
                                                                                                                                                       GACCTCTCATGGAGACCATTATCATTACTATAATGGCAAGGTTCCTTATGATGCCATCAT
                                                                                                                                                                              CACTTCACATGGCGACCACTATCATTATTACAATGGTAAGGTTCCTTATGACGCTATCAT
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TGAAATCAAGGGTGGTTATGTCATTAAGGTAAACGGTAAATACTATGTNTACCTTAAGGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEPHONE: (301) 309-8504
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
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Pred. No. 2.9e-225;
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        TGATGAATCGACTAATAAAGAAAAATTGGTAGATGATTTATTGGCATTCCTAGCACCAAT 1485
                                                                                        TGNAAATAAGGGTCGTAATTCTGATTTCCAAGCCTTAGACAAATTATTAGAACGCTTGAA
                                                                                                                                                              TGACCAAGAATTTTATGATAAAGCATATAATCTGTTAACTGAGGCTCATAAAGCCTTGTT
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Sequence 5, Application US/09884465A
Publication No. US20030077293A1
GENERAL INFORMATION:
APPLICANT: Shire Biochem, Inc.
APPLICANT: Hamel, Josee
APPLICANT: Brodeur, Bernard
APPLICANT: Martin, Denis
APPLICANT: Charland, Nathalie
APPLICANT: Charland, Nathalie
APPLICANT: Ouellet, Catherine
TITLE OF INVENTION: Streptococcus Antigens
FILE REFERENCE: 055190-0044
CURRENT FILING DATE: 2001-06-20
PRIOR APPLICATION NUMBER: 60/212,683
PRIOR FILING DATE: 2000-06-20
NUMBER OF SEQ ID NOS: 384
SOPTWARE: Patentin version 3.1
SEQ ID NO 5
LENGTH: 2639
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US-09-884-465A-5
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|---|--|--|--|--|--|--|--|--|---|--|--|--|--|--|---|--|---|---|
| AATGTCTGAATTGGAAGAACGAATCGCTCGTATTATTCCCCCTTCGTTATCGTTCAAACCA 1 | AACAGCTAGAGGTGTTGCAGTGCCACACGGAGATCATTACCACTTCATCCCTTACTCTCA | 838 GAGTCAACGACATGTAGAATCTGATGGCCTTGTCTTTGATCCAGCACAAATCACAAGTCG 897 | 778 TCAAGCAAGTCAAAGTAATGACATTGATAGTCTCTTGAAACAGCTCTACAAACTGCCTTT 837 | 718 TTCTGTAAGCAATCCAGGAACTACAAATACTAACACAAGCAACAACAGCAACACTAACAG 777 | 658 AAATTCAAGAACCTATCGCCGACAAAATAGCGATAACACTTCAAGAACAAACTGGGTACC 717 | 598 GTTATCAGCTAGCGAGTTGGCTGCTGCAGAAGCCTTCCTATCTGGTCGAGGAAATCTGTC 657 | 538 TACTGGTGATGCTTATATCGTTCCTCATGGAGATCATTACCATTACATTCCTAAGAATGA 597 | 478 GCAAGGACGCTATACTACAGATGATGGTTATATCTTTAATGCTTCTGATATCATAGAGGA 537 | 418 TAGTCAACATCGTGAAGGTGGAACTCCAAGAAACGATGGTGCTGTTGCCTTTGGCACGTTC 477 | 358 TGCTGCCCACGCGCATAACGTCCGTACAAAAGAGGAAATCAATC | 298 TGAGGTCAAGGGTGGATATGTTATCAAGGTAGATGGAAAATACTATGTTTACCTTAAGGA 357 | 238 CAGTGAAGAATTACTCATGAAAGATCCAAACTATAAGCTAAAAGATGAGGATATTGTTAA 297 | 178 CACTTCACATGGCGACCACTATCATTATTACAATGGTAAGGTTCCTTATGACGCTATCAT 237 | 118 CAAGCGTGAAGGAATCAATGCTGAGCAAATCGTCATCAAGATAACAGACCAAGGCTATGT 177 | 58 CTATATAGATGGAAAACAAGCGACGCAAAAAACGGAGAATTTGACTCCTGATGAGGTTAG 117 | 1 TTCTTACGAGTTGGGACTGTATCAAGCTAGAACGGTTAAGGAAAATAATCGTGTTTC 57 | Query Match 41.1%; Score 980.8; DB 11; Length 2639; Best Local Similarity 67.8%; Pred. No. 1.3e-223; Matches 1473; Conservative 0; Mismatches 638; Indels 60; Gaps 5; | TYPE: DNA ORGANISM: Streptococcus pneumoniae -09-884-465A-5 |
| Q   | p Q  | 99<br>20   | Db Q   | ) B &  | Db Qy  | B 6  | ) B &  | ) B &  | P &   | ) B &  | D 50   | ) B 9  | p &  | ) B 4  | S B 8   | 3 da 4   | S B &   | Db  |
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                                                                                                                                                                                                                                                                                              Matches
                                                                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INFORMATION FOR SEQ ID NO: 181: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                 Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REFERENCE/DOCKET NUMBER: PB340P2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 309-8504
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: 08/961,083
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/765,272
FILING DATE: 22-Jan-2001
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb
                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE DESCRIPTION: SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Choi et. al.
TITLE OF INVENTION: Streptococcus pneumoniae
NUMBER OF SEQUENCES: 452
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TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
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AGTTCCTTATGATGCCCTCTTTAGTGAAGAACTCTTGATGAAGGATCCAAACTATCAACT
                                GGTTCCTTATGACGCTATCATCAGTGAAGAATTACTCATGAAAGATCCAAACTATAAGCT
                                                                                                          GATAACAGACCAAGGCTATGTCACTTCACATGGCGACCACTATCATTATTACAATGGTAA
                                                                                                                                               CTTGACACCAGACCAGGTTAGCCAGAAAGAAGGAATTCAGGCTGAGCAAATTGTAATCAA
                                                                                                                                                                                 TTTGACTCCTGATGAGGTTAGCAAGCGTGAAGGAATCAATGCTGAGCAAATCGTCATCAA 156
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Brookes, A. Anders REGISTRATION NUMBER: 36,
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OPERATING SYSTEM: MSDOS version 6.2
SOFTWARE: ASCII Text
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TELEFAX: (301) 30
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                                                                                                                                                                                                                                                                                                               Score 385.4; DB 9
Pred. No. 1.4e-81;
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                                                                                                                                                                                                                                                                                              Mismatches 276;
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                                                                  APPLICANT: Microbial Technics Limited
APPLICANT: Gilbert, Christophe FG
APPLICANT: Gilbert, Christophe FG
APPLICANT: Hansbro, Philip M
TITLE OF INVENTION: Proteins
FILE REFERENCE: PWC/P21129WO
CURRENT APPLICATION NUMBER: US/09/769,787
CURRENT FILING DATE: 2001-01-26
PRIOR APPLICATION NUMBER: US/09/125164
PRIOR APPLICATION NUMBER: US/01/25164
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                                                                                                                                                                                                                                                        Sequence 246, Application US/09769787 Publication No. US20030091577A1 GENERAL INFORMATION:
 SOFTWARE: PatentIn
SEQ ID NO 246
                                  NUMBER OF SEQ ID NOS: 388
                                                     PRIOR FILING DATE: 1999-03-19
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; LENGTH: 1455
; TYPE: DNA
; ORGANISM: Streptococcus
US-09-769-787-246
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                                                                                                                   TCCAGCACAAATCACAAGTCGAACAGCTAGAGGTGTTGCAGTGCCACACGGAGATCATTA
                                                                                                                                                         GGAACTCTATGATTCACCTAGCGCCCAACGTTACAGTGAATCAGATGGCCTGGTCTTTGA
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                    CCACTTTATTCCTTACAGCAAGCTTTCTGCCTTAGAAGAAAAGATTGCCAGAATGGTGCC
                                                 CCACTTCATCCCTTACTCTCAAATGTCTGAATTGGAAGAACGAATCGCTCGTATTATTCC
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Pred. No. 1.5e-81;
0; Mismatches 276;
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APPLICANT: Hansbro, Philip M
ITITLE DE INVENTION: Proteins
FILE REFERENCE: PWC/P21122WO
CCURRENT APPLICATION NUMBER: US/09/769,744A
CURRENT FILING DATE: 2001-01-26
PRIOR APPLICATION NUMBER: PCT/GB99/02452
PRIOR FILING DATE: 1999-07-27
PRIOR FILING DATE: 1998-07-27
PRIOR APPLICATION NUMBER: GB 9816336.3
PRIOR FILING DATE: 1998-07-27
PRIOR APPLICATION NUMBER: US 60/125329
PRIOR FILING DATE: 1999-03-19
PRIOR FILING DATE: 1999-03-19
NUMBER OF SEQ ID NOS: 196
SOUTWARE: Patentin Ver: 2.1
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LENGTH: 1455
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Publication No.
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Matches 631;
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APPLICANT: Wells, Jeremy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: DNA
ORGANISM: Streptococcus
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CCATTACATTCCTAAGAATGAGTTATCAGCTAGCGAGTTGGCTGCTGCAGAAGCCTTCCT
                                                                                                                                                                                                                                                                           ATACTATGTTTACCTTAAGGATGCTGCCCACGCGGATAACGTCCGTACAAAAGAGGAAAT
                                                                                                                                                                                                                                                                                                                   TAAAGACGCTGATATTGTCAATGAAGTCAAGGGTGGTTATATCATCAAGGTCGATGGAAA
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                                TCCAGCTGATATTATCGAAGATACGGGTAATGCTTATATCGTTCCTCATGGAGGTCACTA
                                                                                                        TAATGTTGCTGTAGCAAGGTCTCAGGGACGATATACGACAAATGATGGTTATGTCTTTAA
                                                                                                                                                                                                         CAATCGACAAAAACAAGAGCATAGTCAACATCGTGAAGGTGGAACTCCAAGAAACGATGG
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                                                        TGCTTCTGATATCATAGAGGATACTGGTGATGATTATCGTTCCTCATGGAGATCATTA
                                                                                                                            TGCTGTTGCCTTGGCACGTTCGCAAGGACGCTATACTACAGATGATGATGTTATATCTTTAA
                                                                                                                                                                          CAATCGTCAAAAACAAGAACATGTCAAAGATAATGAGAAGGTTA--
                                                                                                                                                                                                                                               ATATTATGTCTACCTGAAAGATGCAGCTCATGCTGATAATGTTCGAACTAAAGATGAAAT
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No. US20030134407A1
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APPLICANT: Ouellet, Catherine
TITLE OF INVENTION: Streptcoccus Antigens
FILE REFERENCE: 055190-0044
CURRENT APPLICATION NUMBER: US/09/884,465A
CURRENT FILING DATE: 2001-06-20
PRIOR APPLICATION NUMBER: 60/212,683
PRIOR FILING DATE: 2000-06-20
NUMBER OF SEQ ID NOS: 384
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US-09-884-465A-1
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SEQ ID NO 1
LENGTH: 3120
TYPE: DNA
ORGANISM: Streptococcus pneumoniae
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Best Local S
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Pred. No. 2.3e-81;
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Sequence 2, Application US/09884465A
Publication No. US20030077293A1
GENERAL INFORMATION:
APPLICANT: Shire Biochem, Inc.
APPLICANT: Hamel, Josee
APPLICANT: Brodeur, Bernard
APPLICANT: Martin, Denis
APPLICANT: Martin, Denis
APPLICANT: Charland, Nathalie
APPLICANT: Ouellet, Catherine
APPLICANT: Ouellet, Catherine
APPLICANT: Ouellet, Catherine
APPLICANT: Ouellet, Catherine
APPLICANTION: Streptococcus Antigens
FILE REFERENCE: 055190-004
CURRENT APPLICATION NUMBER: US/09/884,465A
CURRENT FILLING DATE: 2001-06-20
PRIOR APPLICATION NUMBER: 60/212,683
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NUMBER OF SEQ ID NOS: 384
SOFTWARE: PatentIn version 3
SEQ ID NO 2
LENGTH: 5048
TYPE: DNA
ORGANISM: Streptococcus pne
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CCCTGCTAAGATTATCAGTCGTACACCAAATGGAGTTGCGATTCCGCATGGCGACCATTA
                               TCCAGCACAAATCACAAGTCGAACAGCTAGAGGTGTTGCAGTGCCACACGGAGATCATTA
                                                                 GGAACTCTATGATTCACCTAGCGCCCAACGTTACAGTGAATCAGATGGCCTGGTCTTTGA
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GENERAL INFORMATION:
APPLICANT: Shire Biochem, Inc.
APPLICANT: Hamel, Josee
APPLICANT: Brodeur, Bernard
APPLICANT: Brodeur, Bernard
APPLICANT: Charland, Nathalie
APPLICANT: Charland, Nathalie
APPLICANT: Ochellet, Catherine
TITLE OF INVENTION: Streptococcus An
FILE REFERENCE: 055190-0044
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; ORGANISM: Streptococcus pneumoniae
US-09-884-465A-9
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US-09-884-465A-9
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SEQ ID NO 9
LENGTH: 2528
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Best Local Similarity 73.0%;
Matches 465; Conservative
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                      TGCTTCTGATATCATAGAGGATACTGGTGATGCTTATATCGTTCCTCATGGAGATCATTA
                                                              ---TGTTGCTGTAGCAAGGTCTCAGGGACGATATACGACAAATGATGGTTATGTCTTTAA
                                                                                   TGCTGTTGCCTTGGCACGTTCGCAAGGACGCTATACTACAGATGATGGTTATATCTTTAA
                                                                                                                               CAATCGTCAAAAACAAGAACATGTCAAAGATAATGAGAAGGTTAACTCTAA------
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Pred. No. 3e-72;
0; Mismatches 160;
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; ORGANISM: Streptococcus
US-09-769-736-23
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US-09-769-736-23
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CURRENT FILING DATE: 2003-02-14
PRIOR APPLICATION NUMBER: GB 9816335.5
PRIOR FILING DATE: 1998-07-27
PRIOR APPLICATION NUMBER: US 60/125163
PRIOR FILING DATE: 1999-03-19
NUMBER OF SEQ ID NOS: 212
SOFTWARE: Patentin Ver: 2.1
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LENGTH: 1146
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Best Local
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APPLICANT: Hanniffy, Sean B
TITLE OF INVENTION: Proteins
FILE REFERENCE: PMC/P21089wo
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454 TGGTGCTGTTGCCTTGGCACGTTCGCAAGGACGCTATACTACAGATGATGGTTATATCTT
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                                                            AACTAAAGAAGCTAAAGAAAAAGGTTTAGCTCAAGTGGCCCATCTCAGTAAAGAAGAAGT
                                                                                              TAGTCAACATCGTGAAG-----
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Pred. No. 4.8e-40;
0; Mismatches 231;
                                                                                              GTGGAACTCCAAGAAACGA
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US-09-769-736-17
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APPLICANT: He Bage, Richard WF
APPLICANT: Wells, Jeremy M
APPLICANT: Hanniffy, Sean B
TITLE OF INVENTION: Proteins
FILE REFERENCE: PMC/Ppl1089wo
CURRENT APPLICATION NUMBER: US/09/769,736
CURRENT FILING DATE: 2003-02-14
PRIOR APPLICATION NUMBER: GB 9816335.5
PRIOR FILING DATE: 1998-07-27
PRIOR APPLICATION NUMBER: US 60/125163
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Best Local :
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NUMBER OF SEQ ID NOS: 212
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       TAGTCAACATCGTGAAG--
                                                                                                                                     TGAGGTCAAGGGTGGATATGTTATCAAGGTAGATGGAAAATACTATGTTTACCTTAAGGA 357
                                                                                                                                                                                      TAGTGAAGAGTTGTTGATGACGGATCCTAATTACCATTTTAAACAATCAGACGTTATCAA
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                                         AGGTAGTAAGCGCAAAAACATTCGAACCAAACAACAAATTGCTGAGCAAGTAGCCAAAGG
                                                                           TTACCATTACATTCCTAAGAATGAGTTATCAGCTAGCGAGTTGGCTGCTGCAGAAGCCTT
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                                                                                                                TGAAATCTTAGACGGTTACGTTATTAAAGTCAATGGCAACTATTATGTTTACCTCAAGCC 425
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Pred. No. 7.2e-40;
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30;

Gaps

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230

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; LOCATION: Complement((4351)..(5214)) US-09-252-088-13
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Publication No. US20030031682A1
GENERAL INFORMATION:
                             Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQ ID NO 13
                 Matches
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APPLICANT: HAMEL, Jose
APPLICANT: MARTIN, Josie
TITLE OF INVENTION: NOVEL GROUP B STREPTOCOCCUS ANTIGENS
FILE REFERENCE: 8331-9002
CURRENT APPLICATION NUMBER: US/09/252,088
CURRENT FILING DATE: 1999-02-18
CURRENT FILING DATE: 1999-02-18
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EARLIER FILING DATE: 1998-02-20
NUMBER OF SEQ ID NOS: 44
SOFTWARE: Patentin Ver. 2.0
                                                                                                FEATURE:
NAME/KEY: CDS
LOCATION: Comp
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LOCATION:
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LOCATION:
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NAME/KEY:
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ORGANISM: group
FEATURE:
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Complement ((2716)..(2946))
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                                                                                                                                                  Complement ((3837) .. (4124))
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              Score 209.8; DB 11; Length 5215; Pred. No. 2.6e-39; 0; Mismatches 232; Indels 30;
              Gaps
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US-09-884-465A-257
Sequence 257, Application US/09884465A
Publication No. US20030077293A1
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                                                             SOFTWARE: PatentIn version 3.1 SEQ ID NO 257
                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
APPLICANT: Shire Biochem, Inc.
APPLICANT: Hamel, Josee
APPLICANT: Brodeur, Bernard
                                                                                             PRIOR APPLICATION NUMBER: 60/212, PRIOR FILING DATE: 2000-06-20 NUMBER OF SEQ ID NOS: 384
                                                                                                                                             APPLICANT: Charland, Nathalie
APPLICANT: Ouellet, Catherine
TITLE OF INVENTION: Streptococcus Antigens
FILE REFERENCE: 055190-0044
CURRENT APPLICATION NUMBER: US/09/884,465A
CURRENT FILING DATE: 2001-06-20
       TYPE: DNA ORGANISM: Artificial Sequence
FEATURE:
                                               ENGTH: 819
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Sequence 71, Application US/09769736
Publication No. US20330138775A1
GENERAL INFORMATION:
APPLICANT: Microbial Technics Limited
APPLICANT: Le Page, Richard WF
APPLICANT: Wells, Jerremy M
APPLICANT: Hanniffy, Sean B
TITLE OF INVENTION: Proteins
FILE REFERENCE: PWC/P21089wo
CURRENT APPLICATION UMBER: US/09/769,736
CURRENT FILING DATE: 2003-02-14
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Pred. No. 1.1e-37;
0; Mismatches 313;
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PRIOR FILING DATE: 1998-07-27
PRIOR PELICATION NUMBER: US 60
PRIOR FILING DATE: 1999-03-19
NUMBER OF SEQ ID NOS: 212
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 71
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                                                                                                                                                                                                                           Sequence 34, Application US/09452599 Patent No. US20020055101A1
                                                                                                                                                                                                            GENERAL INFORMATION:
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Best Local
                                                     APPLICANT: Ouellette, Marc
APPLICANT: Roy, Paul H.
APPLICANT: ROy, Paul H.
INVENTION: Specific and Universal Probes and Amplification Primers
TITLE OF INVENTION: to Rapidly Detect and Identify Common Bacterial
TITLE OF INVENTION: Pathogens and Antibiotic Resistance Genes from Clinical
TITLE OF INVENTION: Specimens for Routine Diagnosis in Micro
FILE REFERENCE: 12287.31
   CURRENT APPLICATION NUMBER: US/09/452,599
CURRENT FILING DATE: 1999-12-01
PRIOR APPLICATION NUMBER: 08/526,840
                                                                                                                                                                                         APPLICANT:
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les 306; Conserv
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FILING DATE: 1998-07-27
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Ouellette, Marc
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Pred. No. 1.5e-17;
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US-10-121-120-34/c
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; ORGANISM: Streptococcus pneumoniae
US-09-452-599-34
                                                                                                                                                                                                                              US-10-121-120-34
                                                                                                                                                                                                                                        SEQ ID NO 34
LENGTH: 841
TYPE: DNA
ORGANISM: Streptococcus pneumoniae
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Best Local Similarity
Matches 176; Conserv
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SOFTWARE: PatentIn Ve
SEQ ID NO 34
LENGTH: 841
                                                                                                                                     Matches 176;
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Best Local Similarity
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APPLICANT: Ouellette, Marc
APPLICANT: Ouellette, Marc
APPLICANT: Roy, Paul H.
TITLE OF INVENTION: Specific and Universal Probes and Amplification
TITLE OF INVENTION: Primers
TITLE OF INVENTION: to Rapidly Detect and Identify Common Bacterial
TITLE OF INVENTION: to Rapidly Detect and Identify Common Bacterial
                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION NUMBER: US/10/121,120
CURRENT FILING DATE: 2002-04-11
PRIOR APPLICATION NUMBER: 09/452,599
PRIOR FILING DATE: 1999-12-01
PRIOR APPLICATION NUMBER: 08/304,732
PRIOR FILING DATE: 1994-09-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION: Pathogens and Antibiotic Resistance Generalize OF INVENTION: Specimens for Routine Diagnosis in MicroFILE REFERENCE: 12287.31
                                                                                                                                                                                                                                                                                                                                          SOFTWARE: PatentIn
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PRIOR APPLICATION NUMBER: 08/
PRIOR FILING DATE: 1994-09-12
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2150 CCAGAAGTCCCTCAAGTAGAGACTGAAAAAGTAGAAGCCCCAACTCAAAGAAGCAGAAGTT 2209
                                                                                  2090 GAAGATCCAAATAAGAACTTCAAAGCGGATGAAGAGCCAGTAGAGGAAACACCTGCTGAG 2149
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                                          GAGTCTCCAAAAACCAACAGAAGGAACCAGAAGAAGAATCACCAGAAGAATCACCAGAGGAA
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ilarity 65.4%;
Conservative
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                                                                                                                                Score 109; DB 12;
Pred. No. 1.1e-15;
0; Mismatches 90;
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Pred. No. 1.1e-15;
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APPLICANT: ABURATANI, HIROYUKI
TITLE OF INVENTION: NOVEL G PROTEIN-COUPLED RECEPTORS
FILE REFERENCE: 084335/0152
CURRENT APPLICATION NUMBER: US/10/017,161
CURRENT FILING DATE: 2002-12-18
PRIOR APPLICATION NUMBER: UP 2001/246789
PRIOR FILING DATE: 2001-06-18
PRIOR FILING DATE: 2010-06-18
NUMBER OF SEQ ID NOS: 2430
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 2179
LENGTH: 1168
RESULT 21
US-10-029-386-25433; A:
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; LOCATION: (201)..(968)
US-10-017-161-2179
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Best Local Similarity
Matches 143; Conserv
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APPLICANT: SUWA, MAKIKO
APPLICANT: ASAI, KIYOSHI
APPLICANT: AKIYAMA, YUTAKA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY:
LOCATION:
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ORGANISM: Homo sapiens
FEATURE:
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                                                                                                                                                           ATGATGATGGTGGTGAGGACGATGGTGATGATGATGCTGGTGATGATGATGATA
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                                                                                                                                                                                            CTGTTGCCTTGGCACGTTCGCAAGGACGCTATACTACAGATGATGGTTATATCTTTAATG
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ilarity 48.3%;
Conservative
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Pred. No. 0.087;
0; Mismatches 153;
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Application US/10029386

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APPLICANT: Penn, Sharron G.
APPLICANT: Rank, David K.
APPLICANT: Hanzel, David K.
APPLICANT: Hanzel, David K.
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NITITLE OF INVENTION: EXPRESSION ANALYSIS TWO FILE REFERENCE: AEOMICA-X-2
CURRENT APPLICATION NUMBER: US/10/029,386
CURRENT FILING DATE: 2001-12-20
NUMBER OF SEQ ID NOS: 34288
SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
SEQ ID NO 25433
LENGTH: 573
TYPE: DNA
                APPLICANT: Hanzel, David K.

APPLICANT: Chen, Wensheng
TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
FILE REFERENCE: Acomica x-1
CURRENT APPLICATION NUMBER: US/09/864,761
CURRENT FILING DATE: 2001-05-23
PRIOR APPLICATION NUMBER: US 60/180,312
PRIOR APPLICATION NUMBER: US 60/180,312
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR APPLICATION NUMBER: US 09/632,366
PRIOR APPLICATION NUMBER: US 09/632,366
PRIOR APPLICATION NUMBER: GB 24263.6
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Matches
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Best Local
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OTHER INFORMATION: MAP TO AL133232.9

OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 0.16

OTHER INFORMATION: NT HIT: U63807.1, EVALUE 8.50e+00

-10-029-386-25433
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APPLICANT: Rank, David R.
APPLICANT: Hanzel, David K
APPLICANT: Chen, Wensheng
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162; Conser
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DATE:
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Pred. No.
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PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/006
PRIOR FILING DATE: 2001-01-30
PRIOR FILING DATE: 2001-01-30
PRIOR FILING DATE: 2001-01-30
PRIOR FILING DATE: 2001-09-21
PRIOR APPLICATION NUMBER: US 60/234,68
PRIOR APPLICATION NUMBER: US 99/608,40
PRIOR APPLICATION NUMBER: US 09/774,20
PRIOR APPLICATION NUMBER: US 09/774,20
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Best Local Similarity
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TYPE: DNA
ORGANISM: Homo
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APPLICATION NUMBER: PCT/US01/00663
FILING DATE: 2001-01-30
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FILING DATE: 2001-01-30
APPLICATION NUMBER: PCT/US01/00668
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R OF SEQ ID NOS: 49117
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: PCT/US01/00662 FILING DATE: 2001-01-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: PCT/US01/00669
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: PCT/US01/00670
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                                                GGGATGATGACAGTGATGATGATGATGATGATGATGATGATGATGATGAT
                                                                                                CTTCTGATATCATAGAGGATACTGGTGATGCTTATATCGTTCCTCATGGAGAT 571
                                                                                                                                                                                        CTGTTGCCTTGGCACGTTCGCAAGGACGCTATACTACAGATGATGGTTATATCTTTAATG 518
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                                                                                                                                                     GTGATGATGGGGGAAGATG----ATGACAGTGATGGTGGTGATGATGACGATAGCGATGATG
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                                                                                                                                                                                                                                                                                                      ATCGACAAAAACAAGAGCATAGTCAACATCGTGAAGGTGGAACTCCAAGAAACGATGGTG 458
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EXPRESSED IN BT474
EXPRESSED IN BRAIN
EXPRESSED IN HBLIN
EXPRESSED IN HBLIN
EXPRESSED IN HELA,
EXPRESSED IN PLACE
EXPRESSED IN ADULT
EXPRESSED IN ADULT
EXPRESSED IN BONE (
EXPRESSED IN HEART
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2.1%;
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D IN BRAIN, SIGNAL = 2.1
ED IN LUNG, SIGNAL = 1.7
ED IN HBL100, SIGNAL = 2.3
ED IN HELA, SIGNAL = 2.3
ED IN PLACENTA, SIGNAL = 2.2
ED IN ADULT LIVER, SIGNAL = 2.2
ED IN ADULT LIVER, SIGNAL = 2.2
ED IN BONE MARROW, SIGNAL = 2.3
ED IN BONE MARROW, SIGNAL = 2.3
ED IN BONE MARROW, SIGNAL = 2.3
ED IN HEART, SIGNAL = 2.3
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Pred. No. 0.25;
0; Mismatches 142;
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OTHER INFORMATION: MAP TO AC002070.1
OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 1.1
OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 0.79
OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1.2
OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 0.91
OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1.2
OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1.2
OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 1.1
US-10-029-386-20619
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US-10-029-386-20619/c
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APPLICANT: Penn, Sharron G.
APPLICANT: Rank, David R.
APPLICANT: Hanzel, David K.
APPLICANT: HOLD BAVID K.
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL
TITLE OF INVENTION: EXPRESSION ANALYSIS TWO
FILE REFERENCE: AEOMICA-X-2
CURRENT APPLICATION NUMBER: US/10/029,386
CURRENT FILING DATE: 2001-12-20
NUMBER OF SEQ ID NOS: 34288
                                                                                                                                                               Sequence 3, Application US/09901152
Publication No. US20030022824A1
GENERAL INFORMATION:
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LENGTH: 506
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Best Local Similarity
 SEQ ID
                            APPLICANT: HU, Song et al.
TITLE OF INVENTION: ISOLATED HUMAN SECRETED
TITLE OF INVENTION: NUCLEIC ACID MOLECULES
TITLE OF INVENTION: USES THEREOF
FILE REFERENCE: CLO01248
CURRENT APPLICATION NUMBER: US/09/901,152
CURRENT FILING DATE: 2001-07-10
NUMBER OF SEC ID NOS: 5
SOFTWARE: FastSEQ for Windows Version 4.0 EQ ID NO 3
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ORGANISM: Homo sapiens
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Pred. No. 0.7;
0; Mismatches 169;
                                                                                                                  PROTEINS,
ENCODING HUMAN
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; FEATURE:
, NAME/KEY: misc feature
; LOCATION: (1)...(143601)
; OTHER INFORMATION: n = A,T,C or
US-09-855-824-3
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US-09-855-824-3/c
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                                                                                                                         Query Match 1.9%;
Best Local Similarity 46.4%;
Matches 148; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 3, Application US/0985824 Publication No. US20030166048A1 GENERAL INFORMATION:
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                 SEQ ID NO 3
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                                                                                                                                                                                                                                                                                                                           CURRENT FILING DATE: 2001-05-16
NUMBER OF SEQ ID NOS: 6
SOFTWARE: FastSEQ for Windows Version
                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: YAN, Chunhua et al.
TITLE OF INVENTION: ISOLATED HUMAN SECRETED PROTEINS,
TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN SECRETED PROTEINS,
TITLE OF INVENTION: USES THEREOF
                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION NUMBER: US/09/855,824
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LOCATION: (1)...(58985)
OTHER INFORMATION: n =
                                                                                                                                                                                                                                                                   ORGANISM: Human
                                                                                                                                                                                                                                                                                   TYPE: DNA
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                                                                                                                       Score 45.4; DE Pred. No. 28; 0; Mismatches
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Pred. No. 17;
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                                                                                                                                                     Length 143601;
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RESULT 26
US-09-864-761-18355
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CURRENT FILING DATE: 2001-05-23
PRIOR APPLICATION NUMBER: US 60/180,312
PRIOR FILING DATE: 2000-02-04
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: US 09/632,366
PRIOR APPLICATION NUMBER: US 09/632,366
PRIOR FILING DATE: 2000-08-03
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR APPLICATION NUMBER: US 60/236,359
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                                                                                                                                                                                                                                                                                          PRIOR
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SOFTWARE: Annomax
SEQ ID NO 18355
LENGTH: 423
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Penn, Sharron
                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE: 2001-01-30
APPLICATION NUMBER: PCT/US01/00667
FILING DATE: 2001-01-30
APPLICATION NUMBER: PCT/US01/00664
FILING DATE: 2001-01-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE: 2000-09-27
APPLICATION NUMBER: PCT/US01/00666
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APPLICATION NUMBER: PCT/US01/00662
FILING DATE: 2001-01-30
APPLICATION NUMBER: PCT/US01/00661
                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: PCT/US01/00665 FILING DATE: 2001-01-30
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                                                                                                                                                   FILING DATE: 2001-01-30
APPLICATION NUMBER: US 60/234,687
FILING DATE: 2000-09-21
                                                                                                                                                                                                           FILING DATE: 2001-01-30
APPLICATION NUMBER: PCT/US01/00670
                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: PCT/US01/00668 FILING DATE: 2001-01-30
                                                                      FILING DATE: 2000-06-30
APPLICATION NUMBER: US 09/774,203
FILING DATE: 2001-01-29
                                                                                                                                   APPLICATION NUMBER: US 09/608,408
                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: PCT/US01/00663
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5. US20020048763A1
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Chen, Wensheng
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l, David K.
                                      sequence
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                                    Listing
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                                                                                                             CURRENT FILLING DATE: 2001-05-23
PRIOR APPLICATION NUMBER: US 60/180,312
PRIOR APPLICATION NUMBER: US 60/180,312
PRIOR FILING DATE: 2000-02-04
PRIOR PRILING DATE: 2000-05-26
PRIOR PRILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR APPLICATION NUMBER: US 99/632,366
PRIOR FILING DATE: 2000-08-03
PRIOR FILING DATE: 2000-08-03
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR APPLICATION NUMBER: DET/US01/00666
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00667
PRIOR APPLICATION NUMBER: PCT/US01/00667
PRIOR APPLICATION NUMBER: PCT/US01/00664
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Best Local
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                                                                   APPLICATION NUMBER: PCT/US01/00665
                                                                                APPLICATION NUMBER: PCT/US01/00669 FILING DATE: 2001-01-30
                                                 FILING DATE:
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                             APPLICATION NUMBER: PCT/US01/00668
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Chen, Wensheng
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EXPRESSED IN HBL10

EXPRESSED IN HELA,

EXPRESSED IN LUNG,

EXPRESSED IN FETAL

EXPRESSED IN HEART

EXPRESSED IN HEART
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PCT/US01/00663
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D IN BONE MARROW, SIGNAL = 1.4
D IN LUNG, SIGNAL = 1.7
D IN FETAL LIVER, SIGNAL = 1.9
D IN HEART, SIGNAL = 1.9
D IN BRAIN, SIGNAL = 3.2
D IN PLACENTA, SIGNAL = 3.2
D IN BT474, SIGNAL = 2.2
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FILING DATE:

FILING DATE:

APPLICATION NUMBER: PCT/US01/00661 FILING DATE: 2001-01-30
APPLICATION NUMBER: PCT/US01/00662

2001-01-30

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RESULT 28
US-10-312-841-2
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; OTHER INFORMATION:
; OTHER INFORMATION:
US-09-864-761-1597
                                                                                                                                                                                                                                         Sequence 2, Application US/10312841 Publication No. US20030186277A1 GENERAL INFORMATION:
                                                                                                SEQ ID NO 2
LENGTH: 3673778
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Best Local
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                                                                                                                            APPLICANT: Epigenomics AG
TITLE OF INVENTION: Diagnose von bedeutenden
FILE REFERENCE: E01/1208/WO
CURRENT APPLICATION NUMBER: US/10/312,841
CURRENT FILING DATE: 2002-12-30
NUMBER OF SEQ ID NOS: 2
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                                                          TYPE: DNA ORGANISM: Artificial Sequence
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ORGANISM: Homo sapiens
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WAME/KEY: unsure
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FILING DATE: 2000-09-21
APPLICATION NUMBER: US 09/608,408
FILING DATE: 2000-06-30
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FILING DATE: 2001-01-29
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APPLICATION NUMBER: PCT/US01/00670
FILING DATE: 2001-01-30
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N: EXPRESSED IN HBLIAO, SIGNAL = 3.1

N: EXPRESSED IN HELA, SIGNAL = 2.8

N: EXPRESSED IN BONE MARROW, SIGNAL = 4.2

N: EXPRESSED IN FETAL LIVER, SIGNAL = 2.6

N: EXPRESSED IN HEART, SIGNAL = 1.9

N: EXPRESSED IN BRAIN, SIGNAL = 3.2

N: EXPRESSED IN BRAIN, SIGNAL = 1.9

N: EXPRESSED IN BRAIN, SIGNAL = 1.9

N: EXPRESSED IN BRAIN, SIGNAL = 1.9

N: EXPRESSED IN ADULT LIVER, SIGNAL = 1.9

N: EXPRESSED IN BT474, SIGNAL = 1.6
                           chemically treated genomic DNA (Homo sapiens)
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US-10-312-841-2
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PRIOR APPLICATION NUMBER: US 09/632,366
PRIOR TILING DATE: 2000-08-03
PRIOR PILLING DATE: 2000-08-03
PRIOR PILLING DATE: 2000-10-04
PRIOR PILLING DATE: 2000-10-04
PRIOR PILLING DATE: 2000-09-27
PRIOR PILLING DATE: 2000-09-27
PRIOR PILLING DATE: 2000-09-27
PRIOR PILLING DATE: 2001-01-30
PRIOR PILLING DATE: 2001-01-30
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PRIOR FILLING DATE: 2001-01-30
PRIOR FILLING DATE: 2001-01-30
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Best Local Similarity
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CURRENT FILING DATE: 2001-05-23
PRIOR APPLICATION NUMBER: US 60/180,312
PRIOR FILING DATE: 2000-02-04
PRIOR APPLICATION NUMBER: US 60/207,456
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APPLICANT: Chen, Wensheng
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
FILE REFERENCE: Aeomica-X-1
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APPLICATION NUMBER: PCT/US01/00667
FILING DATE: 2001-01-30
APPLICATION NUMBER: PCT/US01/00664
FILING DATE: 2001-01-30
                                                        APPLICATION NUMBER: PCT/US01/00662
FILING DATE: 2001-01-30
APPLICATION NUMBER: PCT/US01/00661
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                                       FILING DATE:
                                                                                                                  FILING DATE: 2001-01-30
                                                                                                                                       FILING DATE: 2001-01-30
APPLICATION NUMBER: PCT/US01/00663
                                                                                                                                                                             APPLICATION NUMBER: PCT/US01/00668
                                                                                                                                                                                                APPLICATION NUMBER: PCT/US01/00665
FILING DATE: 2001-01-30
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Pred. No. 2.1e+02;
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                                                                                                                                                                    GENERAL INFORMATION:
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SEQ ID NO 19608
LENGTH: 766
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Best Local
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                                     APPLICANT: Penn, Sharron G.
APPLICANT: Rank, David R.
APPLICANT: Hanzel, David K.
APPLICANT: Chen, Wensheng
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL
TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
FILE REFERENCE: Acomica-X-1
CURRENT APPLICATION NUMBER: US/09/864,761
CURRENT FILING DATE: 2001-05-23
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PRIOR APPLICATION NUMBER: US 09/608,408
PRIOR FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: US 09/774,203
PRIOR FILING DATE: 2001-01-29
NUMBER OF SEQ ID NOS: 49117
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          NT FILING DATE: 2001-05-23
APPLICATION NUMBER: US 60/180,312
FILING DATE: 2000-02-04
APPLICATION NUMBER:
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ESSED IN BY474, SIGNAL = 1.1
ESSED IN PLACENTA, SIGNAL = 0.89
ESSED IN HBL100, SIGNAL = 1.1
ESSED IN HELA, SIGNAL = 1
ESSED IN HELA, SIGNAL = 1
ESSED IN HEART, SIGNAL = 1.2
ESSED IN HEART, SIGNAL = 1.2
ESSED IN FETAL LIVER, SIGNAL = 1.2
SPROT HIT: P17164, EVALUE 4.10e+00
HUMAN HIT: AW844901.1, EVALUE 2.90e+00
US 60/207,456
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Best Local Similarity
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APPLICATION NUMBER: US 60/234,687
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GTAGTGÁTGGTGATGAAGATGATGÁTGTTGGCGATGAAGATGACGATGAAGAGAGGAGG
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I EXPRESSED IN BT474, SIGNAL = 1.1

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EXPRESSED IN HBL100, SIGNAL = 1.1

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Pred. No. 7.5;
0; Mismatches
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371

431

491

305 607 245

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APPLICANT: Penn, Sharron G.
APPLICANT: Rank, David R.
APPLICANT: Rank, David R.
APPLICANT: Hanzel, David K.
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXC
TITLE OF INVENTION: EXPRESSION ANALYSIS TWO
FILE REFERENCE: AEOMICA-X-2
CURRENT APPLICATION NUMBER: US/10/029,386
CURRENT FILING DATE: 2001-12-20
NUMBER OF SEQ ID NOS: 34288
SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
SEQ ID NO 20406
LENGTH: 538
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OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 3.5

OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 3.7

OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 3.7

OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 4.2

OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 6.9

OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 6.9

OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 3.2

OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 3.2

OTHER INFORMATION: EXPRESSED IN HEAT, SIGNAL = 3.6

OTHER INFORMATION: MITHIT: AB021651.1, EVALUE 2.00e+00

OTHER INFORMATION: EST_HUMAN HIT: BI039161.1, EVALUE 1.00e-08
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US-10-029-386-20406
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Best Local
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ORGANISM: Homo sapiens
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 476
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     164 GACCAAGGCTATGTCACTTCACATGGCGACCACTATCATTATTACAATGGTAAGGTTCCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           181;
                                                                                                                                                                                                                                                                                                                                 GAGGATATTGTTAATGAGGTCAAGGGTGGATATGTTATCAAGGTAGATGGAAAATACTAT
                                                                                                                                                                                                                                                                                                                                                                        GATGATGACGATAGTGATGGTGATGGTGGTGATGATGATGATGACGATAGTGATGGT
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                               GATATCATAGAGGATACTGGTGATGCTTATATCGTTCCTCATGGAGATCAT
                                                                                                          GCCTTGGCACGTTCGCAAGGACGCTATACTACAGATGATGGTTATATCTTTAATGCTTCT
                                                                                                                                                                                    CAAAAACAAGAGCATAGTCAACATCGTGAAGGTGGAACTCCAAGAAACGATGGTGCTGTT
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Pred. No. 5.2;
0; Mismatches
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           Sequence 19488, Application US, Patent No. US20020048763A1
GENERAL INFORMATION:
APPLICANT: Penn, Sharron G.
APPLICANT: Rank, David R.
APPLICANT: Hanzel, David K.
                                                                                                                          RESULT 33
US-09-864-761-19488
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APPLICANT:
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; OTHER INFORMATION: MAP TO AC007540.3
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 0.94
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1.1
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 1.5
OTHER INFORMATION: EXPRESSED IN HELLA, SIGNAL = 0.73
; OTHER INFORMATION: EST_HUMAN HIT: BE767903.1, EVALUE 1.00e-03
; OTHER INFORMATION: NT HIT: AJ252124.1, EVALUE 1.20e-02
US-10-029-386-22627
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US-10-029-386-22627/c
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Publication No. US20030194704A1
GENERAL INFORMATION:
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SEQ ID NO 22627
LENGTH: 785
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Best Local Similarity
Matches 188; Conserv
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APPLICANT: Rank, David R.
APPLICANT: Hanzel, David K.
APPLICANT: HOZEL, DAVID K.
TITLE OF INVENTION: HUMAN GENOME-DERIVED
TITLE OF INVENTION: EXPRESSION ANALYSIS
FILE REFERENCE: AEOMICA-X-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION NUMBER: US/10/029,386
CURRENT FILING DATE: 2001-12-20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               670 ÁTTATGGTGATAGTGÁTGATGATGAGGAGATGÁTGGTGATGATGATGATGATTÁTG
AAGGCTATGTCACTTCACATGGCGACCACTATCATTATTACAATGGTAAGGTTCCTTATG
                                                                                                                                                        TGGCACGTTCGCAAGGACGCTATACTACAGATGATGGTTATATCTTTAATGCTTCTGATA
                                                                                                                                                                                                                                                               AACAAGAGCATAGTCAACATCGTGAAGGTGGAACTCCAAGAAACGATGGTGCTGTTGCCT
                                                                                                                                                                                                                                                                                                                   TTGGTGATGATGGTGATGTCTGAGATGATGGTGGTGATGATAATGGTGATGGTGATG
                                                TCATAGAGGATACTGGTGATGCTTATATCGTTCCTCATGGAGATCATTACCAT 580
                                                                                                       ATGATGGTGACGGTGATGATTATGATGGAGATGATGGTGATGGCGATAATGACGGAGATG
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David R. David K.

US/09864761

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Best Local
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CURRENT FILING DATE: 2001-05-23
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                                                                                                                                                                                                                                                                                                                                         OTHER
OTHER
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                                                                                                                                       Local
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APPLICATION NUMBER: US 09/774,203
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APPLICATION NUMBER: US 09/632,366
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US 09/608,408
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US 60/234,687
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: PCT/US01/00670
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APPLICATION NUMBER: PCT/US01/00662
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: PCT/US01/00665
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US 60/236,359
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: GB 24263.6
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                                                             108
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                                                                                                                                       Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Annomax Sequence Listing Engine vers.
                            TACTATGTTTACCTTAAGGATGCTGCCCACGCGGATAACGTCCGTACAAAAGAGGAAATC
GGTTATGGTGGTGATGATGCTGATGGTGATGGTGATGGTGATGGTGAGGATGCT
                                                             AATGGTGATGATGATGATGATGGATGGTGGTGATGATGCTGATGGTGATGATGAT
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Pred. No. 8.1;
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IN BONE MARROW, SIGNAL = 6
IN LUNG, SIGNAL = 2.9
IN BRAIN, SIGNAL = 6.5
IN ADULT LIVER, SIGNAL = 5
IN FETAL LIVER, SIGNAL = 1
IN PEACEBYA, SIGNAL = 1
IN HEART, SIGNAL = 1.1
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PRIOR APPLICATION NUMBER: US 6/
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                                                                                                                                                 NUMBER OF SOFTWARE:
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APPLICANT: Hanzel, David K.

APPLICANT: Chen, Wensheng

TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL

TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY

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PRIOR FILING DATE: 2000-02-04
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: US 09/632,366
PRIOR FILING DATE: 2000-08-03
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                                                 LENGTH: 962
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: MAP TO AC008125.9
OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL
                                                                                                                                                                  FILING DATE: 2001-01-
R OF SEQ ID NOS: 49117
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CURRENT FILING DATE: 2001-03-21
PRIOR APPLICATION UNMEER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR PILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR APPLICATION NUMBER: 60/253,625
                                NUMBER OF SEQ ID NOS: 14110
SOFTWARE: FASTSEQ for Windows Version
SEQ ID NO 4843
LENGTH: 4047
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Best Local Similarity
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Patent No. US20020061569A1
                                                                                                                                                    PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION: Identification of TITLE OF INVENTION: Prokaryotes
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APPLICANT: Ohlsen, Kari L.
APPLICANT: Zyskind, Judith W.
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Pred. No. 9.9;
0; Mismatches 151;
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(IN ADULT LIVER, SIGNAL = 5.8
(IN FETAL LIVER, SIGNAL = 1.8
(IN PLACENTA, SIGNAL = 5
(IN HEART, SIGNAL = 1.1
(IN HELA, SIGNAL = 3.8
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LUNG, SIGNAL = 2 0
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Query Match
Best Local Similarity
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                                                                                                                       NAME/KEY: CDS
LOCATION: (1)
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PRIOR FILING DATE: 2001
NUMBER OF SEQ ID NOS: 1
SOFTWARE: FastSEQ for V
SEQ ID NO 9039
LENGTH: 4050
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Patent No. US2002006
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Xu, H. Howard
TITLE OF INVENTION: Identification of
TITLE OF INVENTION: Prokaryotes
FILE REFERENCE: ELITRA.011A
CURRENT APPLICATION NUMBER: US/09/815,
CURRENT FILLING DATE: 2001-03-21
                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION NUMBER: 60/206,848
PRIOR TILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26.
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR FILING DATE: 2000-05-26.
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                                                                                                                                                                                                                                                                                 PRIOR APPLICATION NUMBER: 60/2
PRIOR FILING DATE: 2001-02-16
                                                                                                                                                                                                                                                                                                                                                                                          PRIOR FILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/253,625
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
                                                                                                                                                                                                                                                                                                                                                                      PRIOR FILING DATE: 2000-11-27
                                                                                                                           TYPE: DNA ORGANISM: Staphylococcus aureus FEATURE:
                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: 60/257,931 FILING DATE: 2000-12-22
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Yamamoto, Robert T.
Xu, H. Howard
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                                                                               ...(4050)
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Pred. No. 21;
0; Mismatches 146;
Score
Pred.
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No. 21;
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               Length 4050;
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US-08-781-986A-454/c
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                                                                                               Query Match
                                                                                                                                                                                                                          FILLING AGENT IN.
ATTORNEY/AGENT IN.
ATTORNEY/AGENT IN.
ANAME: Benson, Bob
REGISTRATION NUMBER: 30,446
REGISTRATION NUMBER: PB248
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION 309-8504
(301) 309-8512
(301) 309-8512
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
                                                                                                                                                                                                                                TELEFAX: (301) 309-85
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Charles Kunsch
TITLE OF INVENTION: Staph
                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES:
                                                                                                                                                            LENGTH: 4358 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OPERATING SYSTEM: MS
SOFTWARE: ASCII Text
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CITY: Rockville
STATE: Maryland
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                                                                                Local
                                                                                                                                               TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER:
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                                1695 AAAAAGTTGCAGCTCAAGCCTATACTAAAGAAAAAGGTATCCTACCTCCATCTCCAGACG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1815 GGGAAAAACGAATTCCACTCGTTCGACTTCCATATATGGTTGAGCATACAGTTGAGGTTA 1874
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                                                                                Similarity
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 ATAAAGTTGAAGTTTCAACTGCCAAATCAGATGAGCAAGCTTCACCAAAATCTACGAATG
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                                                                Conservative
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                                                                                1.8%;
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                                                               ; Score 42.4; Di
; Pred. No. 22;
0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 269927, Application US Publication No. US20030204075A9 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                           Best Local Similarity Matches 77; Conserv
                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION NUMBER: US PRIOR FILING DATE: 1999-09-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILE REFERENCE: 108827.129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR FILING DATE: 1999-11-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR FILING DATE: 2000-02-24
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ORGANISM: Human
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RESULT 39
US-10-027-632-269927/c
(S-10-027-632-269927, Application US/10027632
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: FastSEQ for Windows Version SEQ ID NO 269927
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION NUMBER: US 60/146,002 PRIOR FILING DATE: 1999-08-09
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PRIOR APPLICATION NUMBER: US 60/193,483
PRIOR FILING DATE: 2000-03-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION NUMBER: US/10/027,632 CURRENT FILING DATE: 2002-04-30 PRIOR APPLICATION NUMBER: US 60/218,006 PRIOR FILING DATE: 2000-07-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification
TITLE OF INVENTION: Polymorphisms
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION NUMBER: US 60/198,676
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                                                                                                                                                                                                                                                                                                                                                                                                          2131 AGAGGAAACACCTGCTGAGCCAGAAGTCCCTCAAGTAGAGACTGAAAAAGTAGAAGCCCA 2190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2071 AGGCAAGAAAGACCACAGTGAAGATCCAAATAAGAACTTCAAAGCGGATGAAGAGCCAGT 2130
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                                                                                                                                                                                                                                                                                                                                                   TTGATGATCACACATACAAAGCTCCAAATGGCTATA 1970
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Pred. No. 8.9;
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US-10-027-632-269927
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PRIOR FILING DATE: 1
PRIOR APPLICATION NU
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PRIOR APPLICATION NU
PRIOR FILING DATE:
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Best Local
                                                                                                                                                                                                         CURRENT APPLICATION NUMBER: US/09/864,761
CURRENT FILING DATE: 2001-05-23
PRIOR APPLICATION NUMBER: US 60/180,312
PRIOR FILING DATE: 2000-02-04
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR FILING DATE: 2000-05-26
                                                                                                                                                          PRIOR
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                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Penn, Sharron G. APPLICANT: Rank, David R.
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PRIOR FILING DATE: 2000-07-12
PRIOR APPLICATION NUMBER: US 60/198,676
PRIOR FILING DATE: 2000-04-20
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CURRENT FILING DATE: 2002-04-30
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           No.
                                             PILING DATE: 2000-09-27
APPLICATION NUMBER: PCT/US01/00666
FILING DATE: 2001-01-30
APPLICATION NUMBER: PCT/US01/00667
                                                                                                                    FILING DATE: 2000-08-03
APPLICATION NUMBER: GB 24263.6
FILING DATE: 2000-10-04
APPLICATION NUMBER: US 60/236,359
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FILING DATE: 1999-11-23
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                                    FILING DATE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         19262, Application US/09864761 o. US20020048763A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AGAAGAAGAAGAAG 252
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Chen, Wensheng
   DATE
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                                    2001-01-30
                                                                                                                                                                                                                                                                                                                                                                                    David K.
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                FILE REFERENCE:
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CURRENT APPLICATION NUMBER: US/09/864,761
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RESULT 41
US-09-864-761-2534/c
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GENERAL INFORMATION:
APPLICANT: Penn, Sharron G.
APPLICANT: Rank, David R.
APPLICANT: Hanzel, David K.
APPLICANT: Chen, Wensheng
TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
Matches 90; Conserv
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SEQ ID NO 19262
                                                                                                                                                                                         Sequence 2534, Application Patent No. US20020048763A1
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PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00670
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: US 60/234,687
PRIOR FILING DATE: 2000-09-21
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION NUMBER: US 09/608,408
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APPLICATION NUMBER: US 09/774,203
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 N: EXPRESSED IN PLACENTA, SIGNAL = 3.6

N: EXPRESSED IN HBL100, SIGNAL = 1.8

N: EXPRESSED IN HEART, SIGNAL = 3.9

N: EXPRESSED IN HEART, SIGNAL = 2.7

N: EXPRESSED IN HEALA, SIGNAL = 2.4

N: EXPRESSED IN HELA, SIGNAL = 2.4

N: EXPRESSED IN LUNG, SIGNAL = 2.8

N: EXPRESSED IN HEALA, SIGNAL = 2.8

N: EXPRESSED IN BT474, SIGNAL = 3.6

N: EXPRESSED IN ADULT LIVER, SIGNAL = 3.6

N: EXPRESSED IN FETAL LIVER, SIGNAL = 2.8

N: EXPRESSED IN FETAL LIVER, SIGNAL = 2.8
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6.7;
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OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 3.6
OTHER INFORMATION: EXPRESSED IN HEALTO, SIGNAL = 1.8
OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 3.9
OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 2.7
OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 2.4
OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 3.5
OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 2.8
OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL = 3.5
OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL = 3.6
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                                                                                                                                                                                                                                                                                        Local
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FILING DATE: 2000-02-04
APPLICATION NUMBER: US 60/207,456
FILING DATE: 2000-05-26
APPLICATION NUMBER: US 09/632,366
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APPLICATION NUMBER: US 09/774,203
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APPLICATION NUMBER: US 09/608,408
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE: 2000-08-03
APPLICATION NUMBER: GB 24263.6
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FILING DATE: 2001-01-30
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                                       2158 CCCTCAAGTAGAGACTGAAAAAGTAGAAGCCCCAACTCAAAGAAGCAGAAG
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AMATAAGAACTTCAMAGCGGATGAAGAGCCAGTAGAGGAAACACCTGCTGAGCCAGAAGT 2157
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8.7;
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US-10-017-161-1913
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Publication No. US20030143668A1
GENERAL INFORMATION:
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SEQ ID NO 1913
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APPLICANT: ASAI, KIYOSHI
APPLICANT: AKIYAMA, YUTAKA
APPLICANT: ABURATANI, HIROYUKI
TITLE OF INVENTION: NOVEL G PROTEIN-COUPLED
FILE REFERENCE: 084335/0152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION NUMBER: US/10/017,161
CURRENT FILING DATE: 2002-12-18
PRIOR APPLICATION NUMBER: JP 2001/246789
PRIOR FILING DATE: 2001-06-18
NUMBER OF SEQ ID NOS: 2430
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LOCATION: (26)
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LOCATION: (201)..(437)
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Local Similarity 45.8%;
les 184; Conservative
3011
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TGATAGTGATAACGGTGATGATGGTGGTGATGATAATGGTGA 3052
                                                                                                         AGATGATGGTTATATCTTTAATGCTTCTGATATCATAGAGGATACTGGTGATGCTTATAT 555
                                                                                                                                                                                                                                TGACGGTGATTATAGTGATAATGATGGTGATCATGGTGATGATGGTGCTGCTGCTGATGG
                                    CGTTCCTCATGGAGATCATTACCATTACATTCCTAAGAATGA
                                                                                                                                                                                                                                                                     CCGTACAAAAGAGGAAATCAATCGACA---AAAACAAGAGCATAGTCAACATCGTGAAGG 435
                                                                                                                                                                                                                                                                                                             TGGTAATGATGATGGTGATAGTGATAGTGATCATGGTGATGGTGATGGTGATGATGATGG 2830
                                                                                                                                                                                                                                                                                                                                                TATCAAGGTAGATGGAAAATACTATGTTTACCTTAAGGATGCTGCCCACGCGGATAACGT 378
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TGATGGTGATGGTGATGATGGTGGTGGTGACAGTGATAAAGGTGATGGTGATGGTAATGA 2710
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TCATTATTACAATGGTAAGGTTCCTTATGACGCTATCATCAGTGAAGAATTACTCATGAA
                                                                                                                                                                                            TGGAACTCCAAGAAACGATGGTGCTTGCCTTGGCACGTTCGCAAGGACGCTATACTAC 495
                                                                          TGATAGTGGTGATGATGATGATGGTGATGATGGAGATCATGTTGATGTTGATGT
                                                                                                                                                       TGGTAATGGTAATCATGGTGATGATGGTGGTGATAGTAATCATGGTGACGGTAATGA 2950
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RESULT 43 US-10-029-386-5350/c

GENERAL INFORMATION:

APPLICANT: Penn,

Rank, David

Sequence 5350, Application US/10029386 Publication No. US20030194704A1

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RESULT 44

US-10-029-386-24901/c

; Sequence 24901, Application US/10029386
; Publication No. US20030194704A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Barron G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-10-029-386-5350
                           APPLICANT: Rank, David K.

APPLICANT: Hanzel, David K.

TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL TITLE OF INVENTION: EXPRESSION ANALYSIS TWO FILE REFERENCE: AEOMICA-X-2 CURRENT APPLICATION NUMBER: US/10/029,386

CURRENT FILING DATE: 2001-12-20

NUMBER OF SEQ ID NOS: 34288

SOFTWARE A ARCONANCE AND ANALYSIS TO SEC TO NOS: 34288
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     SEQ ID
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Best Local (
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OTHER INFORMATION: EXPRESSE
OTHER INFORMATION: EST HUMA
OTHER INFORMATION: MT HIT:
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TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL TITLE OF INVENTION: EXPRESSION ANALYSIS TWO FILE REFERENCE: AEOMICA-X-2
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CURRENT FILING DATE: 2001-12-20
NUMBER OF SEQ ID NOS: 34288
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ORGANISM: Homo sapiens
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                     Annomax Sequence
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NN: EXPRESSED IN LING, SIGNAL = 5.6

NN: EXPRESSED IN FETAL LIVER, SIGNAL = 7

NN: EXPRESSED IN BONE MARROW, SIGNAL = 6.1

NN: EXPRESSED IN PLACENTA, SIGNAL = 6.8

NN: EXPRESSED IN ADULT LIVER, SIGNAL = 7.2

NN: EXPRESSED IN HEART, SIGNAL = 7.2

NN: NT HIT: AL163283.2, EVALUE 6.00e-10
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Pred. No. 10;
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US-10-312-841-1/c
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APPLICANT: Epigenomics AG
TITLE OF INVENTION: Diagnose von bedeutenden
FILE REFERENCE: E01/1208/wo
                                                                                                                                                                                                                                                                                                                                                                                                      SEQ ID NO 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 1, Application US/10312841 Publication No. US20030186277A1
                                                                                                                                                       Matches
                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                               FEATURE:
NAME/KEY: unsure
NAME/KEY: (3294164)
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CURRENT FILING DATE: 2002-12-30
NUMBER OF SEQ ID NOS: 2
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OTHER INFORMATION:
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                                                                                                                                                                                                                                                                                                      OTHER INFORMATION:
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                                                                                                                                                     l Similarity 67; Conserv
                       ACTACAAATACTAACACAAGCAACAACAGCAACACTAACAGTCAAGCAA
                                                                         CAACTAAATAAAACTAAACGAACAACAACCACACCCTCACCTCTAACCAAAACAAAA
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SWISSPROT HIT: Q28084, EVALUE 6.50e+00
NT HIT: U13008.1, EVALUE:3.90e+00
EST_HUMAN HIT: BE409401.1, EVALUE 5.70e+00
                                                                                                                                                                                                                                                                                                    chemically treated genomic DNA
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Pred. No. 6.3e+02;
0; Mismatches 42;
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Pred. No. 14;
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OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 2.2

OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 1.7

OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 2.1

OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 3.2

OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 1.7

OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1.7

OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 1.5

OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 1.6

OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 1.6

OTHER INFORMATION: STREET INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 1.6

OTHER INFORMATION: STREET INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 1.6

OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 1.7

OTHER INFORMATION: E
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US-10-029-386-14986/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 1284, Application US/10029386 Publication No. US20030194704A1 GENERAL INFORMATION:
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APPLICANT: Rank, David R.
APPLICANT: Hanzel, David K.
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
TITLE OF INVENTION: EXPRESSION ANALYSIS TWO
FILE REFERENCE: ABOMICA-X-2
                                                                                                                                                                                                                                                                                APPLICANT: Penn, Sharron G.
APPLICANT: Rank, David R.
APPLICANT: Hanzel, David K.
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR TITLE OF INVENTION: EXPRESSION ANALYSIS TWO
FILE REFERENCE: AEOMICA-X-2
                                                                                                                                                    CURRENT APPLICATION NUMBER: US/10/029,386
CURRENT FILING DATE: 2001-12-20
NUMBER OF SEQ ID NOS: 34288
SOFTWARE: Annomax Sequence Listing Engine
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CURRENT FILING DATE: 2001-12-20
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TYPE: DNA
OKGANISM: Homo sapiens
FEATURE:
FEATURE:
                          ORGANISM: Homo sapiens
                                                            TYPE: DNA
                                                                                          ENGTH: 571
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              211 CAACATCATGATGAGCAAATCCCACTAAGGGGTGTTGCTTTTCCACGGGCCTGTCTCCAT
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                                                                                                                                                       Engine vers.
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Best Local
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US-10-029-386-1284
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LENGTH: 611
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Mannion, Jane
APPLICANT: Benson, Darin R.
APPLICANT: Benson, Darin R.
APPLICANT: Carter, Darrick
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
TITLE OF INVENTION: AND DIAGNOSIS OF OVARIAN CANCER
FILE REFERENCE: 210121.523
CURRENT APPLICATION NUMBER: US/09/864,864
CURRENT FILING DATE: 2001-05-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQ ID NOS: 341
                                                                                                                                                                                                                                                            NAME/KEY: misc_feature
LOCATION: (1)...(611)
OTHER INFORMATION: n =
                                                                                                                                                                                                                                                                                                                                        TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                     Local Similarity
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2140 ACCTGCTGAGCCAGAAGTCCCTCAAGTAGAGACTGAAAAAGTAGAAGCCCAACTCAAAGA 2199
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       542 GGTGATGCTTATATCGTTCCTCATGGAGATCA 573
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            482 GGACGCTATACTACAGATGATGGTTATATCTTTAATGCTTCTGATATCATAGAGGATACT 541
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                                                                     AGAAAAGAAAGCAAAAGCAGAAGCTAAACGGAAGGAGCAAGAAGCTAAAGAAAAAACAAAG 161
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Fling, Steve P.
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NN: EXPRESSED IN LUNG, SIGNAL = 1.7

EXPRESSED IN HELA, SIGNAL = 2.1

NN: EXPRESSED IN ADULT LIVER, SIGNAL = 3.2

NN: EXPRESSED IN FETAL LIVER, SIGNAL = 1.7

NN: EXPRESSED IN HONE MARROW, SIGNAL = 1.5

NN: EXPRESSED IN HEART, SIGNAL = 4.1

NN: EXPRESSED IN PLACENTA, SIGNAL = 1.6

NN: EXPRESSED IN PLACENTA, SIGNAL = 1.6
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Pred. No. 12;
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US-09-919-497-50
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US-09-864-864-313
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Sequence 50, Application US/09919497
Patent No. US20020106662A1
GENERAL INFORMATION:
APPLICANT: Mutter, George L.
TITLE OF INVENTION: PROGNOSTIC CLASSIFICATION OF ENDOMETRIAL CANCER FILE REFERENCE: B0801/7225
CURRENT APPLICATION NUMBER: US/09/919,497
CURRENT FILING DATE: 2001-07-31
PRIOR APPLICATION NUMBER: US 60/221,735
PRIOR FILING DATE: 2000-07-31
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Best Local Similarity
Matches 95; Conserv
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SEQ ID NO 313
LENGTH: 1845
TYPE: DNA
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CURRENT FILING DATE: 2001-05-23
NUMBER OF SEQ ID NOS: 341
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TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF OVARIAN CANCER
FILE REFERENCE: 210121.523
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                                                                                                                                                                                                                                                                                                                                          TCTA 2263
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Benson, Darin R.
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Fling, Steve P.
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Dillon, Davin C.
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Lodes, Michael J.
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Best Local Similarity

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The present sequence represents a protein from Streptococcus pneumoniae. The nucleic acid sequence encoding the Streptococcus pneumoniae protein can be useful in vaccines for inducing protective annibodies against Streptococcus pneumoniae, for treatment or prevention of infection e.g. pneumonia, otitis media or meningitis. Probes based on the nucleic acid are used to detect Streptococcus infection (by usual hybridisation or amplification methods), also for isolating Streptococcus genes or their allelic variants. The protein can be used similarly to detect specific antibodies in standard immunoassays, especially for diagnosing or
                                                                                                                                           Nucleic acid encoding antigenic peptide(s) from Streptococcus pneumoniae - or their epitope-containing fragments, useful in protective or therapeutic vaccines, and for diagnosis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                monitoring infections. Antibodies which bind the protein are used to detect corresponding antigens, to purify the protein and for passive immunisation (optionally coupled to a toxin). Vaccines are administered, e.g. by injection, orally or through the skin, typically at 0.01-1000 (especially 10-300) mu g/ml per dose.
                ABP54584
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                                                                                                                                                                                                                                                                                                            KEKLVDDLLAFLAPITHPERLGKPNSQIEYTEDEVRIAQLADKYTTSDGYIFDEHDIISD
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                standard;
                                                                                    LLKGSNPSSVSKEKIN
                                                                                                                                                                                 LFATIKYYVEHPDERPHSNDGWGNASEHVLGKKDHSEDPNKNFKADEEPVEETPAEPEVP
                                                                                                                                                                                                                   NRVKGEKRIPLVRLPYMVEHTVEVKNGNLIIPHKDHYHNIKFAWFDDHTYKAPNGYTLED
                                                                                                                                                                                                                                NRVKGEKRI PLVRLPYMVEHTVEVKNGNLI I PHKDHYHNI KFAWFDDHTYKAPNGYTLED
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AHADNVRTKEEINRQKQEHSQHREGGTPRNDGAVALARSQGRYTTDDGYIFNASDIIEDT
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                                                                          LLKGSNPSSVSKEKIN
                                                                                                                      QVETEKVEAQLKEAEVLLAKVTDSSLKANATETLAGLKNNLTLQIMDNNSIMAEAEKLLA
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                Protein;
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Pred. No. 3.5e-299;
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Best Local
                                                                                                                                                                                                                                                                                                         ABQ84792 to ABQ84904 represents nucleic acids which encode the Streptococcus pneumoniae antigens given in ABP54557 to ABP54669. The S. pneumoniae antigens have antibacterial activity and can be used in vaccines. The S. pneumoniae antigens can also be used to prevent or attenuate a Streptococcal infection in an animal. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Choi
                                                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                               polynucleotides encoding the S. pneumoniae antigens can be used to detect Streptococcus nucleic acids. ABQ84905 to ABQ85130 represent primers used in the cloning of S. pneumoniae ORFs (open reading frawhich are used in an example from the present invention.
                                                                                                                                                                                                                                                                                                                                                                            Claim
                                                                                                                                                                                                                                                                                                                                                                                              New Streptococcus pneumoniae antigens, useful for detecting Streptococcus and for preventing or attenuating disease caused Streptococcus infection -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Streptococcus
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DB; ABQ84819.
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KUNSCH C A.

BARASH S C.

DILLON P J.

DOUGHERTY B.

FANNON M R.
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                                            GDAYIVPHGDHYHYIPKNELSASELAAAEAFLSGRGNLSNSRTYRRQNSDNTSRTNWVPS
                                                                                     AHADNVRTKEEINRQKQEHSQHREGGTPRNDGAVALARSQGRYTTDDGYIFNASDIIEDT
                                                                                                                              SHGDHYHYYNGKVPYDAIISEELLMKDPNYKLKDEDIVNEVKGGYVIKVDGKYYVYLKDA
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VSNPGTTNTNTSNNSNTNSQASQSNDIDSLLKQLYKLPLSQRHVESDGLVFDPAQITSRT
                                                                                                                  SHGDHYHYYNGKVPYDAIISEELLMKDPNYKLKDEDIVNEVKGGYVIKVDGKYYVYLKDA
                               GDAYIVPHGDHYHYIPKNELSASELAAAEAFLSGRGNLSNSRTYRRQNSDNTSRTNWVPS
                                                                         AHADNVRTKEEINRQKQEHSQHREGGTPRNDGAVALARSQGRYTTDDGYIFNASDIIEDT
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; Streptococcal infection; det;
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                                                                                                                                                                                                   Score 4163; DB 23;
Pred. No. 3.5e-299;
; Mismatches 0;
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RESULT 3
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New proteins and nucleic acid molecules from Streptococcus useful as medicaments for treating or preventing a disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                S. pneumoniae
                                                                                     WPI; 2003-040579/03
N-PSDB; ABX06886.
                                                                                                                                                                     Masignani V,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Streptococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bacterial meningitis; pneumonia; ear infection; antiinflammatory;
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INST GENOMIC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Streptococcus pneumoniae type 4 strain genomic sequence appearing as ABS56494. Also included are an antibody which binds one of the proteins, treating a patient by administering the protein, DNA or antibody (in a composition), a kit comprising first and second primers, which are the nucleic acid cited above or fragments between nucleotides 8-100 of a sequence not defined in the specification, for amplifying a target sequence contained within a Streptococcus nucleic acid sequence, where the first primer is substantially complementary to the target
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         genomic sequence.

Note: The sequence data for this patent did not form of the printed specification, but was obtained in ele
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      medicaments for treating or preventing a disease or infection due to streptococcus bacteria, particularly S. pneumoniae, such as pneumonia, sepsis, otitis media or ear infection. The methods are useful in developing vaccines, diagnostics and antibiotics. The methods are useful for identifying immunodominant proteins. The present sequence is one of the 2469 proteins expressed by the identified coding regions from the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        specification (available on a computer readable format), or its fragment, expressed from 2469 of 2489 identified DNA coding regions from the Streptococcus pneumoniae type 4 streit constants.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ftp.wipo.int/pub/published_pct_sequences
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             to streptococcus bacteria, such as pneumonia, sepsis, otitis media ear infection -
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VSHTLTAKKENVA PRDQEFYDKA YNLLTEAHKALFXNKGRNSDFQALDKLLERLNDESTN
                                                                                  PQPAPNLKIDSNSSLVSQLVRKVGEGYVFEEKGISRYVFAKDLPSETVKNLESKLSKQES
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                  LLKGSNPSSVSKEKIN 796
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                                                                    QVETEKVEAQIKEAEVILLAKVTDSSIKANATETLAGIRNNLTLQIMDNNSIMAEAEKLLA
                                                                                                                                          LFATIKYYVEHPDERPHSNDGWGNASEHVLGKKDHSEDPNKNFKADEEPVEETPAEPEVP
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ad residue; Sp36; antibody; otitis media;
l infection; bronchial infection; bronchitis; sepsis
/label= Coiled coil region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /label= Coiled coil region
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                                                                                                                                                                                                                                                                             'label= Histidine triad residue
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    in the pathogenicity of Streptococcus pneumoniae, there still remains a need to identify polypeptides having epitopes in common from various strains of S. pneumoniae in order to utilise such polypeptides in vaccines to protect against a wide variety of S. pneumoniae. New vaccine compositions are described which comprise S. pneumoniae. New vaccine compositions are described which comprise of Streptococcus pneumoniae polypeptide (or fragments) of 80 - 680 amino acids in length that comprise at least one histidine triad residue (HxxHxH) or a coiled-coil region, or an antibody directed against these features. The vaccine is useful in protecting against infection by Streptococcus pneumoniae. The vaccine composition comprising antibodies to is useful for passive immunization for treating Pneumococcal infections which includes otitis media, nasopharyngeal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Johnson
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                                                                                                                                                                                                                             VSHTLTAKKENVAPRDQEFYDKAYNLLTEAHKALFXNKGRNSDFQALDKLLERLNDESTN
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                                                                                                                                                                                                                                                                              antigens (II) from Streptococcus pneumoniae. The protein antige have bactericidal activity. The nucleic acids, encoding the protein antigens, may be used for the recombinant production of the protein encode. The protein antigens may then be used as vaccines prevention and treatment of Streptococcal infections in mammals (especially humans) which result in, e.g. meningitis, otitis me bacteraemia and/or pneumonia. The present sequence represents s. pneumoniae BVH-11M protein antigen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Streptococcus pneumoniae; BVH-3; BVH-11; BVH-28; antigen; prophylaxis; therapy; infection; diagnosis; meningitis; be otitis media; pneumonia; immunisation; bactericidal.
                                                                                                                                                                                                                                         Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim
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                                                                                                                 Streptococcus pneumoniae; BVH-3; BVH-11; BVH-28; antigen; vaccine; prophylaxis; therapy; infection; diagnosis; meningitis; bacteraemia; otitis media; pneumonia; immunisation; bactericidal.
  20-DEC-1999;
                               06-JUL-2000
                                                           WO200039299-A2
                                                                                     Streptococcus pneumoniae
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Matches 616
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Streptococcal antigens useful for vaccinating otitis media, bacteremia and/or pneumonia -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure; Fig 12; 106pp; English.
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                AAIYNRVKGEKRIPLVRLPYMVEHTVEVKNGNLIIPHKDHYHNIKFAWFDDHTYKAPNGY
                                                          ESTNKEKLYDDLLAFLAPITHPERLGKPNSQIEYTEDEVRIAQLADKYTTSDGYIFDEHD
                                                                                                                                                                       KQESVSHTLTAKKENVAPRDQEFYDKAYNLLTEAHKALFXNKGRNSDFQALDKLLERLND
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EAIYNRVKAAKKVPLDRMPYNLQYTVEVKNGSLIIPHYDHYHNIKFEWFDEGLYEAPKGY
                                                                       IISDEGDAYVTPHMGHSHWIGKDSLSDKEKVAAQAYTKEKGILPPSPDADVKANPTGDSA
                                                                                                                   VSSDKVKLVDDILAFLAPIRHPERLGKPNAQITYTDDEIQVAKLAGKYTTEDGYIFDPRD
                                                                                                                                                                                                                                  PQPAPNPQPAPSNPIDEKLVKEAVRKVGDGYVFEENGVSRYIPAKNISAETAAGIDSKLA
                                                                                                                                                                                                                                                 PQPAPNLK-IDSN---SSLVSQLVRKVGEGYVFEEKGISRYVFAKDLPSETVKNLESKLS
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Pred. No. 3.5e-229;
5; Mismatches 104;
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                                                                                                                              infection (e.g., caused by Streptococcus pneumoniae, group A Streptococcus such as Streptococcus pneumoniae, group B Streptococcus such as Streptococcus propered by Streptococcus proup B Streptococcus such as Streptococcus pyogenes, group B Streptococcus such as Streptococcus and an individual susceptible to the infection. Staphylococcus aureus) in an individual susceptible to the infection. A polynucleotide (III) encoding (I) is useful in DAA immunisation techniques. The Streptococcus polypeptides are useful in a diagnostic test for S. pneumoniae infection. (III) is useful for designing DNA probes for use in detecting the presence of Streptococcus in a biological
                                                   probes for use in detecting the presence of Streptococcus in a biological sample suspected of containing the bacteria. The DNA probes may also be used for detecting circulating S. pneumonia nucleic acid in a sample for diagnosing streptococcal infections. This sequence represents a truncate of a Streptococcus pneumoniae gene used to obtain antigenic peptides,
                                                                                                                                                                                                                                                                                The invention describes an isolated polypeptide (I) with 70-90% identity to Streptococcus pneumonia protein BVH-3, BVH-11, variants BVH-3 or BVH-11, or chimeric sequences derived from them. A vaccine comprising (I) is useful for therapeutic or prophylactic treatment or meningitis, otitis media, bacteraemia or pneumonia infection in an individual susceptible to these disorders. (II) is also useful for therapeutic or prophylactic treatment of any streptococcal bacterial infection (a gaussed by Greentococcal pages of the prophylactic treatment of any streptococcal bacterial infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New Streptococcus pneumoniae BVH-3 and BVH-11 variant and epitope-bearing polypeptides, useful as vaccine components for treating or preventing streptococcal infections such as otitis media,
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described in the method of the invention.

Note: This sequence does not appear in the specification but has been created according to information given in the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                           Example 1; Page -; 113pp; English.
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RESULT 8
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ID AAB1

standard;

Protein;

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BXCXEX

21-NOV-2000

(first entry)

AAB12716;

Streptococcus pneumoniae BVH-11 protein antigen SEQ ID

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KSNAKETLTGLKNNLLFGTQDNNTIMAEAEKLLALLKES
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                                                         EETPREEKPQSEKPESPKPTEEPEEESPEESEEPQVETEKVEEKLREAEDLLGKIQDPII
                                                                                                                     TLEDLLATVKYYVEHPNERPHSDNGFGNASDHVQRNKNGQADTNQTEKPSEEKPQTEKPE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Streptococcus pneumoniae; BVH-3; BVH-11; BVH-28; antigen; prophylaxis; therapy; infection; diagnosis; meningitis; be otitis media; pneumonia; immunisation; bactericidal.
                                                                                                                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                   Claim
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KQESVSHTLTAKKENVAPRDQEFYDKAYNLLTEAHKALFXNKGRNSDFQALDKLLERLND
                                                                     ARGVAVPHGDHYHFIPYSQMSELEERIARIIPLRYRSNHWVPDSRPEQPSPQPTPEPSPG
                                                                                                                                 GDAYIVPHGDHYHYIPKNELSASELAAAEAFLSGRENLSNLRTYRRONSDNTPRTNWVPS
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                          PQPAPNPQPAPSNPIDEKLVKEAVRKVGDGYVFEENGVSRYIPAKNLSAETAAGIDSKLA
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KSNAKETLTGLKNNLLFGTQDNNTIMAEAEKLLALLKES
                                                         EETPREEKPQSEKPESPKPTEEPEESSPESSEEPQVETEKVEEKLREAEDLLGKIQDPII
                                                                                                                                                                                                                   EAI YNRVKAAKKVPLDRMPYNLQYTVEVKNGSLI I PHYDHYHNI KFEWFDEGLYEAPKGY
                                                                                                                                                                                                                                     AAIYNRVKGEKRIPLVRLPYMVEHTVEVKNGNLIIPHKDHYHNIKFAWFDDHTYKAPNGY
                                                                                                                                                                                                                                                                                        ITSDEGDAYVTPHMTHSHWIKKDSLSEAERAAAQAYAKEKGLTPPSTDHQDSGNTEAKGA
                                                                                                                                                                                                                                                                                                            IISDEGDAYVTPHMGHSHWIGKDSLSDKEKVAAQAYTKEKGILPPSPDADVKANPTGDSA
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                                 KANATETLAGLRUNLTLQIMDUNSIMAEAEKLLALLKGS
                                                                                                                                              TLEDLLATVKYYVEHPNERPHSDNGFGNASDHVQRNKNGQADTNQTEKPSEEKPQTEKPE
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AAU75933 standard; Protein;

AAU75933;

08-MAY-2002

(first

entry

Streptococcus pneumoniae BVH-11 protein

BVH-11; vaccine; meningitis; otitis monia; streptococcal bacterial infection media; bacteraemia;

Streptococcus pneumoniae.

WO200198334-A2

19-JUN-2001; 2001WO-CA00908

20-JUN-2000; 2000US-212683P

SHIRE BIOCHEM INC.

Ouellet ū Charland z Martin Ö Brodeur

В

N-PSDB; 2002-122272/16. ABK15103

New Streptococcus pneumoniae BVH-3 and BVH-11 variant and epitope-bearing polypeptides, useful as vaccine components for preventing streptococcal infections such as otitis media, meningitis, and bacteraemia for treating

Example 1; Fig 7; 113pp; English.

The invention describes an isolated polypeptide (I) with 70-90% identity to Streptococcus pneumonia protein BVH-3, BVH-11, variants BVH-3 or BVH-11, or chimeric sequences derived from them. A vaccine comprising (I) is useful for therapeutic or prophylactic treatment or meningitis, oticis media, bacteraemia or pneumonia infection in an individual susceptible to these disorders. (II) is also useful for therapeutic or prophylactic treatment of any streptococcal bacterial infection (e.g., caused by Streptococcus pneumoniae, group A Streptococcus such as Streptococcus pyogenes, group w Streptococcus of. (II) such

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                                                                                                                                                                                     TLEDLFATIKYYVEHPDERPHSNDGWGNASEHVLGKKDHSEDPNKNFKAD--
                                                                                                                                                                                                                                                                AAIYNRVKGEKRIPLVRLPYMVEHTVEVKNGNLIIPHKDHYHNIKFAWFDDHTYKAPNGY
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KSNAKETLTGLKNNLLFGTQDNNTIMAEAEKLLALLKES
                         KANATETLAGLRNNLTLQIMDNNSIMAEAEKLLALLKGS
                                                                               EETPREEKPQSEKPESPKPTEEPEEESSEESQVETEKVEEKLREAEDLLGKIQDPII
                                                                                                                                                             TLEDLLATVKYYVEHPNERPHSDNGFGNASDHVQRNKNGQADTNQTEKPSEEKPQTEKPE
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                                                                                                                                                                                                                                                                                                            The present invention describes nucleic acids (I) encoding protein antigens (II) from Streptococcus pneumoniae. The protein antigens have bactericidal activity. The nucleic acids, encoding the protein antigens, may be used for the recombinant production of the protein they encode. The protein antigens may then be used as vaccines for prevention and treatment of Streptococcal infections in mammals (especially humans) which result in, e.g. meningitis, otilis media, bacteraemia and/or pneumonia. The present sequence represents the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Streptococcus pneumoniae; BVH-3; BVH-11; BVH-28; prophylaxis; therapy; infection; diagnosis; meniotitis media; pneumonia; immunisation; bactericio
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Streptococcal otitis media,
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VSNPGTTNTNTSNNSNTNSQASQSNDIDSLLKQLYKLPLSQRHVESDGLVFDPAQITSRT
                                              GDAYIVPHGDHYHYIPKNELSASELAAAEAFLSGRGNLSNSRTYRRQNSDNTSRTNWVPS
                                                                                                 AHADNVRTKEEINRQKQEHSQHREGGTPRNDGAVALARSQGRYTTDDGYIFNASDIIEDT
                                                                                                                                             SHGDHYHYYNGKVPYDAIISEELLMKDPNYKLKDEDIVNEVKGGYVIKVDGKYYVYLKDA
                                                                                                                                                                               AYELGLHQAQTVKENNRVSYIDGKQATQKTENLTPDEVSKREGINAEQIVIKITDQGYVT
                                                                               AHADNVRTKEEINRQKQEHSQHREGGTSANDGAVAFARSQGRYTTDDGY1FNASD11EDT
                                                                                                                               SHGDHYHYYNGKVPYDAIISEELLMKDPNYQLKDSDIVNEIKGGYVIKVNGKYYVYLKDA
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                                                                                                                                                                                                                                                                              690 AA;
                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                antigens useful for vaccinating bacteremia and/or pneumonia -
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Pred. No. 2.9e
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The invention describes an isolated polypeptide (I) with 70-90% identity to Streptococcus pneumonia protein BVH-3, BVH-11, variants BVH-3 or BVH-11 or chimeric sequences derived from them. A vaccine comprising (I) is useful for therapeutic or prophylactic treatment comeningitis, otitis media, bacteraemia or pneumonia infection in an individual susceptible to these disorders. (II) is also useful for therapeutic or prophylactic treatment of any streptococcal bacterial infection (e.g., caused by Streptococcus pneumoniae, group A
                                                                                                                                                                                                                                                                                               New Streptococcus pneumoniae BVH-3 and BVH-11 variant and epitope-bearing polypeptides, useful as vaccine components or preventing streptococcal infections such as otitis medimeningitis, and bacteraemia
                                                                                                                                                                                                                                                Example 1; Page -; 113pp; English.
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streptococcal bacterial infection; mutant; mutein.
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Note: This sequence does not appear in the specification but has been created according to information given in the invention.
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                                                                                  AAIYNRVKGEKRIPLVRLPYMVEHTVEVKNGNLIIPHKDHYHNIKFAWFDDHTYKAPNGY
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                                                           EATYNRVKAAKKVPLDRMPYNLQYTVEVKNGSLIIPHYDHYHNIKFEWFDEGLYEAPKGY
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                                                                                                                                                                                                                                                                                                                                                                 The present sequence, isolated from Streptococcus pneumoniae, is a human C3-degrading protein of about 92 kDa. This sequence may encompass a smallerr, approximately 20 kDa protein (see AAY9138), also having human C3-degrading activity. The DNA sequences (AAA08556-57) can be used for producing an immune response to Streptococcus pneumoniae in a mammal. Antibodies against the proteins can be used to inhibit S. pneumoniae-mediated C3 degradation. C3-mediated inflammation and rejection in xenotransplantation can be inhibited by expressing the nucleic acid sequences on the surface of an organ of an animal. In particular, the polypeptides are useful for stimulating the immune system and are effective to immunize or treat a mammalian subject against Streptococcus pneumoniae infection or colonization.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Isolated polypeptide is used to stimulate immune system and immunize treat a mammalian subject against Streptococcus pneumoniae infection colonization
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human C3-degrading protein; 92 kDa; immunostimulatory; vaccine; inhibitor; inflammation; organ rejection; xenotransplantation.
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                                                                                                                                                                                                                                                                                                                                             Sequence
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31-MAR-1999;
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AMERICAN CYANAM
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NPAQPRLSENHNLTVTPTYHQ-NQGENISSLLRELYAKPLSERHVESDGLIFDPAQITSR
                 SVSNPGTTNTNTSNNSNTNSQASQSNDIDSLLKQLYKLPLSQRHVESDGLVFDPAQITSR
                                                                         TGDAYIVPHGDHYHYIPKNELSASELAAAEAFLSGRGNLSNSRTYRRQNSDNTSRTNWVP
                                                                                                              AAHADNIRTKEEIKROKQEHSHNHGGGS--NDQAVVAARAQGRYTTDDGYIFNASDIIED
                                                                                                                             AAHADNVRTKEEINRQKQEHSQHREGGTPRNDGAVALARSQGRYTTDDGYIFNASDIIED
                                                                                                                                                                      TSHGDHYHYYNGKVPYDAIISEELLMKDPNYQLKDSDIVNEIKGGYVIKVDGKYYVYLKD
                                                                                                                                                                                        TSHGDHYHYYNGKVPYDAIISEELLMKDPNYKLKDEDIVNEVKGGYVIKVDGKYYVYLKD
                                                                                                                                                                                                                             SYELGRHQAGQVKKESNRVSYIDGDQAGQKAENLTPDEVSKREGINAEQIVIKITDQGYV
                                                                                                                                                                                                                                                SYELGLYQARTV-KENNRVSYIDGKQATQKTENLTPDEVSKREGINAEQIVIKITDQGYV
                                                        TGDAYIVPHGDHYHYIPKNELSASELAAAEAYWNG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             inflammation; organ rejection; xenotransplantation.
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                                                                                                                                                                                                                                                                                       Conservative
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99US-0283094.
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Pred. No. 4.1e-199;
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                                                                          Masignani V,
                                                                                                                                27-MAR-2001; 2001GB-0007658
                                                                                                                                                      27-MAR-2002; 2002WO-IB02163
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DB; ABX06885.
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                                                                                                                                                                                                                                             respiratory; gene therapy; vaccine
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New proteins and nucleic acid molecules from Streptococcus useful as medicaments for treating or preventing a disease due to streptococcus bacteria, such as pneumonia, sepsis, o

us pneumoniae, se or infection , otitis media

ear infection

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Streptococcus pneumoniae type 4 strain genomic sequence appearing as ABS56454. Also included are an antibody which binds one of the proteins, treating a patient by administering the protein, DNA or antibody (in a composition), a kit comprising first and second primers, which are the nucleic acid cited above or fragments between nucleotides 8-100 of a sequence not defined in the specification, for amplifying a target sequence contained within a Streptococcus nucleic acid sequence, where the first primer is substantially complementary to the target
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            of the printed specification, but format directly from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Note: The sequence data for this patent of the printed specification, but was o
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             identity to any of the 2469 amino acid sequences, identified in the specification (available on a computer readable format), or its fragment, expressed from 2469 of 2489 identified DNA coding regions from the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim
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                                                                                     SPQPAPSNPID--EKLVKEAVRKVGDGYVFEENGVSRYIPAKDLSAETAAGIDSKLAKQE
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SLSHKLGTKKTDLPSSDREFYNKAYDLLARIHQDLLDNKGRQVDFEALDNLLERLKDVSS
                                       SVSHTLTAKKENVAPRDQEFYDKAYNLLTEAHKALFXNKGRNSDFQALDKLLERLNDEST
                                                                                                                                                                             TARGVAVPHGNHYHFIPYEQMSELEKRIARIIPLRYRSNHWVPDSRPEEPSPQPTPEPSP
                                                                                                                                                                                                                                                                                                               SVSNPGTTNTNTSNNSNTNSQASQSNDIDSLLKQLYKLPLSQRHVESDGLVFDPAQITSR
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Pred. No. 4.8e-198;
14; Mismatches 138;
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AAY81501 to AAY81679 represent specifically claimed protein sequences isolated from Streptococcus pneumoniae. AAA05407 to AAA05590 represent specifically claimed nucleotide sequences isolated from S. pneumoniae. The sequences have antibacterial and antiinflammatory properties. The protein sequences, and fragments of them, are useful as immunogens and/or antigens. The nucleotide sequences can be used in vaccines and idiagnostic assays. The proteins and nucleotides can be useful for the detection and diagnosis of S. pneumoniae. The protein sequences are alsuseful for screening an agent capable of antagonising, inhibiting or interfering with the function or expression of the proteins in which the
                                                                                                                                                                                                                                            New Streptococcal protein, useful as a vaccine, for diagnosis of pneumococcal diseases and for screening agents capable of antagonizing or inhibiting expression of the protein -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Streptococcus pneumoniae; vaccine; screening; protein antigen; antibacterial; antiinflammatory; meningitis; infection; diagnosis;
                                                                                                                                                                                                          Claim 2; Page 99-100; 108pp; English.
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19-MAR-1999;
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99US-0125164
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RESULT 15
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Best Local Sim
Matches 549;
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          AAB01469
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                                                                                                                                                              YTLEDLFATIKYYVEHPDERPHSNDGWGNASEHVLGKKDHSEDPNKNFKADEE------P
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                                                                                                                                                                                                                                          DIISDEGDAYVTPHMGHSHWIGKDSLSDKEKVAAQAYTKEKGILPPSPDADVKANPTGDS
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                                                                                                                                                   YTLEDLLATVKYYVEHPNERPHSDNGFGNASDHVQRNKNGQADTNQTEKPSEEKPQTEKP
                                                                                                                                                                                         AEAIYNRVKAAKKVPLDRMPYNLQYTVEVKNGSLIIPHYDHYHNIKFEWFDEGLYEAPKG
                                                                                                                                                                                                                              DITSDEGDAYVTPHMTHSHWIKKDSLSEAERAAAQAYAKEKGLTPPSTDHQDSGNTEAKG
                                                                                                                                                                                                                                                                                       DESTNKEKLVDDLLAFLAFITHPERLGKPNSQIEYTEDEVRIAQLADKYTTSDGYIFDEH
                                                                                                                                                                                                                                                                                                          AKQESLSHKLGAKKTDLPSSDREFYNKAYDLLARIHQDLLDNKGRQVDFEALDNLLERLK
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                                                                         KSNAKETLTGLKUNLLFGTQDNNTIMAEAEKLLALLKES
                                                                                          KANATETLAGLRNNLTLQIMDNNSIMAEAEKLLALLKGS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             for treatment or prophylaxis of S. pneumoniae infection AAA05591 to AAA05614 represent primers used in the of the present invention.
                            Protein;
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67.0%;
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Pred.
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No. 7
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Streptococcus
                                                                                                                                meningitis; lo
                                                                                                                                                               Streptococcus pneumoniae; infection; vaccine; coiled coil region; histidine triad residue; Sp36; antibody; otitis media;
21-DEC-1999;
                                 29-JUN-2000
                                                                                                                                lobar pneumonia
                                                                                                                                                                                                                                                     (first entry)
                                                                                               pneumoniae
                                                                                                                                                   infection;
99WO-US30390
                                                                                                                                                                                                                    of Sp36
                                                                                                                                                   bronchial
                                                                                                                                                                                                                    (Sp36B)
                                                                                                                                                infection; bronchitis; sepsis;
                                                                                                                                                                                                                    of
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                                                                                                                                                                                                                  pneumoniae
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Vaccine useful for prophylaxis and treatment of such as otitis media, nasopharyngeal and bronch Johnson LS, (MEDI-) MEDIMMUNE INC 2000-452129/39. Koenig 98US-0113048 ß Adamou

pneumoniae proteins ment of pnemococcal infections bronchial infections,

Claim 1; Page 65-69; 70pp; English

Although a number of proteins have been suggested as being involved in the pathogenicity of Streptococcus pneumoniae, there still remains a need to identify polypeptides having epitopes in common from various strains of S. pneumoniae in order to utilise such polypeptides in vaccines to protect against a wide variety of S. pneumoniae. New vaccine compositions are described which comprise Streptococcus pneumoniae polypeptide (or fragments) of 80 - 680 amino acids in length that comprise at least one histidine triad residue (HxxHxH) or a coiled-coil region, or an antibody directed against these features. The vaccine is useful in protecting against infection by Streptococcus pneumoniae. The vaccine composition comprising antibodies to is useful for passive immunization for treating pneumonocccal infections which includes otitis media, nasopharyngeal bronchial infections.

Sequence 819 AA;

DB 21;

Length

819;

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Query Match
Best Local Similarity
Matches 544; Conserv
                                                                  198
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 247
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                          SVSNPGTTNTNTSNNSNTNSQASQSNDIDSLLKQLYKLPLSQRHVESDGLVFDPAQITSR 299
                                                                                                                                                          AAHADNVRTKEEINRQKQEHSQHREGGTPRNDGAVALARSQGRYTTDDGYIFNASDIIED
                                                                                                                                                                                                                    TSHGDHYHYYNGKVPYDAIISEELLMKDPNYKLKDEDIVNEVKGGYVIKVDGKYYVYLKD
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NPAQPRLSENHULTVTPTYHQ-NQGENISSLLRELYAKPLSERHVESDGLIFDPAQITSR
                                                                                      TGDAYIVPHGDHYHYIPKNELSASELAAAEAFLSGRGNLSNSRTYRRQNSDNTSRTNWVP
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                                                                                                                                  AAHADNIRTKEEIKROKQERSHNHNS---RADNAVAAARAQGRYTTDDGYIFNASDIIED
                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                      67.0%;
                                                                                                                                                                                                                                                                                                                                        85;
                                                                                                                                                                                                                                                                                                                                                      Score 2788.5;
Pred. No. 2.2e
                                                                                                                                                                                                                                                                                                                                        Mismatches
                                                                                                                                                                                                                                                                                                                                                      2e-197;
                                                                                                                                                                                                                                                                                                                                        139;
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                                                                  KQGSRPSSSSSYNA
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52;

Gaps

61 59

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ARBIJZ
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AXX ARBIJZ
AXX Strep
CXX Strep
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CXX STREP
XXX POPP

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                                     Disclosure; Fig 12; 106pp; English.
                                                                           Streptococcal otitis media,
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                                                             IKSNAKETLIGLKNNLLFGTQDNNTIMAEAEKLLALLKES
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Pred. No. 3.3e-197;
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                       TARGVAVPHGDHYHFIPYSQMSELEERIARIIPLRYRSNHWVPDSRPEQPSPQPTPEPSP
                                                                         NPAQPRLSENHULTVTPTYHQ-NQGENISSILRELYAKPLSERHVESDGLIFDPAQITSR
                                                                                                                                                                                                                               AAHADNIRTKEBIKRQKQEHSHNHGGGS--NDQAVVAARAQGRYTTDDGYIFNASDIIBD
                                                                                                                                                                                                                                                          AAHADNVRTKEEINRQKQEHSQHREGGTPRNDGAVALARSQGRYTTDDGYIFNASDIIED
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                                                                                                SVSNPGTINTNTSNNSNTNSQASQSNDIDSLLKQLYKLPLSQRHVESDGLVFDPAQITSR
                                                                                                                                                                                 TGDAYIVPHGDHYHYIPKNELSASELAAAEAFLSGRGNLSNSRTYRRQNSDNTSRTNWVP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
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therapy; infection; diagnosis; meningitis;
pneumonia; immunisation; bactericidal.
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3.7e-196;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Streptococcus pneumoniae; infection; vaccine; coiled chistidine triad residue; Sp36; antibody; otitis media; nasopharyngeal infection; bronchial infection; bronchi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              meningitis;
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                     (MEDI-) MEDIMMUNE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Although a number of proteins have been suggested as being involved in the pathogenicity of Streptococcus pneumoniae, there still remains a need to identify polypeptides having epitopes in common from various strains of S. pneumoniae in order to utilise such polypeptides in vaccines to protect against a wide variety of S. pneumoniae. New vaccine compositions are described which comprise a Streptococcus pneumoniae polypeptide (or fragments) of 80 - 600 amino acids in length that comprise at least one histidine triad residue (HxxHxH) or a coiled-coil region, or an antibody directed against these features. The vaccine is useful in protecting against infection by Streptococcus pneumoniae. The vaccine composition comprising antibodies to is useful for passive immunization for treating pneumococcal infections which includes otitis media, nasopharyngeal
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                                                  DIISDEGDAYVTPHMGHSHWIGKDSLSDKEKVAAQAYTKEKGILPPSPDADVKANPTGDS
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                               DITSDEGDAYVTPHMTHSHWIKKDSLSEAERAAAQAYAKEKGLTPPSTDHQDSGNTEAKG
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                   identity to any of the 2469 amino acid sequences, identified in the specification (available on a computer readable format), or its fragment, capacification (available on a computer readable format), or its fragment, capacification 2469 of 2489 identified DNA coding regions from the Streptococcus pneumoniae type 4 strain genomic sequence appearing as ABS56454. Also included are an antibody which binds one of the proteins, treating a patient by administering the protein, DNA or antibody (in a composition), a kit comprising first and second primers, which are the nucleic acid cited above or fragments between nucleotides along the sequence not defined in the specification, for amplifying a target sequence contained within a Streptococcus nucleic acid sequence, where the first primer is substantially complementary to the target sequence and the second primer is substantially complementary to the complement of the target sequence, and where the parts of the primers complement of the target sequence to be amplified, assay comprising contacting a test compound with the protein, and determining whether the termin of the target sequence to be amplified, assay comprising contacting a test compound with the protein, and determining whether the termining by the compound binds to the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              useful as medicaments for treating or preventing due to streptococcus bacteria, such as pneumonia, or ear infection
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The invention relates to a protein comprising or having at least 50% identity to any of the 2469 amino acid sequences, identified in the
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    pneumoniae type 4 strain protein from coding region #993.

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Note: The sequence data for this patent did not form part
of the printed specification, but was obtained in electronic
format directly from WIPO at
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                                                                                                                                                                                                                                                   AAAIYNRVKGEKRIPLVRLPYMVEHTVEVKNGNLIIPHKDHYHNIKFAWFDDHTYKAPNG
                                                                                                                                                                                                                                                                                                                                                  DIISDEGDAYVTPHMGHSHWIGKDSLSDKEKVAAQAYTKEKGILPPSPDADVKANPTGDS
                                                                                                                                                                                                                                                                                                                                                                                                           DVPSDKVKLVDDILAFLAPIRHPERLGKENAQITYTDDEIQVAKLAGKYTTEDGYIFDPR
                                                                                                                                                                                                                                                                                                                                                                                                                                     DESTNKEKLYDDLLAFLAFITHPERLGKFNSQIEYTEDEVRIAQLADKYTTSDGYIFDEH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SPQPAPNPQPAPSNPIDEKLVKEAVRKVGDGYVFEENGVSRYIPAKDLSAETAAGIDSKL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TARGVAVPHGDHYHFIPYSQMSELEERIARIIPLRYRSNHWVPDSRPEQPSPQPTPEPSP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAHADNVRTKEEINRQKQEHSQHREGGTPRNDGAVALARSQGRYTTDDGYIFNASDIIED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SYELGRHQAGQVKKESNRVSYIDGDQAGQKAENLTPDEVSKREGINAEQIVIKITDQGYV
                                                                                                                                                                YTLEDLFATIKYYVEHPDERPHSNDGWGNASEHVLGK-------KDHSE------
                                                                                                                                                                                                                           AEAIYNRVKAAKKVPLDRMPYNLQYTVEVKNGSLIIPHYDHYHNIKFEWFDEGLYEAPKG
                                                                                                                                                                                                                                                                                                                   DITSDEGDAYVTPHMTHSHWIKKDSLSEAERAAAQAYAKEKGLTPPSTDHQDSGNTEAKG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AKQESLSHKLGAKKTDLPSSDREFYNKAYDLLARIHQDLLDNKGRQVDFEALDNLLERLK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GPQPAPNLK-IDSN---SSLVSQLVRKVGEGYVFEEKGISRYVFAKDLPSETVKNLESKL
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AKVTDSSLKANATETLAGLRNNLTLQIMDNNSIMAEAEKLLALLKGSNPSSV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SKQESVSHTLTAKKENVAPRDQEFYDKAYNLLTEAHKALFXNKGRNSDFQALDKLLERLN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TARGVAVPHGNHYHFIPYEQMSELEKRIARIIPLRYRSNHWVPDSRPEQPSPQSTPEPSP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TSHGDHYHYYNGKVPYDAIISEELLMKDPNYQLKDSDIVNEIKGGYVIKVDGKYYVYLKD
                                          ESDEKENHAGINPSADNIYKPSTDTEETEEEAEDTTDEAEIPQVENSVINAKIADAEALL
                                                                                                                                  YTLEDLLATVKYYVEHPNERPHSDNGFGNÅSDHVRKNKVDQDSKPDEDKEHDEVSEPTHP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TGDAYIVPHGDHYHYIPKNELSASELAAAEAYWNG------KQGSRPSSSSSYNA
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                                                                                     -DPNKNFKADEEPVEETPAEPEVPQVETEKVEAQLKEAEVLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 2772;
Pred. No. 3
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.9e-196;
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Best Local
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                                                                                                                                                                                                                                                                                                                            The present invention describes nucleic acids (I) encoding protein antigens (II) from Streptcoccus pneumoniae. The protein antigens have bactericidal activity. The nucleic acids, encoding the protein antigens, may be used for the recombinant production of the proteins they encode. The protein antigens may then be used as vaccines for the prevention and treatment of Streptcoccal infections in mammals (especially humans) which result in, e.g. meningitis, ortis media, bacteraemia and/or pneumonia. The present sequence represents a s. pneumoniae BVH-11 protein antigen, from the present invention.
                                                                                                                                                                                                                                                                                                        Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Streptococcal otitis media,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Streptococcus pneumoniae; BVH-3; BVH-11; BVH-28; prophylaxis; therapy; infection; diagnosis; meni
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure; Fig 12; 106pp; English.
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AAHADNVRTKEEINRQKQEHSQHREGGTPRNDGAVALARSQGRYTTDDGYIFNASDIIED
                                                                                           AAHADNIRTKEEIKROKOERSHNHNS---RADNAVAAARAOGRYTTDDGYIFNASDIIED
                                                                                                                                                TSHGDHYHYYNGKVPYDAIISEELLMKDPNYQLKDSDIVNEIKGGYVIKVDGKYYVYLKD
                                                                                                                                                                       TSHGDHYHYYNGKVPYDAIISEELLMKDPNYKLKDEDIVNEVKGGYVIKVDGKYYVYLKD
                                                                                                                                                                                                SYELGRHQAGQVKKESNRVSYIDGDQAGQKAENLTPDEVSKREGINAEQIVIKITDQGYV
                                         TGDAYIVPHGNHFHYIPKSDLSASELAAAQAYWNG
                                                               TGDAYIVPHGDHYHYIPKNELSASELAAAEAFLSGRGNLSNSRTYRRONSDNTSRTNWVP
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                                                                                                                                                                                                                                                                                                         807 AA;
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                                                                                                                                                                                                                                                     87;
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Pred. No. 4.3e-196;
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                                                                                                                                                                                                                                                    Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Martin
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 Disclosure; Fig 12; 106pp; English
                           otitis
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                          media,
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                                     TDSSLKANATETLAGLRNNLTLQIMDNNSIMAEAEKLLALLKGS
                                                                                                                                                                                                                                          DIISDEGDAYVTPHMGHSHWIGKDSLSDKEKVAAQAYTKEKGILPPSPDADVKANPTGDS
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TGDAYIVPHGDHYHYIPKSDLSASELAAAQAYWNG------KQGSRPSSSSSSHNA
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                                                                                                                                      YTLEDLFATIKYYVEHPDERPHSNDGWGNASEHVLGKKDHSEDPNKNFKADEE-----P
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Pred. No. 2.8e-195;
87; Mismatches 141;
                                                                                       PAEPEVPQVETEKVEAQLKEAEVLLAKV 741
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TARGVAVPHGDHYHFIPYSQMSELEERIARIIPLRYRSNHWVPDSRPEQPSPQPTPEPS-
                                                    SVSNPGTTNTNTSNNSNTNSQASQSNDIDSLLKQLYKLPLSQRHVESDGLVFDPAQITSR
                                                                                            TGDAYIVPHGDHYHYIPKNELSASELAAAEAFLSGRGNLSNSRTYRRQNSDNTSRTNWVP
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                                                                              TGDAYIVPHGDHYHYIPKNELSASELAAAEAYWNG-------KQGSRPSSSSSYNA
                                                                                                                                  AAHADNIRTKEEIKROKOEHSHNHNS---RADNAVAAARAQGRYTTDDGYIFNASDIIED
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The present invention describes nucleic acid antigens (II) from Streptococcus pneumoniae.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      have bactericidal activity. The nucleic acids, encoding the protein antigens, may be used for the recombinant production of the proteins they encode. The protein antigens may then be used as vaccines for the prevention and treatment of Streptococcal infections in mammals (especially humans) which result in, e.g. meningitis, otitis media, bacteraemia and/or pneumonia. The present sequence represents a spneumoniae BVH-11-2 protein antigen, from the present invention.
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38; Conservative
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LLEKVTDPSIRQNAMETLTGLKSSLLLGTKDNNTISAEVDSLLALLKESQPAPI
                                 LLAKVTDSSLKANATETLAGLRNNLTLQIMDNNSIMAEAEKLLALLKGSNPSSV
                                                                     HPESDEKENHAGLNPSADNLYKPSTDTEETEEEAEDTTDEAEIPQVENSVINAKIADAEA
                                                                                                                                            KGYSLEDLLATVKYYVEHPNERPHSDNGFGNASDHVRKNKADQDSKPDEDKEHDEVSEPT
                                                                                                                                                                            NGYTLEDLFATIKYYVEHPDERPHSNDGWGNASEHVLGK---
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Best Local Similarity
Matches 538; Conserv
                                                                                                                                                                                                                                                                                                                                   infection (e.g., caused by Streptococcus pneumoniae, group A Streptococcus such as Streptococcus propers, group B Streptococcus such as Streptococcus propers, group B Streptococcus such as Streptococcus agalactiae, S. dysgalactiae, S. uberis, S. nocardia or Staphylococcus aureus) in an individual susceptible to the infection. A streptococcus polynucleotide (III) encoding (I) is useful in DNA immunisation techniques. The Streptococcus polypeptides are useful in a diagnostic test for S. pneumoniae infection. (III) is useful for designing DNA probes for use in detecting the presence of Streptococcus in a biological sample suspected of containing the bacteria. The DNA probes may also be used for detecting circulating S. pneumonia nucleic acid in a sample for diagnosing streptococcal infections. This sequence represents a truncate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The invention describes an isolated polypeptide (I) with 70-90% identity to Streptococcus pneumonia protein BVH-3, BVH-11, variants BVH-3 or BVH-10, or chimeric equences derived from them. A vaccine comprising (I) is useful for therapeutic or prophylactic treatment emeningitis, otitis media, bacteraemia or pneumonia infection in an individual susceptible to these disorders. (II) is also useful for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New Streptococcus pneumoniae BVH-3 and BVH-11 variant and epitope-bearing polypeptides, useful as vaccine components for treating or preventing streptococcal infections such as otitis media, meningitis, and bacteraemia
                                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                             Note: This sequence does not appear in the specification but has been created according to information given in the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           therapeutic or prophylactic treatment of any streptococcal bacterial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 20-JUN-2000; 2000US-212683P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Streptococcus pneumoniae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BVH-3; BVH-11; vaccine; meningitis; otitis media; bacteraemia; pneumonia; streptococcal bacterial infection; mutant; mutein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAU84087 standard; Peptide; 819
                                                                                                                                                                                                                                                                                                  Streptococcus pneumoniae gene used to obtain antigenic ribed in the method of the invention
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                   TSHGDHYHYYNGKVPYDAIISEELLMKDPNYKLKDEDIVNEVKGGYVIKVDGKYYYYLKD 119
                                                                                               SYELGLYQARTV-KENNRVSYIDGKQATQKTENLTPDEVSKREGINAEQIVIKITDQGYV
 TSHGDHYHYYNGKVPYDAIISEELLMKDPNYQLKDSDIVNEIKGGYVIKVDGKYYVYLKD
                                                                          SYELGRHQAGQVKKESNRVSYIDGDQAGQKAENLTPDEVSKREGINAEQIVIKITDQGYV
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                                                                                                                                                  Score 2750.5; DB 23; Pred. No. 1.5e-194; 90; Mismatches 145;
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Matches 538
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Streptococcal antigens useful fo otitis media, bacteremia and/or
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                            PRDITSDEGDAYVTPHMTHSHWIKKDSLSEAERAAAQAYAKEKGLTPPSTDHQDSGNTEA
                                                                                                 EHDIISDEGDAYVTPHMGHSHWIGKDSLSDKEKVAAQAYTKEKGILPPSPDADVKANPTG
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                                                                            CC identity to Streptococcus pneumonia protein BVH-3, BVH-11, variants of CC identity to Streptococcus pneumonia protein BVH-3, BVH-11, variants of CC BVH-3 or BVH-11, or chimeric sequences derived from them. A vaccine (II) CC comprising (I) is useful for therapeutic or prophylactic treatment of CC meningitis, otitis media, bacteraemia or pneumonia infection in an CC individual susceptible to these disorders. (II) is also useful for therapeutic or prophylactic treatment of any streptococcul bacterial CC infection (e.g., caused by Streptococcus pneumoniae, group A CC Streptococcus such as Streptococcus pyogenes, group B Streptococcus such as Streptococcus pyogenes, group B Streptococcus such as Streptococcus pyogenes, S. uberis, S. nocardia or CC staphylococcus agalactiae, S. dysgalactiae, S. uberis, S. nocardia or CC Staphylococcus aureus) in an individual susceptible to the infection. CC A polymucleotide (III) encoding (I) is useful in DNA immunisation CC techniques. The Streptococcus polypetides are useful in a diagnostic test for S. pneumoniae infection. (III) is useful for designing DNA CC probes for use in detecting the presence of Streptococcus in a biological sample suspected of containing the bacteria. The DNA probes may also be CC used for detecting circulating S. pneumonia nucleic acid in a sample for CC Streptococcus pneumoniae protein BVH-11-2, used to create the antigenic CC peptides described in the method of the invention.
 Query Match
Best Local Similarity
Matches 538; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                        New Streptococcus pneumoniae BVH-3 and BVH-11 variant and epitope-bearing polypeptides, useful as vaccine components for treating or preventing streptococcal infections such as otitis media, meningitis, and bacteraemia
                                                       Sequence
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                                                       therapy;
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                                                       pneumoniae; BVH-3; BVH-11; BVH-28; antigen; vaccine;
therapy; infection; diagnosis; meningitis; bacteraemi
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Streptococcal otitis media,
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                                                                                             SKQESVSHTLTAKKENVAPRDQEFYDKAYNLLTBAHKALFXNKGRNSDFQALDKLLERLN
                                                                                                                                                      GPQPAPNLK-IDSN---SSLVSQLVRKVGEGYVFEEKGISRYVFAKDLPSETVKNLESKL
                                                                                                                                                                                                                                             NPAOPRLSENHULTVTPTYHO-NOGENISSLLRELYAKPLSERHVESDGLIFDPAOITSR
DIISDEGDAYVTPHMGHSHWIGKDSLSDKEKVAAQAYTKEKGILPPSPDADVKANPTGDS
                                                   DESTNKEKLVDDLLAFLAFITHPERLGKPNSQIEYTEDEVRIAQLADKYTTSDGYIFDEH
                                                                              AKQESLSHKLGAKKTDLPSSDREFYNKAYDLLARIHQDLLDNKGRQVDFEALDNLLERLK
                                                                                                                                   SPOPAPNPOPAPSNPIDEKLVKEAVRKVGDGYVFEENGVPRYIPAKDLSAETAAGIDSKL
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                The present invention describes nucleic acids (I) encoding protein antigens (II) from Streptococcus pneumoniae. The protein antigens have bactericidal activity. The nucleic acids, encoding the protein antigens, may be used for the recombinant production of the proteins they encode. The protein antigens may then be used as vaccines for the prevention and treatment of Streptococcal infections in mammals (especially humans) which result in, e.g. meningitis, ottis media, bacteraemia and/or pneumonia. The present sequence represents a S. pneumoniae BVH-11-2 protein antigen, from the present invention.
                                                                                                                                                                                                                                                                                                                                                                                              Streptococcus pneumoniae; BVH-3; BVH-11; BVH-28; antigen; prophylaxis; therapy; infection; diagnosis; meningitis; bootitis media; pneumonia; immunisation; bactericidal.
 Sequence
                                                                                                                                         Disclosure; Fig 12; 106pp; English
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Query Match Best Local Similarity

63

Score Pred.

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Length

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RESULT 29
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                                                                            QESVSHTLTAKKENVAPRDQEFYDKAYNLLTEAHKALFXNKGRNSDFQALDKLLERLNDE 477
                                                                                                                                  TARGVAVPHGDHYHFIPYSQMSELEERIARIIPLRYRSNHWVPDSRPEQPSPQ--PTPEP
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                                                                                                                  APNPOPAPSNPID--EKLVKEAVRKVGDGYVFEENGVSRYIPAKDLSAETAAGIDSKLAK
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                                                                                                                                           The present invention describes nucleic acids (I) encoding protein antigens (II) from Streptococcus pneumoniae. The protein antigens have bactericidal activity. The nucleic acids, encoding the protein antigens, may be used for the recombinant production of the proteins they encode. The protein antigens may then be used as vaccines for the prevention and treatment of Streptococcal infections in mammals (especially humans) which result in, e.g. meningitis, otitis media, bacteraemia and/or pneumonia. The present sequence represents a s. pneumoniae BVH-11 protein antigen, from the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Streptococcus pneumoniae; BVH-3; BVH-11; BVH-28; antigen; prophylaxis; therapy; infection; diagnosis; meningitis; bactitis media; pneumonia; immunisation; bactericidal.
                                                                                                                                                                                                                                                                                                                                                                 Streptococcal antigens useful for vaccinating otitis media, bacteremia and/or pneumonia -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              240 SVSNPGTTNTNTSNNSNTNSQASQSNDIDSLLKQLYKLPLSQRHVESDGLVFDPAQITSR
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                                                                                                    DEKENHAGLNPSADNLYKPSTDTEETEEEAEDTTDEAEIPQVEHSVINAKIADAEALLEK
                                                                                                                                                                                                    LEDLLATVKYYVEHPNERPHSDNGFGNASDHVRKNKADQDSKPDEDKGHDEVSEPTHPES
                                                                                                                                                                                                                                                                                                                                                 AIYNRVKGEKRIPLVRLPYMVEHTVEVKNGNLIIPHKDHYHNIKFAWFDDHTYKAPNGYT
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               antigens (II) from Streptococcus pneumoniae. The protein antigens have bactericidal activity. The nucleic acids, encoding the protein antigens, may be used for the recombinant production of the proteins they encode. The protein antigens may then be used as vaccines for the prevention and treatment of Streptococcal infections in mammals (especially humans) which result in, e.g. meningitis, ottis media, bacteraemia and/or pneumonia. The present sequence represents a s. pneumoniae BVH-11 protein antigen, from the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  present invention describes nucleic acids (I) encoding protein igens (II) from Streptococcus pneumoniae. The protein antigens
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TSDEGDAYVTPHMTHSHWIKKDSLSEAERAAAQAYAKEKGLTPPSTDHQDSGNTEAKGAE
                    ISDEGDAYVTPHMGHSHWIGKDSLSDKEKVAAQAYTKEKGILPESPDADVKANPTGDSAA
                                                    STNKEKLVDDLLAFLAPITHPERLGKPNSQIEYTEDEVRIAQLADKYTTSDGYIFDEHDI
                                                                                                              QESLSHKLGTKKTDLPSSDREFYNKAYDLLARIHQDLLDNKGRQVDFEALDNLLERLKDV
                                                                                                                                 QESVSHTLTAKKENVAPRDQEFYDKAYNLLTEAHKALFXNKGRNSDFQALDKLLERLNDE
                                                                                                                                                                     APNPOPAPSNPID--EKLVKEAVRKVGDGYVFEENGVSRYIPAKDLSAETAAGIDSKLAK
                                                                                                                                                                                               SPGPQPAPNLKIDSNSSLVSQLVRKVGEGYVFEEKGISRYVFAKDLPSETVKNLESKLSK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       antigens useful for bacteremia and/or
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 2720; DB 21;
Pred. No. 2.6e-192;
B; Mismatches 142;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           for vaccinating
or pneumonia -
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                                                                             have bactericidal activity. The nucleic acids, encoding the protein antigens, may be used for the recombinant production of the protein they encode. The protein antigens may then be used as vaccines for t prevention and treatment of Streptococcal infections in mammals (especially humans) which result in, e.g. meningitis, otitis media, bacteraemia and/or pneumonia. The present sequence represents as some protein antigen, from the present invention.
                                                                                                                                                                                                                          Streptococcal antigens useful for vaccinating otitis media, bacteremia and/or pneumonia -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Streptococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAB12758
                                                        Sequence
                                                                                                                                                                The present invention describes nucleic acids (I) encoding protein antigens (II) from Streptococcus pneumoniae. The protein antigens
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                                                                                                                                                                                                                                                                                      Hamel J,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           prophylaxis; therapy; inf
otitis media; pneumonia;
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Local 528;
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                                                                                                                                                                                                                                                                                      Brodeur BR,
                                                        816 AA;
                                                                                                                                                                                                   Fig 12; 106pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      pneumoniae; BVH-3; BVH-11; BVH-28; antigen; vaccine;
therapy; infection; diagnosis; meningitis; bacteraemia;
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                    65.2%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            immunisation;
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        Score 2714; DB 21;
Pred. No. 7.3e-192;
0; Mismatches 146;
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                                                                                                    therapy; infection; pneumonia; immunisa
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                                                                                                     pneumoniae; BVH-3; BVH-11; BVH-28; antigen; vaccine;
therapy; infection; diagnosis; meningitis; bacteraemi
pneumonia; immunisation; bactericidal.
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Matches 528
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8; Mismatches 143;
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        The present sequence represents a protein from Streptococcus pneumoniae. The nucleic acid sequence encoding the Streptococcus pneumoniae protein can be useful in vaccines for inducing protective antibodies against Streptococcus pneumoniae, for treatment or prevention of infection e.g. pneumonia, otitis media or meningitis. Probes based on the nucleic acid are used to detect Streptococcus infection (by usual hybridisation or amplification methods), also for isolating Streptococcus genes or their allelic variants. The protein can be used similarly to detect specific antibodies in standard immunoassays, especially for diagnosing or monitoring infections. Antibodies which bind the protein are used to
                                                                                                                                       Claim
                                                                                                                                                          Nucleic acid encoding antigenic peptide(s) from Streptococcus pneumoniae - or their epitope-containing fragments, useful in protective or therapeutic vaccines, and for diagnosis
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tis media; meningitis.
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RESULT 35
ABP54589
ID ABP54
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04-SEP-2002

(first entry) SP042

pneumoniae

protein

sequence

SEQ ij NO:66 ABP54589

standard;

Protein;

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Best Local S
Matches 519
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                                                                                                                    AAAIYNRVKGEKRIPLVRLPYMVEHTVEVKNGNLIIPHKDHYHNIKFAWFDDHTYKAPNG
                                                                                                                                                                           DIISDEGDAYVTPHMGHSHWIGKDSLSDKEKVAAQAYTKEKGILPPSPDADVKANPTGDS
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                           VEET--
                                                   YTLEDLLATVKYYVEHPNERPHSDNGFGNASDHVQRNKNGQADTNQTEKPSEEKPQTEKP
                                                               YTLEDLFATIKYYVEHPDERPHSNDGWGNASEHVLGKKDHSEDPNKNFKADEE-----P
                                                                                                                                                                                                               DVXSDKVKLVXDILAFLAPIRHPERLGKPNAQITYTDDEIQVAKLAGKYTTEDGYIFDPR
                                                                                                                                                                                                                                                                    AKQESLSHKLGAKKTDLPSSDREFYNKAYDLLARIHQDLLDNKGRQVDFEALDNLLERLK
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Pred. No. 3.9e-187;
77; Mismatches 132;
                          PAEPEVPOVETEKVEAQLKEAEVLLAKVTD
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Query Match
Best Local Similarity
Matches 519; Conserv
                                                                                                                                                                                                                                                                                                                                                                                              ABQ84792 to ABQ84904 represents nucleic acids which encode the Streptococcus pneumoniae antigens given in ABP54557 to ABP54669. The S. pneumoniae antigens have antibacterial activity and can be used in vaccines. The S. pneumoniae antigens can also be used to prevent or attenuate a Streptococcal infection in an animal. The polynucleotides encoding the S. pneumoniae antigens can be used to detect Streptococcus nucleic acids. ABQ84905 to ABQ85130 represent primers used in the cloning of S. pneumoniae ORFs (open reading fra which are used in an example from the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New Streptococcus pneumoniae antigens, useful for Streptococcus and for preventing or attenuating di Streptococcus infection -
                                                                                                                                                                                                                                                                                                                                                                          Sequence
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(KUNS/)
(BARA/)
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KUNSCH C A.
BARASH S C.
DILLION P J.
DOUGHERTY B.
FANNON M R.
ROSEN C A.
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              TARGVAVPHGNHYHFIPYEQMSELEKRIARIIPLRYRSNHWVPDSRPEQPSPQSTPEPSP
                                                                  NPAQPRLSENHNLTVTPTYHQ.
                                                                                                                   TGDAYIVPHGDHYHYIPKNELSASELAAAEAYWNG------
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7; Mismatches 132;
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The present serotype 4 t
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: sequence is a 79 kDa protein of Streptococcus pneumoniae that is capable of degrading human complement protein C3

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meningitis; pneum
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(HCPC3). The sequence was deduced from the open reading frame of an isolated gene (see AAX25394). A smaller (20 kDa) HCPC3 protease is encoded by an open reading frame of S. pneumoniae serotype 3, and this open reading frame may be part of a larger open reading frame corresponding to the present sequence from the S. pneumoniae serotype 4 genome. Amino acids 1-58 and 90-132 of the 20 kDa protein have substantial sequence identity with amino acids 170-227 and 258-300 of the 79 kDa protein. Proteins and peptides or polypeptides containing these regions, and DNA sequences encoding them, are claimed. HCPC3 proteases and polypeptides can be used as immune system stimulating compositions (claimed). They can produce an immune response against infection or colonization (claimed). They can produce an ammalian subject against infection or colonization (claimed). They can produce a B cell response, a T cell response, an epithelial cell response, or an endothelial cell response (claimed). The expression of the proteins on the surface of an inhibit Claimed used in xenotransplantation can be used to inhibit Claimed used in firm and rejection.
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                                             --PAEPEVPQVETEKVEAQLKEAEVLLAKVTDSSLKANATETLAGLRNNLTLQIMDNNSI
                                                                                                                                                   GWGNASEHVLGKKDHSEDPNKNFKADEE-----PVEET-------
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ESPEESEEPQVETEKVEEKLREAEDLLGKIQDPIIKSNAKETLTGLKNNLLFGTQDNNTI
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Best Local Similarity
Matches 419; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The present invention describes nucleic acids (I) encoding protein antigens (II) from Streptococcus pneumoniae. The protein antigens have bactericidal activity. The nucleic acids, encoding the protein antigens, may be used for the recombinant production of the proteins they encode. The protein antigens may then be used as vaccines for the prevention and treatment of Streptococcal infections in mammals (especially humans) which result in, e.g. meningitis, oticis media, bacteraemia and/or pneumonia. The present sequence represents the S. pneumoniae BVH-11C protein antigen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Streptococcus pneumoniae; BVH-3; BVH-11; BVH-28; antigen; vaccine; prophylaxis; therapy; infection; diagnosis; meningitis; bacteraemia; otitis media; pneumonia; immunisation; bactericidal.
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                  The invention describes an isolated polypeptide (I) with 70-90% identity to Streptococcus pneumonia protein BVH-3, BVH-11, variants BVH-3 or BVH-11, or chimeric sequences derived from them. A vaccine comprising (I) is useful for therapeutic or prophylactic treatment omeningitis, otitis media, bacteraemia or pneumonia infection in an individual susceptible to these disorders. (II) is also useful for therapeutic or prophylactic treatment of any streptococcal bacterial
                                                                                                                                                                                                                                                                           New Streptococcus pneumoniae BVH-3 and BVH-11 variant and epitope-bearing polypeptides, useful as vaccine components for treating or preventing streptococcal infections such as otitis media, meningitis, and bacteraemia
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Streptococcus such as Streptococcus pyogenes, group B Streptococcus such as Streptococcus agalactiae, S. uberis, S. nocardia or Staphylococcus aureus) in an individual susceptible to the infection. A polynucleotide (III) encoding (I) is useful in DNA immunisation techniques. The Streptococcus polypeptides are useful in a diagnostic test for S. pneumoniae infection. (III) is useful for designing DNA probes for use in detecting the presence of Streptococcus in a biological sample suspected of containing the bacteria. The DNA probes may also be used for detecting circulating S. pneumonia nucleic acid in a sample for diagnosing streptococcus pneumoniae gene used to obtain antigenic peptides, described in the method of the invention.

Note: This sequence does not appear in the specification but has
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601
                               774
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       268 DSLLKQLYKLPLSQRHVESDGLVFDPAQITSRTARGVAVPHGDHYHFIPYSQMSELEERI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        208 AEAFLSGRGNLSNSRTYRRQNSDNTSRTNWVPSVSNPGTTNTNTSNNSNTNSQASQSNDI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity
EAEKLLALLKES
                                 EAEKLLALLKGS
                                                                 PEESEEPQVETEKVEEKLREAEDLLGKIQDPIIKSNAKETLTGLKNNLLFGTQDNNTIMA
                                                                                                PAEPEVPQVETEKVEAQLKEAEVLLAKVTDSSLKANATETLAGLRNNLTLQIMDNNSIMA
                                                                                                                                  NASDHVQRNKNGQADTNQTEKPSEEKPQTEKPEEETPREEKPQSEKPESPKPTEEPEEES
                                                                                                                                                                   NASEHVLGKKDHSEDPNKNFKAD----
                                                                                                                                                                                                     VKNGSLIIPHYDHYHNIKFEWFDEGLYEAPKGYTLEDLLATVKYYVEHPNERPHSDNGFG
                                                                                                                                                                                                                          VKNGNLIIPHKDHYHNIKFAWFDDHTYKAPNGYTLEDLFATIKYYVEHPDERPHSNDGWG
                                                                                                                                                                                                                                                                      AERAAAQAYAKEKGLTPPSTDHQDSGNTEAKGAEAIYNRVKAAKKVPLDRMPYNLQYTVE
                                                                                                                                                                                                                                                                                                      KEKVAAQAYTKEKGILPPSPDADVKANPTGDSAAAIYNRVKGEKRIPLVRLPYMVEHTVE
                                                                                                                                                                                                                                                                                                                                       PNAQITYTDDEIQVAKLAGKYTTEDGYIFDPRDITSDEGDAYVTPHMTHSHWIKKDSLSE
                                                                                                                                                                                                                                                                                                                                                                         PNSQIEYTEDEVRIAQLADKYTTSDGYIFDEHDIISDEGDAYVTPHMGHSHWIGKDSLSD
                                                                                                                                                                                                                                                                                                                                                                                                          YDLLARIHQDLLDNKGRQVDFEALDNLLERLKDVSSDKVKLVDDILAFLAFIRHFERLGK
                                                                                                                                                                                                                                                                                                                                                                                                                            YNLLTEAHKALFXNKGRNSDFQALDKLLERLNDESTNKEKLVDDLLAFLAPITHPERLGK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GDGYVFEENGVSRYIPAKNISAETAAGIDSKLAKQESISHKLGAKKTDIPSSDREFYNKA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GEGYVFEEKGISRYVFAKDLPSETVKNLESKLSKQESVSHTLTAKKENVAPRDQEFYDKA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ARIIPLRYRSNHWVPDSRPEEPSPQPTPEPSPSPQPAPNPQPAPSNPIDEKLVKEAVRKV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ARIIPLRYRSNHWVPDSRPEQPSPQPTPEPSPGPQPAPNLK-IDSN----SSLVSQLVRKV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DSLLKQLYKLPLSQRHVESDGLIFDPAQITSRTARGVAVPHGNHYHFIPYEQMSELEKRI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AEAFLSGRENLSNLRTYRRQNSDNTPRTNWVPSVSNPGTTNTNTSNNSNTNSQASQSNDI
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                               785
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Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
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No. 8
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.9e-152;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    34;
                                                                                                                                                                  EEPVEET
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                                                                                                                                                                                                                                                                                                   CC therapeutic or prophylattic treatment of any streptococcal bacterial
CC infection (e.g., caused by Streptococcus pneumoniae, group A
CC Streptococcus such as Streptococcus pyogenes, group B Streptococcus such
CC as Streptococcus agalactiae, S. dysgalactiae, S. uberis, S. nocardia or
CC Apolynucleotide (III) encoding (I) is useful in DNA immunisation
CC Apolynucleotide (III) encoding (I) is useful in DNA immunisation
CC techniques. The Streptococcus polypeptides are useful in a diagnostic
CC test for S. pneumoniae infection. (III) is useful for designing DNA
CC probes for use in detecting the presence of Streptococcus in a biological
CC sample suspected of containing the bacteria. The DNA probes may also be
CC used for detecting circulating S. pneumonia nucleic acid in a sample for
CC diagnosing streptococcal infections. This sequence represents a chimeric
CC gene created from fragments and variant fragments of Streptococcus
CC pneumoniae genes, described in the method of the invention.

CC Note: This sequence does not appear in the specification but has
                                                                                                                                                                                                                                     Matches
                                                                                                                                                                                                                                                  Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The invention describes an isolated polypeptide (I) with 70-90% identity to Streptococcus pneumonia protein BVH-3, BVH-11, variants BVH-3 or BVH-11, or chimeric sequences derived from them. A vaccine comprising (I) is useful for therapeutic or prophylactic treatment of meningitis, otitis media, bacteraemia or pneumonia infection in an individual susceptible to these disorders. (II) is also useful for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Example 1; Page -; 113pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New Streptococcus pneumoniae BVH-3 and BVH-11 variant epitope-bearing polypeptides, useful as vaccine compon or preventing streptococcal infections such as otitis meningitis, and bacteraemia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hamel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      20-JUN-2000; 2000US-212683P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      19-JUN-2001;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Streptococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Preumonia;
BVH-11-2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BVH-3; BVH-11;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (SHIR-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        pneumoniae
                                                                                                                                                                                                                                                                                                                                   created
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 442
                                  122
                                                                 382
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                                                                                                                                                                                                                                   366;
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                                                                                                                                                                   N
                                                                                                                                                                                                                                                    Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SHIRE
                                                                                                                   RIARIIPLRYRSNHWVPDSRPEQPSPQPTPEPSPGPQPAPNLK-IDSN---SSLVSQLVR
                                                                                                                                                                                   DIDSLLKQLYKLPLSQRHVESDGLVFDPAQITSRTARGVAVPHGDHYHFIPYSQMSELEE
                                                            KVGEGYVFEEKGISRYVFAKDLPSETVKNLESKLSKQESVSHTLTAKKENVAPRDQEFYD
 KAYNLLTEAHKALFXNKGRNSDFQALDKLLERLNDESTNKEKLVDDLLAFLAPITHPERL
                                  KVGDGYVFEENGVSRYIPAKNLSAETAAGIDSKLAKQESLSHKLGAKKTDLPSSDREFYN
                                                                                                RIARIIPLRYRSNHWVPDSRPEEPSPQPTPEPSPSPQPAPNPQPAPSNPIDEKLVKEAVR
                                                                                                                                                                DIDSLLKQLYKLPLSQRHVESDGLIFDPAQITSRTARGVAVPHGNHYHFIPYEQMSELEK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ouellet C,
                                                                                                                                                                                                                                                                                                   1126 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -11; vaccine; netreptococcal
                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                according to information given
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2001WO-CA00908
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BIOCHEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        derived
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      pneumoniae
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Charland
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       meningitis;
l bacterial :
                                                                                                                                                                                                                                   63;
                                                                                                                                                                                                                                 Score 1898; D)
Pred. No. 3.2e
63; Mismatches
                                                                                                                                                                                                                                                                                                                                  appear in the specification but formation given in the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         infection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      otitis media; bacteraemia;
infection; mutant; mutein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NEW31
                                                                                                                                                                                                                                                 DB 23;
.2e-131;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     'n
                                                                                                                                                                                                                                   101;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     cine components for as otitis media,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Brodeur
                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                  Length
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                                                                                                                                                                                                                                                                    1126;
                                                                                                                                                                                                                                 34;
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                                                                                                                                                                                                                                 Gaps
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                                                                                                          New Streptococcus pneumoniae BVH-3 and BVH-11 veepitope-bearing polypeptides, useful as vaccine or preventing streptococcal infections such as
                                                                                                                                                                                                                                                                                                                        BVH-3; BVH-11; vaccine; meningitis; pneumonia; streptococcal bacterial i BVH-11-2.
                                                                                                                                                                                                                                                                                           Streptococcus pneumoniae Synthetic.
                                                                               Example
                                                                                                                                                     WPI; 2002-122272/16.
                                                                                                                                                                        Hamel J,
                                                                                                                                                                                                              20-JUN-2000; 2000US-212683P
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                                                                                                                                                                                                                                                                        WO200198334-A2
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                                                                                                                                                                                                                                                                                                                                                                                                                           AAU84057
                                                                                                                                                                                           (SHIR-)
                                                                                                                                                                                                                                 19-JUN-2001; 2001WO-CA00908
                                                                                                                                                                                                                                                                                                                                                               pneumoniae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           542
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               362
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                                                                               <u>ب</u>
                                                                                                                                                                                                                                                                                                                                                                                                                          standard; Peptide; 1365
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GKPNAQITYTDDEIQVAKLAGKYTTEDGYIFDPRDITSDEGDAYVTPHMTHSHWIKKDSL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GKPNSQIEYTEDEVRIAQLADKYTTSDGYIFDEHDIISDEGDAYVTPHMGHSHWIGKDSL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MAEAEKLLALLKGSNPSSVSKEKI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WGNASEHVLGKKDHSEDPNKNFKAD------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VEVKNGNLIIPHKDHYHNIKFAWFDDHTYKAPNGYTLEDLFATIKYYVEHPDERPHSNDG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEAERAAAQAYAKEKGLTPPSTDHQDSGNTEAKGAEAIYNRVKAAKKVPLDRMPYNLQYT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MAEAEKLLALLKESKGPDLTEEQI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ESPEESEEPQVETEKVEEKLREAEDLLGKIQDPIIKSNAKETLTGLKNNLLFGTQDNNTI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ETPAEPEVPQVETEKVEAQLKEAEVLLAKVTDSSLKANATETLAGLRNNLTLQIMDNNSI 771
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FGNASDHVQRNKNGQADTNQTEKPSEEKPQTEKPEEETPREEKPQSEKPESPKPTEEPEE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VEVKNGSLI I PHYDHYHNI KFEWFDEGLYEAPKGYTLEDLLATVKYYVEHPNERPHSDNG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SDKEKVAAQAYTKEKGILPPSPDADVKANPTGDSAAAIYNRVKGEKRIPLVRLPYMVEHT
                                                                                                                                                                       Ouellet C,
                                                                              Page -;
                                                                                                    and bacteraemia
                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                                                                           BIOCHEM
                                                                                                                                                                                                                                                                                                                                                               derived chimeric peptide,
                                                                              113pp;
                                                                                                                                                                                            INC
                                                                                                                                                                         Charland
                                                                              English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              795
                                                                                                                                                                         Martin
                                                                                                                                                                                                                                                                                                                                  otitis media; bacteraemia;
infection; mutant; mutein;
                                                                                                                                                                                                                                                                                                                                                                 NEW30
                                                                                                                                                                        ā
                                                                                                                                variant
                                                                                                                                                                         Brodeur
                                                                                                             e components for otitis media,
                                                                                                                               and
                                                                                                                       treating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EEPVE
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The invention describes an isolated polypeptide (I) with 70-90% identity to Streptococcus pneumonia protein BVH-3, BVH-11, variants BVH-3 or BVH-11, or chimeric sequences derived from them. A vaccine comprising (I) is useful for therapeutic or prophylactic treatment omeningitis, otitis media, bacteraemia or pneumonia infection in an individual susceptible to these disorders. (II) is also useful for

t of (II)

therapeutic

prophylactic treatment

any

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Query Match
Best Local S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         techniques. The Streptococcus polypeptides are useful in a diagnostic test for S. pneumoniae infection. (III) is useful for designing DNA probes for use in detecting the presence of Streptococcus in a biological sample suspected of containing the bacteria. The DNA probes may also be used for detecting circulating S. pneumonia nucleic acid in a sample for diagnosing streptococcal infections. This sequence represents a chimeric gene created from fragments and variant fragments of Streptococcus pneumoniae genes, described in the method of the invention.

Note: This sequence does not appear in the specification but has been created according to information given in the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   infection (e.g., caused by Streptococcus pneumóniae, group A Streptococcus such as Streptococcus pyogenes, group B Streptococcus such as Streptococcus guberis, S. nocardia or streptococcus agalactiae, S. dysgalactiae, S. uberis, S. nocardia or Staphylococcus aureus) in an individual susceptible to the infection. A polynucleotide (III) encoding (I) is useful in DNA immunisation
                     Streptococcus
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67; Conservative
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                                                                                                                                            standard;
                                                                                                                                                                                                                                                                                      MAEAEKLLALLKGS----NPSSVS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   WGNASEHVLGKKDHSEDPNKNFKAD----
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                                                           (first entry)
                     pneumoniae NEW4
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Matches 364
                                                                                                                                                                                                                                                                                                                                                                                                                            antigens (II) from Streptococcus pneumoniae. The protein antigens have bactericidal activity. The nucleic acids, encoding the protein antigens, may be used for the recombinant production of the proteins they encode. The protein antigens may then be used as vaccines for the prevention and treatment of Streptococcal infections in mammals (especially humans) which result in, e.g. meningitis, otitis media, bacteraemia and/or pneumonia. The present sequence represents the S. pneumoniae NEW4 protein antigen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Streptococcus pneumoniae; BVH-3; prophylaxis; therapy; infection; otitis media; pneumonia; immunisa
                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Streptococcal otitis media,
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   WGNASEHVLGKKDHSEDPNKNFKAD---
                                                                                                                                       KAYDLLARIHQDLLDNKGRQVDFEALDNLLERLKDVSSDKVKLVDDILAFLAPIRHPERL
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                                        VEVKNGNLIIPHKDHYHNIKFAWFDDHTYKAPNGYTLEDLFATIKYYVEHPDERPHSNDG
                                                                         SEAERAAAQAYAKEKGLTPPSTDHQDSGNTEAKGAEAIYNRVKAAKKVPLDRMPYNLQYT
                                                                                                                         GKPNAQITYTDDEIQVAKLAGKYTTEDGYIFDPRDITSDEGDAYVTPHMTHSHWIKKDSL
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                                                                                                SDKEKVAAQAYTKEKGILPPSPDADVKANPTGDSAAAIYNRVKGEKRIPLVRLPYMVEHT
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                                                                                                                                                                                                                                                                                                                                                                       59;
                           KFEWFDEGLYEAPKGYTLEDLLATVKYYVEHPNERPHSDNG
                                                                                                                                                                                                                                                                                                                                                                       Score 1888; DB 21;
Pred. No. 5.8e-131;
9; Mismatches 97;
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                                                                                                                                                                                                                                                                   infection (e.g., caused by Streptococcus pneumoniae, group A Streptococcus such as Streptococcus syogenes, group B Streptococcus such as Streptococcus agalactiae, S. dysgalactiae, S. uberis, S. nocardia or Staphylococcus aureus) in an individual susceptible to the infection. A polynucleotide (III) encoding (I) is useful in DNA immunisation techniques. The Streptococcus polypeptides are useful in a diagnostic test for S. pneumoniae infection. (III) is useful for designing DNA probes for use in detecting the presence of Streptococcus in a biological sample suspected of containing the bacteria. The DNA probes may also be used for detecting circulating S. pneumonia nucleic acid in a sample for diagnosing streptococcal infections. This sequence represents a truncate
                                                                                            Sequence
                                                                                                                                                                                                                   of a Streptococcus pneumoniae gene used to obtain antigenic peptides, described in the method of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             comprising (I) is useful for therapeutic or prophylactic treatment of meningitis, otitis media, bacteraemia or pneumonia infection in an individual susceptible to these disorders. (II) is also useful for therapeutic or prophylactic treatment of any streptococcal bacterial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             identity to Streptococcus pneumonia protein BVH-3, BVH-11, variants BVH-3 or BVH-11, or chimeric sequences derived from them. A vaccine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Example 1; Page -; 113pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    meningitis, and bacteraemia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New Streptococcus pneumoniae BVH-3 and BVH-11 variant and epitope-bearing polypeptides, useful as vaccine components for treating or preventing streptococcal infections such as otitis media,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2002-122272/16
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                                                                                                                                                                                         Note: This sequence does
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (SHIR-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             invention describes an isolated polypeptide (I) with 70-90% ntity to Streptococcus pneumonia protein BVH-3, BVH-11, vari
                                                                                                                                                      created according
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streptococcal bacterial infection; mutant; mutein.
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Best Local S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      probes for use in detecting the presence of Streptococcus in a biological sample suspected of containing the bacteria. The DNA probes may also be used for detecting circulating S. pneumonia nucleic acid in a sample for diagnosing streptococcal infections. This sequence represents a truncate of a Streptococcus pneumoniae gene used to obtain antigenic peptides, described in the method of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New Streptococcus pneumoniae BVH-3 and BVH-11 variant and epitope-bearing polypeptides, useful as vaccine components for treating or preventing streptococcal infections such as otitis media,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          meningitis, and bacteraemia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Note: This sequence does not appear in the specification but has been created according to information given in the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NHWVPDSRPEQPSPQPTPEPS-----PGPQPAPNLKIDSNSSLVSQLVRKVGEGYVFEE
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AEPEVPQVETEKVEAQLKEAEVLLAKVTDSSLKANATETLAGLRNNLTLQIMDNNSIMAE
                                                                                                                       PHYDHYHNIKFEWFDEGLYEAPKGYSLEDLLATVKYYVEHPNERPHSDNGFGNASDHVRK
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                                                                                  KDHSE--
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Pred. No. 5.7e-125;
8; Mismatches 127;
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                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local S
Matches 345
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              antigens (II) from Streptococcus pneumoniae. The protein antigens have bactericidal activity. The nucleic acids, encoding the protein antigens, may be used for the recombinant production of the protein they encode. The protein antigens may then be used as vaccines for the prevention and treatment of Streptococcal infections in mammals (especially humans) which result in, e.g. meningitis, otitis media, bacteraemia and/or pneumonia. The present sequence represents the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Streptococcal otitis media,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              otitis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Streptococcus pneumoniae; BVH-3; BVH-11; BVH-28; antigen; vaccine; prophylaxis; therapy; infection; diagnosis; meningitis; bacteraemia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Streptococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAB12741 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            S. pneumoniae NEW10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The present invention describes nucleic acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 18; Fig 39; 106pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hamel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           23-DEC-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              21-NOV-2000
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YDKAYNLLTEAHKALFXNKGRNSDFQALDKLLERLNDESTNKEKLVDDLLAFLAFITHPE
                                                                          VRKVGDGYVFEENGVSRYIPAKDLSAETAAGIDSKLAKQESLSHKLGAKKTDLPSSDREF
                                                                                                                 VRKVGEGYVFEEKGISRYVFAKDLPSETVKNLESKLSKQESVSHTLTAKKENVAPRDQEF
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Pred. No. 4.3e-124;
1; Mismatches 107;
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or pneumonia
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RESULT 45
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                                                                                    The invention describes an isolated polypeptide (I) with 70-90% identity to Streptococcus pneumonia protein BVH-3, BMH-11, variants of BVH-3 or BVH-11, or chimeric equences derived from them. A vaccine comprising (I) is useful for therapeutic or prophylactic treatment of meningitis, otitis media, bacteraemia or pneumonia infection in an individual susceptible to these disorders. (II) is also useful for therapeutic or prophylactic treatment of any streptococcal bacterial
                                     Streptococcus such as Streptococcus
                                                                                                                                                                                                                                                                                                                                          Example 1; Page -; 113pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                  New Streptococcus pneumoniae BVH-3 and BVH-11 variant and epitope-bearing polypeptides, useful as vaccine components for or preventing streptococcal infections such as otitis media, meningitis, and bacteraemia
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caused by Streptococcus pneumoniae, groch as Streptococcus pyogenes, group B Steptococcus pyogenes, cuberis,
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RESULT 46
AAU84055
ID AAU84
XX AAU84
AC AAU84
XX 08-MA
XX 08-MA
XX DT 08-MA
XX DT 08-MA
XX DT XX Pneum
XX BVH-3
XW BVH-1-1

08-MAY-2002

(first

entry)

pneumoniae

derived chimeric peptide,

NEW28

AAU84055

standard;

Peptide;

1139

B

BVH-3; BVH-11; vaccine; meningitis; otitis media; bacteraemia; pneumonia; streptococcal bacterial infection; mutant; mutein; BVH-11-2.

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Note: This sequence does not appear in the specification but has been created according to information given in the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Staphylococcus aureus) in an individual susceptible to the infection. A polymucleotide (III) encoding (I) is useful in DNA immunisation techniques. The Streptococcus polypeptides are useful in a diagnostic test for S. pneumoniae infection. (III) is useful for designing DNA
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LGTKDNNTISAEVDSLLALLKESQPAPI
                       LQIMDNNSIMAEAEKLLALLKGSNPSSV
                                                           TEETEEEAEDTTDEAEIPQVENSVINAKIADAEALLEKVTDPSIRQNAMETLTGLKSSLL
                                                                                                                                                           DGWGNASEHVLGK---
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                                                                                                                                                                                                                                                                                                                                    RLGKPNSQIBYTEDEVRIAQLADKYTTSDGYIFDEHDIISDEGDAYVTPHMGHSHWIGKD
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                                                                                           FKADEEPVEETPAEPEVPQVETEKVEAQLKEAEVLLAKVTDSSLKANATETLAGLRNNLT 762
                                                                                                                          NGFGNASDHVRKNKADQDSKPDEDKEHDEVSEPTHPESDEKENHAGLNPSADNLYKPSTD
                                                                                                                                                                                                                                                      SLSEAERAAAQAYAKEKGLTPPSTDHQDSGNTEAKGAEATYNRVKAAKKVPLDRMPYNLQ
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                                                                                                                                                           -----KDHSE----
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Pred. No. 4.3e-124;
1; Mismatches 107;
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Best Local Similarity
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Note: This sequence does not appear in the specification but has been created according to information given in the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BVH-3 of BVH-11, or chimeric sequences derived from them. A vaccine (II) comprising (I) is useful for therapeutic or prophylactic treatment of meningitis, otitis media, bacteraemia or pneumonia infection in an individual susceptible to these disorders. (II) is also useful for therapeutic or prophylactic treatment of any streptococcal bacterial infection (e.g., caused by Streptococcus pneumoniae, group A Streptococcus such as Streptococcus aureus) in an individual susceptible to the infection. A polymacleotide (III) encoding (I) is useful in DNA immunisation for the first continuation of the first contin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                identity to Streptococcus pneumonia BVH-3 or BVH-11, or chimeric sequenc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New Streptococcus pneumoniae BVH-3 and BVH-11 variant and epitope-bearing polypeptides, useful as vaccine components for treating or preventing streptococcal infections such as otitis media,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Synthetic.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The invention describes an isolated polypeptide (I) with 70-90%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Example 1; Page -; 113pp; English
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                                                                                                                                                                                                     DIDSLLKQLYKLPLSQRHVESDGLVFDPAQITSRTARGVAVPHGDHYHFIPYSQMSELEE
                                                                                               RIARIIPLRYRSNHWVPDSRPEQPSPQSTPEPSPSLQPAPNPQPAPSNPID--EKLVKEA
                                                                                                                                                                                                                                                                                                                                                RIARIIPLRYRSNHWVPDSRPEQPSPQPTPEDS-----PGPQPAPNLKIDSNSSLVSQL 379
                                                                                                                                                                                                                                                                                                                                                                                                                     NISSLLRELYAKPLSERHVESDGLIFDPAQITSRTARGVAVPHGNHYHFIPYEQMSELEK
RLGKPNAQITYTDDEIQVAKLAGKYTTEDGYIFDPRDITSDEGDAYVTPHMTHSHWIKKD
                           RLGKPNSQIEYTEDEVRIAQLADKYTTSDGYIFDEHDIISDEGDAYVTPHMGHSHWIGKD
                                                                                                                                                   YDKAYNLLTEAHKALFXNKGRNSDFQALDKLLERLNDESTNKEKLVDDLLAFLAPITHPE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ä
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     43.1%; Score 1795.5; DB 2 60.7%; Pred. No. 1.3e-123;
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Infection (e.g., caused by Streptococcus pneumoniae, group A Streptococcus such as Streptococcus pneumoniae, group A streptococcus such as Streptococcus pogenes, group B Streptococcus agalactiae, S. dysgalactiae, S. uberis, S. nocardia Staphylococcus aureus) in an individual susceptible to the infection. A polynucleotide (III) encoding (I) is useful in DNA immunisation techniques. The Streptococcus polynometriae.
                                                                                       The invention describes an isolated polypeptide (I) with 70-90% identity to Streptococcus pneumonia protein BVH-3, BVH-11, variants of BVH-3 or BVH-11, or chimeric sequences derived from them. A vaccine (I BVH-3 or BVH-11) is useful for therapeutic or prophylactic treatment of meningitis, otitis media, bacteraemia or pneumonia infection in an individual susceptible to these disorders. (II) is also useful for therapeutic or prophylactic treatment of any streptococcan bacterial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Streptococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BVH-3; BVH-11; vaccine; meningitis; otitis media; bacteraemia; pneumonia; streptococcal bacterial infection; mutant; mutein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    S. pneumoniae
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                                                                                                                                                                                                                          Example 1;
                                                                                                                                                                                                                                                        meningitis, and bacteraemia
                                                                                                                                                                                                                                                                  New Streptococcus pneumoniae BVH-3 and BVH-11 variant and epitope-bearing polypeptides, useful as vaccine components or preventing streptococcal infections such as otitis med
                                                                                                                                                                                                                                                                                                                                   WPI; 2002-122272/16.
                                                                                                                                                                                                                                                                                                                                                                  Hamel J,
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           Streptococcus
                                      otitis media;
                                                                  Streptococcus
                                                                                            Streptococcus
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                                      is pneumoniae; BVH-3; BVH-11; BVH-28; antigen; vaccine;
therapy; infection; diagnosis; meningitis; bacteraemi
; pneumonia; immunisation; bactericidal.
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           pneumoniae
                                                                                           pneumoniae BVH-11A protein antigen
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   antigens (II) from Streptococcus pneumoniae. The protein antigens have bactericidal activity. The nucleic acids, encoding the protein antigens, may be used for the recombinant production of the proteins they encode. The protein antigens may then be used as vaccines for the prevention and treatment of Streptococcal infections in mammals (especially humans) which result in, e.g. meningitis, otitis media, bacteraemia and/or pneumonia. The present sequence represents the S. pneumoniae BVH-11A protein antigen.
           BVH-3; BVH-11; vaccine; meningitis; otitis media; bacteraemia; pneumonia; streptococcal bacterial infection; mutant; mutein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The present invention describes nucleic acids (I) encoding protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Streptococcal antigens useful for vaccinating otitis media, bacteremia and/or pneumonia -
                                                 Truncated variant of S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2000-452397/39
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                                                                                                                                                                                                                                                                                                                                                                                           VSNPGTTNTNTSNNSNTNSQASQSNDIDSLLKQLYKLPLSQRHVESDGLVFDPAQITSRT
                                                                                                                                                                                                                                                                                                                  GDAYIVPHGDHYHYIPKNELSASELAAAEAFLSGRGNLSNSRTYRRQNSDNTSRTNWVPS
                                                                                                                           standard;
                                                                                                                                                                                                        ARGVAVPHGDHYHFIPYSQMSELEERIARIIPL 333
                                                                                                                                                                                                                                                                                             GDAYI VPHGDHYHYI PKNELSASELAAAEAFLSGRENLSNLRTYRRQNSDNTPRTNWVPS
                                                                                                                                                                                                                                           VSNPGTTNTNTSNNSNTNSQASQSNDIDSLLKQLYKLPLSQRHVESDGLIFDPAQITSRT
                                                                                                                                                                                                                                                                                                                                           AHADNVRTKEEINRQKQEHSQHREGGTSANDGAVAFARSQGRYTTDDGYIFNASDIIEDT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Brodeur BR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  334 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                          (first
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    26; 106pp;
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                                                                                                                           Peptide;
                                                                          entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         94.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pineau I,
                                                pneumoniae BVH-11, BVH-11A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    English.
                                                                                                                            334
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 1666; DB 21;
Pred. No. 7.2e-115;
9; Mismatches 8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Martin
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Comprising (I) is useful for therapeutic or prophylactic treatment of meningitis, otitis media, bacteraemia or pneumonia infection in an individual susceptible to these disorders. (II) is also useful for therapeutic or prophylactic treatment of infection (e.g., caused by Streptococcus pneumoniae, group A Streptococcus such as Streptococcus prophylactic treatment of any streptococcus such as Streptococcus prophylactic, s. dysgalactiae, group B Streptococcus such as Streptococcus prophylactic, s. dysgalactiae, group B Streptococcus such as Streptococcus prophylactic, s. dysgalactiae, s. uberis, s. nocardia or Streptococcus aureus) in an individual susceptible to the infection. A polynucleotide (III) encoding (I) is useful in DNA immunisation test for S. pneumoniae infection. (III) is useful in a diagnostic test for S. pneumoniae infection. (III) is useful in a biological sample suspected of containing the presence of Streptococcus in a biological sample for detecting circulating s. pneumonia nucleic acid in a biological containing the presence of Streptococcus in a biological selection diagnosing streptococcus infections. This sequence represents a truncate of a Streptococcus pneumoniae gene used to obtain antigenic peptides, or more missed in the method of the invention.
                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Sim
Matches 316;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            epitope-bearing polypeptides, or preventing streptococcal in meningitis, and bacteraemia
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2002-122272/16.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hamel J,
                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Example 1; Page -; 113pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WO200198334-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The invention describes an isolated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New Streptococcus pneumoniae BVH-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              20-JUN-2000; 2000US-212683P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              19-JUN-2001; 2001WO-CA00908
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 the invention describes an isolated polypeptide (I) with 70-90% identity to Streptococcus pneumonia protein BVH-3, BVH-11, variants of
                                   241
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This sequence does not appear in the specification but has
                                                                                                                                                                                                                                                                                         N
                                                                                                                                                                                                                                                                                                          1 SYELGLYQARTVKENNRVSYIDGKQATQKTENLTPDEVSKREGINAEQIVIKITDQGYVT
                                                                                                                                                                                                                                                                                                                                                                                   Similarity
                                                                                                                                                                                                                                               SHGDHYHYYNGKVPYDAIISEELLMKDPNYKLKDEDIVNEVKGGYVIKVDGKYYVYLKDA
VSNPGTTNTNTSNNSNTNSQASQSNDIDSLLKQLYKLPLSQRHVESDGLIFDPAQITSRT
                                                                                                          GDAYIVPHGDHYHYIPKNELSASELAAAEAFLSGRGNLSNSRTYRRQNSDNTSRTNWVPS
                                                                                                                                                                    AHADNVRTKEEINRQKQEHSQHREGGTPRNDGAVALARSQGRYTTDDGYIFNASDIIEDT
                                   VSNPGTTNTNTSNNSNTNSQASQSNDIDSLLKQLYKLPLSQRHVESDGLVFDPAQITSRT
                                                                                                                                                                                                                 SHGDHYHYYNGKVPYDAIISEELLMKDPNYQLKDSDIVNEIKGGYVIKVNGKYYVYLKDA
                                                                                                                                                                                                                                                                                      AYELGLHQAQTVKENNRVSYIDGKQATQKTENLTPDEVSKREGINAEQIVIKITDQGYVT
                                                                                                                                             AHADNVRTKEEINRQKQEHSQHREGGTSANDGAVAFARSQGRYTTDDGYIFNASDIIEDT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     information given
                                                                                                                                                                                                                                                                                                                                                             Score 1666; D
Pred. No. 7.2e
9; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             infections such as
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                                                                                                                                                                                                                                                                                                                                                             .2e-115;
les 8;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             e components for treating otitis media,
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                           CC BVH-3 or BVH-11, or chimeric sequences derived from them. A vaccine (II) C comprising (I) is useful for therapeutic or prophylactic treatment of c meningitis, ottitis media, bacteraemia or pneumonia infection in an CC individual susceptible to these disorders. (II) is also useful for therapeutic or prophylactic treatment of any streptococcal bacterial cinfection (e.g., caused by Streptococcus pneumoniae, group A Streptococcus such as Streptococcus supogenes, group B Streptococcus such as Streptococcus pneumoniae, group A Streptococcus such as Streptococcus supogenes, group B Streptococcus such as Streptococcus such as Streptococcus such as Streptococcus such as Individual susceptible to the infection. (I Staphylococcus aureus) in an individual susceptible to the infection. (I Polymucleotide (I II) encoding (I) is useful in DNA immunisation techniques. The Streptococcus polypeptides are useful in a diagnostic test for S. pneumoniae infection. (III) is useful for designing DNA compared to the presence of Streptococcus in a biological sample suspected of containing the bacteria. The DNA probes may also be used for detecting circulating S. pneumonia nucleic acid in a sample for diagnosing streptococcus and variant fragments of Streptococcus cus in a biological sample created from fragments and variant fragments of Streptococcus cus in a biological containing the bacteria. The DNA probes may also be used for detecting circulating S. pneumonia nucleic acid in a sample for diagnosing streptococcus and variant fragments of Streptococcus cus of Streptococcus cus in a biological containing the bacteria. The DNA probes may also be used for detecting circulating S. pneumonia nucleic acid in a sample for claim contains of streptococcus cus cus contains the method of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    epitope-bearing polypeptides, useful as vaccine components for treating or preventing streptococcal infections such as otitis media, meningitis, and bacteraemia -
Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The invention describes an isolated polypeptide (I) with 70-90% identity to Streptococcus pneumonia protein BVH-3, BVH-11, vari BVH-3 or BVH-11, or chimeric sequences derived from them. A vac
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      pneumonia;
BVH-11-2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Example 1; Page -; 113pp; English.
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    pneumoniae derived chimeric peptide, NEW29

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ARGVAVPHGNHYHFIPYEQMSELEKRIARIIPL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ouellet C,
1238
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A
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Matches 314; Best Local Similarity

Conservative

57;

Score 1661; DB 23; Pred. No. 1.3e-113; 7; Mismatches 97;

Indels

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Gaps

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39.9%;

Query Match

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Search completed: November 14, 2003, 10:34:12 Job time : 89 secs
                                                                                                                                                                                                                                                                                                                           682 WGNASEHVLGKKDHSEDPNKNFKADEEPVEETPAEPEVPQVETEKVEAQLKE 733
                                                                                                                                                            622 VEVKNGNLIIPHKDHYHNIKFAWFDDHTYKAPNGYTLEDLFATIKYYVEHPDERPHSNDG 681
||||||:|||||::|
362 VEVKNGSLIIPHYDHYHNIKFEWFDEGLYBAPKGYTLEDLLATVKYYVEHPNERPHSDNG 421
                                                                                                                                                                                                                                                                 562 SDKEKVAAQAYTKEKGILPPSPDADVKANPTGDSAAAIYNRVKGEKRIPLVRLPYMVEHT 621
                                                                                                                                                                                                                                                                                                                                                                                                            182 KAYDLLARIHQDLLDNKGRQVDFEALDNLLERLKDVSSDKVKLVDDILAFLAPIRHPERL 241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          422 FGNASDHVGPNMQPSQLSYSSTASDNNTQSVAKGSTSKPANKSENLQSLLKE 473
                                                                                                                                                                                                                                              302 SEAERAAAQAYAKEKGLTPPSTDHQDSGNTEAKGAEAIYNRVKAAKKVPLDRMPYNLQYT
                                                                                                                                                                                                                                                                                                                                                                                                                                    442 KAYNILITEAHKALFXNKGRNSDFQALDKLLERLNDESTNKEKLVDDLLAFLAPITHPERL 501
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A; rettelin, H.; Nelson, K.E.; Paulsen, I.T.; Eisen, J.A.; Read, T.D.; Peterson, S.; on, J.D.; Umayam, L.A.; White, O.; Salzberg, S.L.; Lewis, M.R.; Radune, D.; Holtzapp, nson, T.; Hickey, E.K.; Holt, I.E.

Science 293, 498-506, 2001

A; Aucthors: Loftus, B.J.; Yang, F.; Smith, H.O.; Venter, J.C.; Dougherty, B.A.; Morri A; Title: Complete Genome Sequence of a virulent isolate of Streptococcus pneumoniae. A; Reference number: A95000; MUID:21357209; PMID:11463916

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A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 1-802 <KUR>
A;Crose-references: GB:AE005672; PI
A;Experimental source: strain TIGR4
C;Genetics:
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C;Superfamily: Streptococcus agalactiae hypothetical 92.4K protein
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A;Molecule type: DNA
A;Residues: 1-828 <KUR>
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                    VSHTLTAKKENVAPRDQEFYDKAYNLLTEAHKALFXNKGRNSDFQALDKLLERLNDESTN 480
                                                                    PQPAPNLKI DSNSSLVSQLVRKVGEGYVFEEKG I SRYVFAKDL PSETVKNLESKLSKQES
                                                                                                                   ARGVAVPHGDHYHFIPYSQMSELEERIARIIPLRYRSNHWVPDSRPEQPSPQPTPEPSPG
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                                                      PQPAPNLKIDSNSSLVSQLVRKVGEGYVFEEKGISRYVFAKDLPSETVKNLESKLSKQES
                                                                                                       ARGVAVPHGDHYHFIPYSQMSELEERIARIIPLRYRSNHWVPDSRPEQPSPQPTPEPSPG
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Pred. No. 3e-219;
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RESULT 3
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histidine Motif-Containing protein [imported] - Streptococcus pneumoniae (strain C;pecies: Streptococcus pneumoniae
C;pecies: Streptococcus pneumoniae
C;Date: 22-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 02-Nov-2001
C;Accession: D98004
R;Hoskins, J.A.; Alborn Jr., W.; Arnold, J.; Blaszczak, L.; Burgett, S.; DeHoff, e, R.; LeBlanc, D.J.; Lee, L.N.; Lefkowitz, E.J.; Lu, J.; Matsushima, P.; McAhren e, R.; LeBlanc, D.J.; Lee, M.Z.; Lefkowitz, E.J.; Lu, J.; Matsushima, P.; McAhren y, P.; Sun, P.M.; Winkler, M.E.
J. Bacteriol. 183, 5709-5717, 2001
J. Bacteriol. 183, 5709-5717, 2001
J. Rathors: Yang, Y.; Young-Bellido, M.; Zhao, G.; Zook, C.; Baltz, R.H.; Jaskunas A;Title: Genome of the Bacterium Streptococcus pneumoniae Strain R6.
A;Reference number: A97872; MUID:21429245; pMID:11544234
A;Accession: D98004
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C; Superfamily:
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C;Genetics:
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                    ARGVAVPHGDHYHFIPYSQMSELEERIARIIPLRYRSNHWVPDSRPEQPSPQPTPEPSPG
                                                              VSNPGTTNTNTSNNSNTNSQASQSNDIDSLLKQLYKLPLSQRHVESDGLIFDPAQITSRT
                                                                                       VSNPGTTNTNTSNNSNTNSQASQSNDIDSLLKQLYKLPLSQRHVESDGLVFDPAQITSRT
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ANGVAVPHGDHYHFIPYSQLSPLEEKLARIIPLRYRSNHWVPDSRPEQPSPQSTPEPSPS
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Pred. No. 3.2e-
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3.2e-168;
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atsushima, P.; McAhren, S.;
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A; Authors: Loftus, B.J.; Yang, F.; Smith, H.O.; Venter, J.C.; Dougherty, A; Title: Complete Genome Sequence of a virulent isolate of Streptococcus, A; Reference number: A95000; MUID:21357209; PMID:11463916
A; Raccession: B95136
A; Raccession: B95136
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A,Wolecule type: DNA
A,Residues: 1-819 < KUR>
A,Experimental source: strain TIGR4
C;Genetics:
A;Gene: SP1174
C;Superfamily: Streptococcus agalactiae hypothetic
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B95136
C;Species: Streptococcus pneumoniae
C;Date: 03-Aug-2001 #sequence_revision 03-Aug-2001
C;Accession: B95136
R;Tettelin, H.; Nelson, K.E.; Paulsen, I.T.; Eisen,
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                                                                                                                                               SYELGRYQAGQDKKESNRVAYIDGDQAGQKAENLTPDEVSKREGINAEQIVIKITDQGYV
                                                                                                                                                                  SYELGLYQA-RTVKENNRVSYIDGKQATQKTENLTPDEVSKREGINAEQIVIKITDQGYV
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                                                                                                   TSHGDHYHYYNGKVPYDAIISEELLMKDPNYKLKDEDIVNEVKGGYVIKVDGKYYVYLKD
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                                                                                                                                                                                                                 Conservative
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                                                                                                                                                                                                               Score 2797.5; DB 2;
Pred. No. 5.7e-145;
94; Mismatches 138;
               RADNAVAAARAQGRYTTDDGYIFNASDIIED
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A; KCtsoacoo.
A; Ktatus: preliminary
A; Molecule type: DNA
A; Residues: 1-839 < KUR>
A; Cross-references: GB: AE005672; PII
A; Cross-references: GB: AE005672; PII
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G95115
G95115
Conserved hypothetical protein SP1003 [imported] -
C;Species: Streptococcus pneumoniae
C;Date: 03-Aug-2001 #sequence_revision 03-Aug-2001
C;Accession: G95115
C;Accession: G95115
R;Tettelin, H.; Nelson, K.E.; Paulsen, I.T.; Eisen,
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                                                                                                                                                                                                                                               nson, T.; Hickey, E.K.; Holt, I.E. Science 293, 498-506, 2001
Science 293, 498-506, 2001
A;Authors: Loftus, B.J.; Yang, F.; Smith, H.O.; Venter, J.C.; Dougherty, A;Title: Complete Genome Sequence of a virulent isolate of Streptococcus A;Reference number: A95000; MUID:21357209; PMID:11463916
A;Accession: G95115
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   SYELGLYQARTV-KENNRVSYIDGKQATQKTENLTPDEVSKREGINAEQIVIKITDQGYV
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                                                                                                       Streptococcus agalactiae hypothetical
                                      Conservative
                                                                                                                                                                                                                                                                                                                                 K.E.; Paulsen, I.T.; Eisen, J.A.; Read, T.D.; Peterson, S.; Hei White, O.; Salzberg, S.L.; Lewis, M.R.; Radune, D.; Holtzapple, Holt, I.E.
                                                      66.6%;
65.0%;
                                      91; Mismatches 144;
                                                                                                                                                                            PIDN: AAK75120.1;
                                                      Score 2772; DB
Pred. No. 1.4e-
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                        AKVTDSSLKANATETLAGLRNNLTLQIMDNNSIMAEAEKLLALLKGSNPSSV
                                                                                           YTLEDLLATVKYYVEHPNERPHSDNGFGNASDHVRKNKVDQDSKPDEDKEHDEVSEPTHP
                                                                                                       DIISDEGDAYVTPHMGHSHWIGKDSLSDKEKVAAQAYTKEKGILPPSPDADVKANPTGDS
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                                              ESDEKENHAGLNPSADNLYKPSTDTEETEEEAEDTTDEAEIPQVENSVINAKIADAEALL
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hypothetical protein phtD [imported] - Streptococcus pneumoni C;Species: Streptococcus pneumoniae C;Species: Streptococcus pneumoniae C;Date: 22-Oct-2001 #sequence_revision 22-Oct-2001 #text_chan C;Accession: C97985

R;Hoskins, J.A.; Alborn Jr., W.; Arnold, J.; Blaszczak, L.; B e, R.; LeBlanc, D.J.; Lee, L.N.; Lefkowitz, E.J.; Lu, J.; Mat y, P.; Sun, P.M.; Winkler, M.E.

J. Bacteriol. 183, 5709-5717, 2001

A;Authors: Yang, Y.; Young-Bellido, M.; Zhao, G.; Zook, C.; B A;Title: Genome of the Bacterium Streptococcus pneumoniae Str A;Reference number: A97872; MUID:21429245; PMID:11544234

A;Accession: C97985
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-853 <XUR>
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conserved hypothetical protein SP1004 [imported] - Streptococcus pneumoniae (strain
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C;Genetics:
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Best Local Similarity
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R;Tettelin, H.; Nelson, K.E.; Paulsen, I.T.; Eisen, J.A.; Read, T.D.; Peterson, on, J.D.; Umayam, L.A.; White, O.; Salzberg, S.L.; Lewis, M.R.; Radune, D.; Holson, T.B.; Science 293, 498-506, 2001
A;Authors: Loftus, B.J.; Yang, F.; Smith, H.O.; Venter, J.C.; Dougherty, B.A.; la;Reference number: A95000; MUID:21357209; PMID:11463916
A;Recession: H95115
A;Recession: H95115
A;Residues: preliminary
A;Molecule type: DNA
A;Residues: 1-1039 <KUR>
A;Cross-references: GB:AE005672; PIDN:AAK75121.1; PID:g14972477; GSPDB:GN00164; A;Constriental source: strain TIGR4
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C;Date: 03-Aug-2001 #sequence_revision 03-Aug-2001
C;Accession: H95115
R;Tettelin, H.; Nelson, K.E.; Paulsen, I.T.; Eisen,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
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  IDEH---KPVGIG--
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                                                                                                                                           NR------VKGEKRIPLVRLPYMV--EHTVEVKNGNLII-PHKDHYHNIKFAW
                                                                                                                                                                                          DESGFVMSHGDHNHYFFKKDLTEEQIKAAQKHLEE
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                                            FDDHTYKAPNGYTLEDLFATIKYYVEHPDERPHSNDG----WGNASEHVLGKKDHSEDPN
                                                                                           EQDYPSNAKEMKDLDKKIEEKIAGIMKQYGVKRESIVVNKEKNAIIYPHGDHHHADP---
                                                                                                                                                                                                                                      EGDAYVTPHMGHSHWIGKDSLSDKEKVAAQAYTKEKGILPPSPDADVKANPTGDSAAAIY
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                                                                                                                                                                                                                                                                                                                                                                                    ----LTTSKELSSASDGYIFNPK-DIVEETATAYIVRHG--DHFHYIPK-----
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  HSHSNYELFKPEEGVAKKEGNKVYTGEELTNVVNLLKNSTFNN
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Pred. No. 3.6e-60;
7; Mismatches 180
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e, D.; Holtzapple,
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, N.; Luet

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RESULT 8
D97985
hypothetical protein phtE [imported] - Streptococcus pneumoniae (strain R6)
c;Species: Streptococcus pneumoniae
C;Species: Streptococcus pneumoniae
C;Date: 22-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 22-Oct-2001
C;Accession: D97985
R;Hoskins, J.A.; Alborn Jr., W.; Arnold, J.; Blaszczak, L.; Burgett, S.; DeHoff, B.:
e, R.; LeBlanc, D.J.; Lee, L.N.; Lefkowitz, E.J.; Lu, J.; Matsushima, P.; McAhren, J.; P.; Sun, P.M.; Winkler, M.E.
y, P.; Sun, P.M.; Winkler, M.E.
y, P.; Sun, P.M.; Winkler, M.E.
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A;Authors: Yang, Y.; Young-Bellido, M.; Zhao, G.; Zook, C.; Baltz, R.H.; Jaskunas, A;Title: Genome of the Bacterium Streptococcus pneumoniae Strain R6.
A;Reference number: A97872; MUID:21429245; PMID:11544234
A;Accession: D97985
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A;Molecule type: DNA
A;Residues: 1-1039 <KUR>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Cross-references: GB:AE007317; PIDN:AAK99712.1; PID:g15458515;
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WFDDHTYKAPNGYTLEDLFATIKYYVEHPDERPHSNDG----WGNASEHVLGKKDHSEDP
                                  HEQDYPGNAKEMKDLDKKIEEKIAGIMKQYGVKRESIVVNKEKNAIIYPHGDHHHADP--
                                                                                                                                            DEGDAYVTPHMGHSHWIGKDSLSDKEKVAAQAYTKEKGILPPSPDADVKANPTG-DSAAA
                                                                                                                                                                                    OPTLPNNSLATPSP---
                                                                                                                                                                                                                      KEKLVDDLLAFLAPITHPERLGKP-NSQIEYTEDEVRIAQLADKYTTSDGYIFDEHDIIS
                                                                                                                                                                                                                                                           ----LTTSKELSSASDGYIFNPK-DIVEETATAYIVRHG--DHFHYIPK-----SNQIG
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41.2%; Pred. No. 5.2e-60;
tive 94; Mismatches 180;
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R;Spellerberg, B.; Rozdzinski, E.; Martin, S.; Weber-Heynemann, J.; Schnitzl Infect. Immun. 67, 871-878, 1999
A;Title: Lmb, a protein with similarities to the LraI adhesin family, mediat A;Reference number: Z24091; MUID:99115568; PMID:9916102
A;Accession: T46758
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A;Residues: 1-822 <SPE>
A;Cross-references: EMBL:AF062533; NID:g4249622; PIDN:AAD13797.1; PA;Experimental source: strain R268
C;Superfamily: Streptococcus agalactiae hypothetical 92.4K protein
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VKAKGQADELVAALDQEQGKEKPLFDTKKVSRKVTKDGKVGYIMPKDGKDYFYARYQLDL 527
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                                    TKEKG----ILPPSPDADVKANPTGDSAAA--
                                                                                                                                                                                                                                                       GISRYVFAKDLPSETVKNLESKLSKQESVSHTLTAKKENVAPRDQEFYDKAYNLLTEAHK 452
                                                                                                                                                                                                                                                                                                                                    LRYRSNHWVPDSRPEQPSPQPTPEPSPGPQPAPNLKIDSNSSLVSQLVRKVGEGYVFEEK 392
                                                                                                                                                                                                                                                                                                                                                                      QLHRLDLKYRHVEEDGLIFEPTQVIKSNAFGYVVPHGDHYHIIPRSQLSPLEMELAD---
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                                                                                                                                                                                      ALFXNKGRNSDFQALDKLLERLNDESTNKEKLVDDLLAFLAPITHPERLGKPNSQIEYTE 512
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                                                                        YDTSDAYVFSKESIHSVDKSGVTAKHGDHFHYIGFGELEQYELDEVANW
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                                      ---IYNR----
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A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-182 <KUR>
A;Cross-references: GB:A;
C;Genetics:
A;Gene: phtE-truncation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           R;HOSKINS, J.A.; Alborn Jr., W.; Arnold, J.; Blaszczak, L.; Burgett, S.; DeHoff, Be, R.; LeBlanc, D.J.; Lee, L.N.; Lefkowitz, E.J.; Lu, J.; Matsushima, P.; McAhren, Y. P.; Sun, P.M.; Winkler, M.E.
J. Bacteriol. 183, 5709-5717, 2001
A;Authors: Yang, Y.; Young-Bellido, M.; Zhao, G.; Zook, C.; Baltz, R.H.; Jaskunas, A,Fitle: Genome of the Bacterium Streptococcus pneumoniae Strain R6.
A;Reference number: A97872; MUID:21429245; pMID:11544234
A,Accession: F97985
trfA protein - slime mold (Dictyostelium C;Species: Dictyostelium discoideum C;Date: 20-Sep-1999 #sequence_revision 20 C;Accession: T14004 #Seaito, J.; Adachi, H.; Sutoh, K. J. Biol. Chem. 273, 24654-24659, 1998 A;Title: Dictyostelium TRFA homologous to
                                                                                                         RESULT
T14004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   hypothetical protein phtE-truncation [imported] - Streptococcus C;Species: Streptococcus pneumoniae C;Date: 22-Oct-2001 #sequence_revision 22-Oct-2001 #text_change C;Accession: F97985
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Matches 61
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   to yeast Ssn6
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A;Accession: T14004
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 1-1390 <SAI>
A;Cross-references: EMBL:AB009080; NID:d1228566; PID:d1(C;Genetics:
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18.1%;
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Pred. No. 0.016;
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                                    E--RPHSNDGWGNASEHVLGKKDHSED----PNKNFKADEEPVEETPA-----EPEVPQV
                                                                                                                                KNGNLIIP-HKDHYHNIKFAWFDDHT-----YKAPNGYTLEDLFATIKYYVEHPD
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A;Residues: 1-1271 <BOR>
A;Residues: 1-1271 <BOR>
A;Cross-references: EMBL.M59706; NID:g160311; PID:g160312
A;Note: sequence extracted from NCBI backbone (NCBIN:77801, NCBIP:77802)
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                                                          DDHTYKAPNGYTLEDLFATIKYYVEHPDE-RPHSNDGWGNAS----EHVLGKKDHSE---
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A;Residues: 1-2481 «KUR»
A;Cross-references: GB:BA000018; PID:g13701961;
A;Experimental source: strain N315
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C;Accession: D90011
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C; Species: Staphylococcus aureus
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                                                                                DNTTGATTEE-----KNAAKDLVLKAKEKAYQDILNAQTTNDVTQIKDQAVADIQGITAD 1433
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                                    ITHPERLGKPNSQIEYTEDEVRIAQLADKYTTSDGYIFDEHDIISDEGDAYVTPHMGHSH 554
                                                                                                                       DKAYNLLTEAHKALFXNKGRNSDFQALDKLLER-LNDESTN-----KEKLVDDLLAFLAP
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                                                                                                                                                                                                        --YVFEEKGISRYVFAKDLPSETVKNLES----KLSKQESVSHTLTAKKENVAPRDQEFY 440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              --QGRYTTDDGYIFNASDIJEDTGDAYIVPHGDHYHYIPKNELSASELAAAEAFLSGRGN 217
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19.4%; Pred. No. 0.5;
htive 140; Mismatches
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Indels

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GSPDB:GN00149

22-Oct-2001

; Cui, L.; Sekimizu,

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C;Species: Saccharomyces cerevisiae
C;Date: 02-Sep-1995 #sequence_revision 19-Oct-1995 #text_change 19-Apr-2002
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A; Residues: 1-1233 < MUR>
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A; Accession: S56271
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R;Murakami, Y.; Naitou,
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Best Local
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                                                                                                                                        NSRTYRRONSDNTSRTNWVPSVSNP-----GTTNTNTSNNSNTNSQASQSNDI-----
                                                                                                                                                                                                                           SSDKTFDIDVPNKDNVDETSSKSENNINEEKAEHTLPREENEILNVNEGNAASFKHQLEP
                                                                                                                                                                                                                                                  GKYYVYLKDAAHADNV-----RTKEBINRQKQEHSQHREGG--TPRNDGAVALARSQ---
                                                                                                                                                                                                                                                                                    NPADTTDLSKOSTLDSILVGIEEYLQEDGS---KNEDIKVNIVQDEPVNVEKMDIRTRNE
                                                                                                                                                                                                                                                                                                           HGDHYHYYNGKVPYDAII--SEELLMKDPNYKLKDEDI-----VNEVKGGYVIKVD
                                                                                                                                                                                                                                                                                                                                          IKETSTNNVAEG-----TENVPP--IKESTGIEVGNSPITRRKKNKKKKTTNRRGRNSS
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                                                                                                                                                                    HGLEAGDE----NGQASTKDVESESLTKNGFNFKENESKHLKAGEKQQTE---SDRDGIS
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 QEAVRNNEVSGTEEESTSKGEEIMGGD
                                                                                                               PSVLAKNQKETEIGKEDHVFEQKDKEDEKCRKELSVNHENNMSHNFNAAGSDSIIPPETE
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                                                       DDETMGPTKRISDNEKNLQHGTNDISVEVEKEEEEEEEEENSTFSKVKKENVTGE
                                                                                  -DSLLKQLYKLPLSQRHV---------ESDGLVFDPAQ---ITSR
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wata Library, May 19
of the nucleotide
                                                                                                                                                                                                                                                                                                                                                                                                               4.1%; Score 171; DB 2; 19.8%; Pred. No. 0.21;
                          TARGVAVPHGDHYHFIPYSQMSELEERIARIIPLRYRSN-----
                                                                                                                                                                                                                                                                                                                                                                                                  142;
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C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001
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EVEETEKETSLPDLVVEENIT---EEKNEIKQEEEE-VSQLDFNETESISKEAPN 1053
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                                                                                                                                                         --HSEDPNKNFKADEEPVEETPAEPEVPQVE----TEKVE-AQLKEAEVLLAKVTDSSL
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                                               KANATETLAGI -----RNNLTLQIMDNNSIMAEAEKLLALLKGSNPSSVSKEKIN 796
                                                                                                    AVTKEDENMENSKIAEALKDVTGDQEIDDINISDEFQRTVELPELEKQDIKDNKGEDKEL
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A; Cross-references: C; Genetics: A;Status: preliminary A;Molecule type: DNA A;Residues: 1-1043 <STO> A;Title: Sequence and analysis of chromosome A;Reference number: A84420; MUID:20083487; PA;Accession: D84900 C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Feb-2001 #sequence\_revision 02-Feb-2001 #text\_change 02-Feb-2001
C;Accession: D84900
C;Accession: Kaul, S; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y. R;Lin, X; Kaul, S; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y. M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, Nature 402, 761-768, 1999 A;Gene: At2g46240 A;Map position: 2 Query Match Best Local Sim Matches 169; 349 143 271 40 Similarity REGGTP---KESSNEGRNLESCPSDLHRNEGQITQAKGK-----EGNFECNVLSDAEEKSSVINIPVAN IVNEVKGGYVIKVDGKYYVYLKDAAHADNVRTKEEI----KREGINAEQIVIKITDQGYVTSHGDHYHYYNGKV---PYDAIISEELLMKDPNYKLKDED KRDDVEASE Conservative GB:AE002093; 4.0%; 18.5%; 108; -RNDGAVALARSQGRYTTDDGYIFNASDIIEDTGDAYIVPHGD NID:g3702325; PIDN:AAC62882.1; Score 168.5; D Pred. No. 0.22; 8; Mismatches -SSNEDRKKMQNGKTVEYPFDISMIKSL-------QDVKEAQNQKNKEEPGQVPYPIFWIPSYGKRKDVEASES ne 2 of the plant Arabidopsis thaliana PMID:10617197 BB 327; 2 Indels Length -----NRQKQEHSQH 142 1043; GSPDB:GN00139 Gaps 190 96 403 348 306 38 η, ...;

| A;Cross-re<br>A;Experime<br>C;Genetics | A;Accession: A;Status: pro A;Molecule to A:Residues:   | Lancet 3 A;Title: A;Refere         | R;Kuroda<br>ma, A.;                             | C;Species:<br>C;Date: 10-   | RESULT 16 G89957 hypothetic  | Db   | Q Db   | Q B   | & B   | Qy   | B &  | P B  | & B  | Qy   | B &  | € ₽  | Q B   | , Q   | рь <b>ў</b>  | § B   | δ     | ₽ \$   | ę       |
|--|--|------------------------------------|---|---|--|--|--|---|---|--|--|--|--|--|--|--|---|---|--|---|-------|--|---------|
| erences<br>tal sou                     | A;Accession: G89957 A;Status: preliminary A;Molecule type: DNA A;Molecule type: DNA A;Molecule type: DNA | icillin-resista<br>52: PMID:114181 | 2 3 3   | Staphylococcus aureus   | al protein (imported)  |  |  | 907 KTASQEETEVDHSPNNSKGIGQQTSEPQDEKEQSPETEVIVKEQPLETEVILNEQAPE 964 717 PEVPQVETEKVEAQLKEAEVLLAKVTDSSLKANATETLAGLRNNLTLQIMDNNSIMAEAE 776 | IVLHSEKNVELSELPVGVIDEETQPLSQDPSS SNDGWGNASEHVLGKKDHSEDPNKNFKADEEP | KAGNLIIPHKDHYHNIKFAWFDDHTYKAPNGYTLEDLFA 6  | 792PSADGNGMTVTNVBENKAMVVESLEEPINELPQMVEETETNSIRDPENASEVSEA 846 | 52GLFETLATDSKQATENAAAASSTTIPEKIGEVETVVPGNP 7                         | 713SDTNLEKVLRLSPEEHPMSVLNRTDEKQAESAAETEEGY 751 533 DEHDIISDEGDAYVTPHMGHSHWIGKDSLSDKEKVAAQAYTKEKGILPPSPDA 585 | PITHPERLGKPNSQIEYTEDEVRIA  | NOSCASAEKEAVKEQVEIKSQP-SDSPVNLEHSQLTEENKNV               | 16 STDQHIEEKEIVVNGELVMNLLLKLDAVEGL                     | 562AKKSFTEEEAARIIQSWYRGYDVRRWEDIKKLKEIATVREQMGDVKKRIEALEA 615 361PQPAPNLKIDSNSSLVSQLVRKVGEGYVFEEKGISRYVFAKDLDSETVKNLESKLS 416 | 15 IPYSQMSELEERIARIIPLRYRSNHWVPDSRPEQPSPQPTPEPSPG | 522 GSLNALRTEKGSVESNSNLQEESNGEIIKPCEAKENREQP 561               | 64 PKERNGGSKSVSHPKRME :                                   |       |  | O 1 HV  |
| RESULT 17<br>A44361                    | Db Qy  | Db .                               | 용   | ν γο  | B &  | Db Qy  | D Qy   | Db Q  | g B   | Qy b   | . Q  | Db Qy  | рЬ   | Q 5  | ş Ş  | D Q  | DЬ  | Q YQ  | Py Qy  | D &   | Match | Query<br>Best L  | A;Gene: |
| 7                                      | 764 QIMDNNSIMAEAEKLLALLKG-SNPSSVSKEK 794   | DKDSNKNKDKVIQLA                    | 703 ADVIEPESDVVKDADNNIDKDVQHDVDHLSDMSDNNHFD 741 | 662 FATIKYYVEHPDERPHSNDGWGNASEHYLGKKDHSEDPNKNFKADEEPVEETPAEPE 718 | 617 MVEHTVEVKNGNLIIPHKDHYHNIKFAMFDDHTYKAPNGYTLEDL 661<br>;   ;   ;   ; | 561 LSDKEKVAAQAYTKEKGILPPSPDADVKANPTGDSAAAIYNRVKGEKRIPLVRLPY 616 | 506 SQIEYTEDEVRIAQLADKYTTSDGYIFDEHDIISDEGDAYVT-PHMGHSHWIGKDS 560 | 432 KALIFANNAKNSUFGALDKULDEKIMUS-SINNEKUNDULDAFUAFIIREKUSKEN 303<br>  | 430 NGTRDVKNVSSIEYGENIHEDYDYTLMVFAQPITNNPDDYVDEETYNLQKLLAPYH 485  | 370 STVEPATVIFTKTGPVIELGLKTASTWKKFEVYEGDKKLPVELVSYDSDKDYAXIRFPVS 429 396 RYVFAKDLPSETVKNLESKLSKQESVSHTLTAKKENVAPRDQEFYD-KAYNLLTEAH 451 | 353 PTPEPSPGPQPAPNLKIDSNSSLVSQLVR-KVGEGYVFEEKGIS 395           | 293 PAQITSRTARGVAVPHGDHYHFIPYSQMSELEERIARIIPLRYRSNHWVPDSRPEQPSPQ 352 | -  | 241 NUQSSUASNQININI-SNQNISIINNANNQFQAIINNSQFAQFKSSANA 289 246TINTNTSNNSNTNSQASQSNDIDSLLKQLYKLPLSQRHVESDGLVFD 292 | 198 NELSASELAAAEAFLSGRGNLSNSRTYRRONSDNTSRTNWVPSVSNPG 245 | 153 AVALARSQGRYTTDDGYIFNASDIIE-DTGDAYIVPHGDHYHYIPK 197 | WKKFEVY   |   | 67 HYYNGKVPYDAIISEELLMKDPNYKLKDEDIVNEVKGGYVIKVDGKYYVYLKDAA 121 | 36 HQAQAAENTNTSDKISENQNNNATTTQQPKDTNQTQPATQPVITAKNYPAA 86 | ш     | / Match 4.0%; Score 165; DB 2; Length 891; Local Similarity 19.0%; Pred. No. 0.27; | SA1552  |

| 569 SAYLQTKNSADSSYKKDDTEKVAVTRIGGRKRITKEQKKLCYSEPEKLD | Db 509 SLMNDYIEKLKVAQKKVLRETSFKRKDLQMSLPCRFKLNPPKRPTIDHFRSYSSSSANEE 568  Qy 592TGDSAAAIYNRVKGEKRIPLVRLPYMVEHTVEVKNGNLIIPHK-D 635 | SLSDKEKVAAQAYTKEKGILPPSPDADVKANP                         | OY 500 RIGKUNSQIEYTEDENTRAÇLADKYTSDOYIFDEHDIISDEGDAYVTPHMGHSHWIGKD 559  Db 477 KLPKNKSLTQLADLHDSVEGGNSGNLNSSAEE 508 |   | 382FQKDATVKSIPULSQQLQQEKCKSHPLSDLNCEKITKASTPMLY 445 NILTEAHKALFXNKGRNSDFQALDKILERINDESTNKEKIVDDIJAFIADTTHDR | 351 SQSLYYESNEDVSGPPLKAMNSKNEVDQTLS        | QY 286 SUGLEVED PAQUESKERAKGVAVEHIGDEN YEE             | 254 KSNEENTERDGPYLTKDGQFVQGQYASDVRTSFKNIRRSLK                       | 201 LDVLQADGDIMTQDSYTQNALYFPQNQPDQYRNTQYPGANRMSKEQFKVNDVQ 226 RQNSDNTSRTNWVPSVSNPGTTNTNTSNNSNTNSQASOSNDIDSLLKOLYKLPLSORHVE  | QY 130EEIN-RQKQEHSQHREGGTPRNDGAVALARSQGRYTTDDGYIFNA 173  | QY 83 LLMKDPNYKLKDEDIVNEVKGGYVIKVDGKYVYYLKDAAHADNVRTK 129  | Qy 42 EGINAEQIVIKITDQGYVTSHGDHYHYYNGKVPYDAIISEE 82   | 03,660,664,988,1038,1211,1273/Binding 3.9%; Score 161; DB 1; milarity 19.8%; Pred. No. 0.89; Conservative 111; Mismatches 318            | e-sensi | source: A6 cells e extracted from NCBI backbone (NCBIP:121141) protein is part of a large molecular complex. | A;Accession: A44361<br>A;Molecule type: mRNA<br>A;Residues: 1-1420 <sta><br/>A;Cross-references: EMBL:214997; NID:g64551; PIDN:CAA78718.1; PID:g64552</sta> | R;Staub, O.; Verrey, F.; Kleyman, T.R.; Benos, D.J.; Rossier, B.C.; Kraehenbuhl, J.P. J. Cell Biol. 119, 1497-1506, 1992 A;Title: Primary structure of an apical protein from Xenopus laevis that participates in A;Reference number: A44361; MUID:93107151; PMID:1334959 | amiloride-sensitive sodium channel Apx protein - African clawed frog N;Alternate names: apical plasma membrane protein C;Species: Xenopus laevis (African clawed frog) C;Date: 30-Apr-1993 #sequence_revision 19-Oct-1995 #text_change 22-Jun-1999 C;Accession: A44361; S25S17 |
|---|--|--|---|---|---|--|--|---|---|--|--|--|--|---------|--|---|---|--|
| Qy 355 354  | Db 1852 DSRARERMENPLLARQIPRAYPYQNGNVVPPPPSSYRAPSPAPTSGDRRG 1901  | 1801 RŚPŚVDILKPPMSRRTPDAMVEĆTYVRPHLAĆSPVGRQTŚRFEEFSALPRĆ | 261 ASQSNDIDSLLKQLYKLP-LSQRHVESDGLVFDPAQITSR  | Qy 201 SASELAAAEAFLSGRGNLSNSRTYRRQNSDNTSRTNWVPSVSNPGTTNTNTSNNSNTNSQ 260 | Qy 146 GTPRNDGAVALARSQGRYTTDDGYIFNASDIIEDTGDAYIVPHGDHYHYIPKNEL 200  | Qy 114YVYLKDAAHADNVRTKEEINRQKQEHSQHREG 145 | Qy 75 -YDAIISBELLMKDPNYKLKDEDIVNEVKGGYVIKVDGKY 113<br> | Qy 19 SYIDGKQATQKTENLTPDEVSKREGINAEQIVIKITDQGYVTSHGDHYHYY-NGKVP- 74 | Query Match . 3.8%; Score 159; DB 2; Length 2810;<br>Best Local Similarity 18.5%; Pred. No. 3.1;<br>Matches 183; Conservative 137; Mismatches 346; Indels 322; Gaps 46; | A;Gene: CESP:P46C3.3<br>A;Map position: X<br>A;Introns: 67/2; 172/3; 204/2; 310/3; 366/2; 431/2; 684/3; 739/3; 786/3; 823/2; 880/2; ]<br>1958/3; 1999/1; 2078/1; 2117/3; 2159/2; 2220/1; 2269/3; 2306/1; 2399/2; 2444/1; 2488/3; | A; Residues: 1-2810 <wil> A; Cross-references: EMBL: Z66563; PIDN:CAA91469.1; GSPDB:GN00028; CESP:F46C3.3 A; Experimental source: clone F46C3 C; Genetics:</wil> | A;Reference number: Z19543 A;Reference number: Z19543 A;Accession: T22298 A;Status: preliminary; translated from GB/EMBL/DDBJ A.Molecule trace. Number: Accession: T2000 A;Status: preliminary; translated from GB/EMBL/DDBJ | netical protein F46C3.3 - Caenorhabditis cies: Caenorhabditis elegans elso 15-Oct 1599 #sequence_revision 15-Oct ession: T22298 tage, A. |         | Qy 782 LKGSNPSSVSK 792<br> :  :    <br>Db 784 LEGSSPSLSQK 794  | Qy 733EAEVLLAKVTDSSLKANATETLAGIRNNLTLQIMDNNSIMAEAEKLLAL 781   | . 694 DHSEDPNK<br>    :    <br>674 QHNALVQYMERKTNQRPNS  | Qy 636 HYHNIKFAWFDDHTYKAPNGYTLEDLFATIKYYVEHPDERPHSNDGWGNASEHVLGKK 693<br>  |

LNRLPQESYTEPAVKNTKNNSEYLSPHRFNLDEQKAVIRHEKETAKNAINMLSDRLRSPV

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C;Species: Plasmodium falciparum
C;Date: 15-Oct.1999 #sequence_revision 15-Oct-1999 #text_change 09-Jun-2000
C;Accession: T18444
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A; Introns: 1597/3; 1625/3
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A; Accession: T18444
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                                                                                                                                                                                                                                                                                                                                                                                                                                                C; Genetics
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                                                                                                                                                                                                                                                                                                                               Query Match
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    KYNCLNFNKSDVMRD--
                                              TDDGYIFNASDIIEDTGDAYIVPHGDHYHYIPKNELSASELAAAEAFLSGRGNLSNSRTY
                                                                                             DEKORWITSNNTNNNIOTHA-----NVKCDDKSVENKTTTLINKDINEITNISKODKNYT
                                                                                                                                         DNVR---TKEEINRQKQEHSQHREGGTPRNDGAVA---
                                                                                                                                                                                        DNVHYTKKNV-----TTHN
                                                                                                                                                                                                                                      DHYHYYNGKVPYDAI I SEELLMKDPNYKLKDEDI VNEVKGGYVI KVDGKYYVYLKDAAHA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SERYTMID-FAT-KYFRKPKDKKKQETWAWEDISQIV----RFSEKPISQSLLADLGNEE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GRNSDFQALDKLLERLN---DESTNKEKLVDDL----LAFLAPI----THPERLGKPN
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                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                3.8%; Score 158; DB 2;
17.7%; Pred. No. 1.6;
tive 127; Mismatches 311
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  YVRYSKKEDSSSNNMNGNNNMNGNNNMNGNNNM
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                                                                                                                                                                                                                                  A;Status: preliminary; nucleic acid sequence not shown; translation not A;Molecule type: DNA A;Molecule type: DNA A;Residues: 1-910 <HIM> A;Residues: 1-910 <HIM> A;Cross-references: EMBL:AE000004; GB:U000089; NID:g1673671; PIDN:AAB9566 A;Cross-references: EMBL:AE0000004; GB:U000089; NID:g1673671; PIDN:AAB9566 A;Note: the nucleotide sequence was submitted to the EMBL Data Library,
                                                                                                                                                                                                                                                                                                                                                   R;Himmelreich, R.; Hilbert, H.; Plagens, H.; Pirkl, E.; Li, B.C.; Herrmann, R. Nucleic Acids Res. 24, 4420-4449, 1996
A;Title: Complete sequence analysis of the genome of the bacterium Mycoplasma pneumoniae A;Reference number: S73327, MUID:97105885; PMID:8948633
A;Accession: S73361
                                                                                                                          A;Genetic code: SGC3
C;Superfamily: Mycoplasma heat shock protein dnaJ homolog CO9_orf910; dnaJ amino-termina
F;7-71/Domain: dnaJ amino-terminal homology <DNJ>
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A;Variety: ATCC 29342
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999
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                                                                                                                                                                                                                                    EMBL:AE000004; GB:U00089; NID:g1673671; PIDN:AAB95683.1; PID:g167368
                                              3.8%; Score 157; DB 1;
19.0%; Pred. No. 0.77;
vative 127; Mismatches 305
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                                                                                             Length 910;
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44;

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RESULT 21

$55101

$55101

Apporthetical protein YMR219w - yeast (Saccharomyces cerevisiae) hypothetical protein YMR261.13; hypothetical protein YMR261.13; hypothetical processes: Saccharomyces cerevisiae

C;Species: Saccharomyces cerevisiae

C;Accession: $55101; $57587

R;Dedman, K.; Brown, D.; Bowman, S.
submitted to the EMBL Data Library, June 1995

A;Reference number: $55089

A;Accession: $55101

A;Molecule type: DNA

A;Residues: 1-711 <DED>
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                                                                                          #text_change 29-Oct-1999
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                STDSPDNFQESNDNT---EFSSTKYKVRNSDLEDDESLKKELTKAEVVDKLDEEESEDSY
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A;Cross-references: EMBL:Z49809; NID:g854459; PI:A;Experimental source: strain AB972
R;Skelton, J; Churcher, C.M.
submitted to the EMBL Data Library, June 1995
A;Reference number: S57587
A;Accession: S57587
A;Accession: S57587
A;Residues: 608-1658 <SKE>
A;Cross-references: EMBL:Z4939; NID:g887599; PII
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Experimental source: C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        193 LEGKQSLIKDFDLENDEYELSEEEKNSDGQSSPSIMI-LSDEEYAEEGALQDVSNDEYAE
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                                                                                                                                                                                                                                                                                                                                EVVISESVYSSTSYEDNTVAMPPQVEYTSPFMNDPFNS---
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AWFDDHTYKAPNGYTLEDLFATIKYYVEHPDERPHSNDGWGNASEHVLGKKD--HSEDPN
                                                                                        SAAAIYNRVKGEKRIPLVRLPYMVEHTV------EVKNGNLIIPHKD--HYHNIKF
                                                                                                                                      NTGDENKNQSKNFPGVANSTDKSTEDNTDEKYFSAINYT---
                                                                                                                                                                                  IISDE--GDAYVTPHMGHSHWIGKDSLSDKEKVAAQAYTKEKGILPPSPDADVKANPTGD
                                                                                                                                                                                                                                   LAALAPAFTKKDAEFVEAGVTKSCLTSTSGHTNIFHTSKETKQVSDLDESTENVTF-ENE
                                                                                                                                                                                                                                                                             LAFLAP-ITHPE----RLGKPNSQIEYTEDEVRI-----AQLADKYTTSDGYIFDEHD
                                                                                                                                                                                                                                                                                                                                                                        NVAPRDQEFYDKAY--NLLTEAHKALFXNKGRNSDFQALDKLLERLNDESTNKEKLVDDL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AKDLPSETVKNL-----ESKLSKQESVSHTL---
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ilarity 19.7%;
Conservative 11
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AB972
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                                              IETASNVEENLRYCEKDMNEAEMSSGDECVKQNDDGSKTQISF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 157;
Pred. No. 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PIDN: CAA89934.1;
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submitted to the EMBL Data Library, August 1995
A;Description: The sequence of Saccharomyces cerevisiae chromosome XVI left arm.
A;Reference number: $59677
A;Rocession: $61103
A;Rolecule to---
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A;Residues: 1-2195 <HAL>
A;Cross-references: EMBL:U41849; NID:g1147608; PID:g1147609; MIPS:YPL085w
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEC16 protein - yeast (Saccharomyces cerevisiae)
N;Alternate names: protein LPF1w; protein YPL085w
C;Species: Saccharomyces cerevisiae
C;Date: 23-Feb-1996 #sequence_revision 01-Mar-1996 #text_change 06-Feb-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Cross-references:
A;Map position: 16L
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TPAEPEVPQVETEKVEAQLKEAEVLLAKVT. 742
                                     SMOTSTEKIAEOKFSFLENDDDLLDDDDSFLASSE----EEDTVPNTDNTTNLTSKPVEE
                                                                         G-YTLEDLFATIKY-YVEHPDERPHSNDGWGNASEHVLGKKDHSEDPNKNFKADEEPVEE
                                                                                                                                                  KRIPLVRLPYMVEHTVEVKNGNLIIPHKDHYHNI-----KFAW----FDDHTYKAPN
                                                                                                                                                                                          --GQNDFTGKNIENESQKLMGEGNHK----LPLSAEADIIEPGKDIQDQAEDLFTQSSGD
                                                                                                                                                                                                                             HMGHSHWIGKDSLSDKEKVAAQAYTKEKGILPPSPDADV--KANPTGDSAAAIYNRVKGE 606
                                                                                                                                                                                                                                                                   NENTHNTQESAPHTDDRDKGYEGNEALKKSESCTAADERSYSEETSEDIFHGHDKQVVE-
                                                                                                                                                                                                                                                                                                        PERLGKPNSQIEYTEDEVR----IAQLADKYTTSDGYIFDE---HDIISDEGDAYVTP
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Pred. No. 2.8;
9; Mismatches 241
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A;Accession: T48429
A;Status: preliminary
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R;Bevan, M.; Peters, S.A.;
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A; Introns: 100/3
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A;Experimental source: cultivar C
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A; Residues: 1-1495 <BEV>
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C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 20-Apr-2000
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Matches 146; Conserv
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                                       --RNLQ---
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                                                                                                                                                                                          LSPKTPRVLPWEPDPETEKIRLRHQEIGGKRNSEEWMLDYALRQAISTLAPSQKRKVSLL
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                                                                           HYHNIKFAWFDDHTYKAPNGYTLEDLFATIKY--YVEHPDERPHSNDGWGNASEHVLGKK 693
                                                                                                                                                                                                                                                                                                                                                                                    PRDQEFYDKAYNLLTEAHKALFXNKGRNSDFQALDKLLERLNDESTNKEKLVDDLLAFLA
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                                                                                                                AQAFDTISLQDMGSGSTPGSAASSRN-ISRQSSISSMAAHYENEANAEIIRGKL-----
                                                                                                                                                    PPSPDA----DVKANPTGDSAAAIYNRVKGEKRIPLVRLPYMVEHTVEVKNGNLIIPHKD
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                                                                                                                                                                                                                                                                                                       PITHPERLGKPNSQIEYTEDEVRIAQLADKYTTS--DGY----IFDEHDIISDEGD---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3.8%; Score 156.5; 18.6%; Pred. No. 1.7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .; van Staveren, M.; Dirkse, W.; Stiekema, Sequence Database, March 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Columbia;
                                     EDLKESAKLDGVSKDLEEKQQCSSLW-----RILCKQ
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| Db 328 SPTNSGEGNSSAYSVEFGNSEFTAAEMKKIAADEKLAEIVMADPKRVKRILANRVSAARS 387 |   | Db 290 APTGRHYRSVSMDSCFMGKLNFGDESSLKLPPSSSAKV 327 | Qy 631 IPHKDHYHNIKFAWFDDHTYKAPNGYTLEDLFATIKYYVEHPDERPHS 678             | Db 248 GTKKTNGGSSSDSEGDSSASGNVKVALSSSSSGVKR                  | Qy 571 AYTKEKGILPPSPDADVKANPTGDSAAAIYNRVKGEKRIPLVRLPYMVEHTVEVKNGNLI 630 | 206 AMDDVFTAYMNLDNIDVLNSFGGEDGKNGNENVEEMESSRGS | OV 511 TEDEVRIAQLADKYTTSDGYIFDEHDIISDEGDAYVTPHWGHSHWIGKDSLSDKEKVAAO 570 | 451 HKALFXNKGRNSDFQALDKLLERLNDESTNKEKLVDDLLAFLAPITHPERLGKPNSQIEY | Db 151 VTFGFSSMMSQNQKSPPLSSLERSISGEDTSDWSNLVKKEPR-EGFY 196      | VAPRDQEFYDKAYNLLTEA 4  | Qy 348 QPSPQPTPEPSPGPQPAPNLKIDSNSSLVSQLVRKVGEGYVFEEKGISR 396                    | Db 42HHHERHPFTGAPPPPIPPISPYSQIPATLQPRHSRSMSQPSSFFSFDSLPPLNPS 96         | Qy 306 VPHGDHYHF    | Db 7 TTDTNMMQRVNSSSGTSSSSIPKHNLHLNPALIRS41                      | Matches 125; Conservative 84; Mismatches 176; Indels 260; Gaps |  | : 1-519<br>ference<br>:<br>2g21230  | 20083487; PMID:10617197                 | K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon,<br>.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter,<br>1999 | S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; | probable bill transcription factor (imported) - Arabidopsis thaliana C;Species: Arabidopsis thaliana (mouse-ear cress) |   | Cy 791 SKEKIN 796 | 1379 NLNNEETROKSETLOVSKVRIDRWSNLKRAILLRRFVKALENVRKFNPREPRFLPPNPEV     | 753 TLAGLRNNLTLQIMDNNSIMAEAEKLLALLKGSNPSSV                              | Db 1319 MEDNEKNOTIPEETRKEEREEELKEDTSVDGEKMRIYOTRAVELLGEVIDGISLERSODO 1378 |
|---|---|---|---|--|---|--|---|--|---|--|---|---|---------------------|---|--|--|---|---|--|---|--|---|-------------------|---|---|---|
| Qy 476  | Db 704 RYAEIOTROYRAPEVILKSGFNETADIWSFACMVFELVTGDFLFNPQKGDRYDKNEEHLS 763 | Oy 460 RNSDFQALDKLLERLN 475                       | Db 644 IDSNNTMNDLGNNQNSHKVVYINTEDGEYCIRPYDPSVYYHEKSCYKICDLGNSLWIDES 703 | Qy 411 LESKLSKQESVSHTLTAKKENVAPRDQEFYDKAYNLLTEAHKALFXNKG 459 | Db 584 QNKNQLEVNLPNNKYPNSNDVYKFFEKDINKFPIYCDMFNHLIHPEALRLHELYMKNKKN 643 | 369 IDSNSSLÝSQLVRKVGEGYVFBEKGISRYVFAKDLPSETVKN | QY 328 ARIIFLRYRSNHWVPDSRPEQPSPQPTPPSPGPQPAPNLK 368                     | 482 KQTKKKNINEPPYVKHKLRPSNSDPSLLTSYSNIHALQETL                    | Qy 276 KLPLSQRHVESDGLVFDPAQITSRTARGVAVPHGDHYHFIPYSQMSELEERI 327 | 426 NNIQTNNINDNTVNEKINNTSKKDMLNNTQNNNDSEKNDVVIEQQLVNEDILKKKN | Db 419NICNNICNNKN 425  Qy 231 NTSRTNWVPSVSNPGTTNTNTSNNSNTNSQASQSNDIDSLLKQLY 275 | Qy 171 FNASDIIEDTGDAYIVPHGDHYHYIPKNELSASELAAAEAFLSGRGNLSNSRTYRRQNSD 230 | 387NNISIKEKINDCHSPN | Qy 119 DAAHADNVRTKEEINRQKQEHSQHREGGTPRNDGAVALARSQGRYTTDDGYI 170 | 63GDHYHYYNGKVPYDAIISEELLMKDPNYKLKDEDIVNEVKGGYVIKVDGKYYVYLK     | Db 277 TQKNDKNIEYDQKCTSSKENIEDNVSFVNDPSDPNQKNNLNNNITDNNIIPSN 329 | Query Match 3.7%; Score 154.5; DB 2; Length 1338; Best Local Similarity 16.6%; Pred. No. 1.8; Matches 153; Conservative 122; Mismatches 287; Indels 357; Gaps | 1 to 0 to | <pre>i: preliminary; translated from GB/EMBL/DDBJ ile type: DNA les: 1-1338 &lt; LAW&gt;</pre>   | ence number: Z18934<br>sion: T18416         | ion: T18416<br>1, D.; Bowman, S.; Barrell, B.<br>d to the EMBL Data Library. July 1997                                 | T18416 hypothetical protein C0105w - malaria parasite (Plasmodium falciparum) C:Species: Plasmodium falciparum C:Species: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jun-2000 | 25                | Qy 758 RNNLTLQIMDNNSIMAEAEKLLALLKGSNPSSVSKEKIN 796  :  : ::   ::   :: | Db 388 KERKTRYMAELE-HKVQTLQTEATTLSAQLTHLQRDSMGLTNQNSELKFRLQAMEQQAQL 446 | Qy 719VPQVETEKVEAQLKEAEVLLAKVTDSSLKANATETLAGL 757                         |

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ASS surface protein - Staphylococcus saprophyticus
C;Species: Staphylococcus saprophyticus
C;Species: Staphylococcus saprophyticus
C;Accession: T30290
C;Accession: T30290
Mol. Microbiol. 29, 871-881, 1998
A;Title: Cloning of aas, a gene encoding a Staphylococcus saprophyticus surf
A;Reference number: Z20809; MUID:98389318; PMID:9723925
A;Accession: T30290
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-1463 - KHEL>
A;Residues: 1-1463 - FMEL>
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                                                                                                                                              HYHFIPYSQMSELEERIARIIPLRYRSNHWVPDSRPEQPSPQPTPEPSPGPQPAPNLKID
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VVEPSPDQYMHANYNNDIVHAV----
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                                                                                                                                                                                                                                                                                                 ----KAETSNEDVASSDVKQDDTHSDANASDVADQNESETQNDN--AESSNEDDVASSD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ---NEPVAQNDKAETSNEDVASSDVK-------QDGTHSDD-NASDD
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-QNESATQDDKA---TSKED
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E71619
E71619
E71619
C; Species: Plasmodium falciparum
C; Species: Plasmodium falciparum
C; Date: 13-Nov-1998 #sequence_revision 13-Nov-1998 #text_change 21-Jul-2000
C; Accession: E71619
R; Gardner, M.J.; Tettelin, H.; Carucci, D.J.; Cummings, L.M.; Aravind, L.; Koonin, ...; Pertea, M.; Salberg, S.; Zhou, L.; Sutton, G.G.; Clayton, R.; White, O.; Smith, Science 282, 1126-1132, 1998
A; Title: Chromosome 2 sequence of the human malaria parasite Plasmodium falciparum. A; Reference number: A71600; MUID:99021743; PMID:9804551
A, Accession: E71619
A, Accession: E71619
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A; Residues: 1-1516 <GAR>
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Best Local Similarity
Matches 165; Conserv
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  487
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                                                                                                                                                                                                                                                                                                                                                                                                                                     IISEELLMKDPNYKLKDEDIVNEVKGGYVIKVDGKYYVYLKDAAHADNVRTKEEINR--- 134
                                                                                                                                                                                                                                                                                                                                                     ---QKQEHSQHREGGTPRNDGAVALARSQGRYTTDDGYIFNASDIIEDTGDAYIVPHGDH 191
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  ITNDEKSININNYNNNNNNNNNNNNNNDNNDVIIEHNKNNMNIYDNKYNVECSSEKIN 546
                                                 -TNWVPSVSNPGTTNTNTSNNSNTNSQASQSNDI-----DSLLKQLYKLPLSQRHVE 285
                                                                                                                                                                                                                                                                                                    DDDDEKEDIQNKNG------
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                                                                                                                                                                                                                                                     YHYIPKN-----ELSAS---
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ilarity 17.3%; Pred. No. 2.2;
Conservative 134; Mismatches
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                                                                                                                                                ELAAAEAFLSGRGNLSN-----SRTYRRQNSDNTSR-----
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A;Residues: 1-3924 <CHA>
A;Cross-references: EMBL:Z26634; NID:9406287; PIDN:CAA81387.1; PID:9406288
R;Otto, E.; Kunimoto, M.; McLaughlin, T.; Bennett, V.
J. Cell Biol. 114, 241-253, 1991
A;Title: Isolation and characterization of cDNAs encoding human brain anky
A;Reference number: A39643; MUID:91302466; PMID:1830053
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ş
        A;Molecule type: mRNA
A;Residues: 1-1443,3585-3924 <OTT>
A;Cross-references: EMBL:X56958
R;Tse, W.T.; Menninger, J.C.; Yang-Feng,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           N;Contains: ankyrin 2, short form
C;Species: Homo sapiens (man)
C;Date: 06-Jan-1995 #sequence revision 06-Jan-1995 #text change 13-Aug-1999
C;Accession: S37431; A39643; B39643; A40334; A49462; S14533; S14569
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ankyrin 2, neuronal long splice form - human
N;Alternate names: ankyrin B, 440K splice form; ankyrin-B;
N;Contains: ankyrin 2, short form
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R;Chan, W.; Kordeli, E.; Bennett, V.

Cell Biol. 123, 1463-1473, 1993
A;Title: 440-kD ankyrinB: structure of the major developmentally regulated A;Reference number: A49462; MUID:94075409; PMID:8253844
A;Accession: A49462
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A;Accession: A40334
A;Molecule type: DNA
A;Residues: 463-474, 'PE', 447-495 <TSE>
A;Cross-references: GB:M37123; NID:g178647; PIDN:AAA62828.1; PID:g178648
R;Chan, W.; Kordeli, E.; Bennett, V.
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A;Map position: 4q25-4q27
C;Superfamily: ankyrin; ankyrin
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F;232-264/Domain: ankyrin repeat homology
F;265-297/Domain: ankyrin repeat homology
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F;2-3924/Product: ankyrin 2, long form #status predicted <MAT>
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A; Cross-references:
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-----IPTAPMENVPFTESKSKIPVR

3274

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R;Zhao, Y.; Kappes, B.; Yang, J.; Franklin, R.M.

Eur. J. Biochem. 207, 305-313, 1992

A;Title: Molecular cloning, stage-specific expression and cellular distribution |
A;Reference number: $23466; MUID:92331669; PMID:1378403

A;Accession: $23467

A;Atatus: preliminary; translation not shown
A;Molecule type: mRNA
A;Residues: 1-749 < ZHA>
A;Residues: 1-749 < ZHA>
A;Cross-references: EMBL:X63648; NID:g9937; PID:g9939
C;Superfamily: human long-chain-fatty-acid-CoA ligase; acetate-CoA ligase homolo C;Keywords: acid-thiol ligase; coenzyme A
F;103-732/Domain: acetate-CoA ligase homology <ACL>
                                                                                                                                                                                                                                                                                                                                                                                                                           probable long-chain-fatty-acid-CoA ligase (EC 6.2.1.3) - malaria parasite ()
C;Species: Plasmodium falciparum
C;Date: 22-Nov-1993 #sequence_revision 01-Dec-1995 #text_change 03-Jun-2002
C;Accession: S23467
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S23467
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SRTYRRONSDNTSRTNWVPSVSNPGTTNTNTSNNSNTNSQASQSND--IDS----LLKQL
                                                                   GYKLYYYKDLIDKYKNRNIIPQTEMHDHDFHKEHNPNNAF-YDKLKKEQADYSNNNNNNN
                                                                                                      GY-IFNASDIIEDTGDAYIVP-----HGDHYHYIPKNELSASELAAAEAFLSGRGNLSN
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                                                                                                                                           Conservative
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                                                                                                                                      3.7%; Score 154; DB 2; Length
18.7%; Pred. No. 0.84;
ative 92; Mismatches 209; Indel
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- NNNNNNNNNNN I QKMNTNNRS I DERNNYLMKQ I
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A36685
                                                                                                                                                                                                                                                                                 A;Gene: FlyBase:Map205
A;Cross-references: FlyBase:FBgn0002645
C;Keywords: alternative splicing
                                                                                                                                                                                                                                                                                                                                       A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-1163 <IRM>
A;Cross-references: GB:X54061; NID:g8201;
C;Genetics:
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                                                                      53
96
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                                                                                                                                                                                                                                 Similarity
                                                                                                      NASDIIEDTGDAYIVPHGDHYHYIPKNELSASELAAAE-----AFLSGRGNLSNS
                             RTYRRQNSDNTSRTNW------VPSVSNPGTTNTNTSNNSNTNS----QASQSND 266
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                                                                    --SDEVDGEED-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IPLVRLPYMVEHTVEVKNGNLIIPHKDHY-HNIKFAWFDDHTYKAPNGYTLEDLFATIKY
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                                                                                                                                           HEDNAQLDNYLQNRLAESLQICGGAGEHNPHLADATGGNGCAPGIAPSK----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -KIIDRAKNIFKLAQGEY-----IEPEKLENLYSN-----SIYIENIFVHGYSYENE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DSLSDKE----KVAAQAYTKEKGILPPSPDADVKANPTGDSAAAIYNR---VKG---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TAKKENVAPRDQEFYDKAYNLLTEAHKALFXNKGRNSDFQALDKLLERLNDESTNKEKLV 485
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               KKNKGNLNDVYT--IIFTSG--SSGTPKGVMITHNSFITFLQAYLIDGNRLGLKKYDVVF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             YKLPLSQRHVESDGLVFDPAQITSRTARGVAVPHGDHYHFI----------
-----DSDNQVHGNGAAAVFNLYEEDVEVIKNDGDFSTNSNTTTSTDEVVARQAQEPNQ 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -----NSRKFHSKIYDLILQPIRNKFGGCIRT-----QVMGSSSMDKNKLI 493
                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VPRILQKIHDSVM---EGLKSKSFIARNLVKTSLKNKTSAYVK--
                                                                                                                                                                                                                3.6%; Sc
20.3%; Pr
tive 105;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        678
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                                                                      -EEWKYI--HEVRQSEKLQQEKLPLTKETGNGFGPGR-----
                                                                                                                                                                                                              Score 151.5; D
Pred. No. 2.2;
05; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -----PERLGKPNSQIEYTEDEV------
                                                                                                                                                                             -EHSQHREGGTPRNDGAVALARSQGRYTTDDGYIF 171
                                                                                                                                                                                                                                                                                                                                                          PID: 98202
                                                                                                                                                                                                                                                    DB 2;
                                                                                                                                                                                                                310;
                                                                                                                                                                                                                                                  Length 1163;
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| 91: S27437  91: S27437  103  104  108, 'AVSPMEM', 1016-1017, 'SRT  108: EMBL:M88606; NID:g172077;  28: SGD:S0005438  15L  3.6%; Score 150.5   | n: S667 type: : 1-117 : erence ference ntal sc M.E. | RESULT 31 S66771 S66771 S66771 S66771 S66771  N;Alternate names: hypothetical protein O1110 C;Species: Saccharomyces cerevisiae C;Date: 12-Uul-1996 #sequence revision 12-Jul-1996 #text_change 19-Apr-2002 C;Accession: S66771; S27437 R;Alexandraki, D.; Katsoulou, C.; Tzermia, M. submitted to the Protein Sequence Database, July 1996 A;Reference number: S66756 | Db 260 DELEGYOPREDELOGITLDLVARSERKEFARINNOSHA   | Qy 267 IDSILKQLYKLPLSQRHVESDGLVFDPAQITSRTARGVAVPHG  |
|---|---|--|---|---|
| RESULT 32  B8253B ribonuclease E XF2607 [imported] - Xylella fastidiosa (strain 9a5c) C;Species: Xylella fastidiosa C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 02-Sep-2000 C;Accession: B8253B R;anonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide Sequence Nature 406, 151-157, 2000 A;Title: The genome sequence of the plant pathogen Xylella fastidiosa. | ::    :  :  : : : : : : : : : : : : : :             | Db 812 DTTDGTINOLSFYKPIIGNEDDIDKTNGSKIDVTVYLYP 851  Qy 654 NGYTLEDLFATIKYYVEHPDERPHSNDGWGNASEHVLGKKDHSEDPN 700   | Qy  215RGNLSNSRTYRRQNSDN-TSRTNWVPSVSNPGTTNTNTSNNSNTNSQAS 262  bb 422 MNRDSKDSRSNSNEFNAQNRDRITPGSSYGKSLLGSEYSERYSNNDSSTMESGEMSLDS 481  Qy  263QSNDIDSLLKQLYKLPLSQRHVESPGLVFDPAQITSRTARGVAVPHGDHY 312  db 482 DMQTNTIPS | Best Local Similarity 18.6%; Pred. No. 2.5;  Matches 157; Conservative 118; Mismatches 254; Indels 313; Gaps 41;  Oy 104 GYVIKUDKYYVYLKDAAHADNVRTKEEINRQKQEHSQHREGGTPRNDGAVALARSQ 160 |

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A;Experimental Source: Strain 9a5c
A;Experimental Source: Strain 9a5c
Briones, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.E.A.; Carraro, D.M.; Carrer, H. Briones, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.E.A.; Carraro, D.M.; Carrer, H. Briones, M.R.S.; Bueno, M.R.P.; Faccincani, A.P.; Ferreira, A.J.S.
submitted to GenBank, June 2000
A;Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; Frohn
J.D.; Junqueira, M.L.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.E.; Kuramae, B.E.; Laigi
Chado, M.A.; Madeira, A.M.B.N.; Madeira, H.M.F.; Marrino, C.L.; Marques, M.V.; Martins, F.
A;Authors: Martins, E.M.F.; Matsukuma, A.Y.; Menck, C.F.M.; Miracca, E.C.; Miyaki, C.Y.;
F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmieri, D.,
F.G.; Nunes, L.R.; Oliveira, M.A.; de Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; Sawasał
A;Authors: da Silva, A.C.R.; da Silva, F.R.; da Silva, A.M.; Silva Jr., W.A.; da Silvei
M.; Tsuhako, M.H.; Vallada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.;
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A;Note: for a complete list
A;Accession: B82538
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C;Superfamily:
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AHSNTTRHTSGRRLETLSTAHTPAKASPSEHITPTSRSNANAKTTKTEIPNKPTNANSDT
                                             GHS----HWIGK-
                                                                                          TAPQSMMETTSRTHVASQMAPQSETSAASTTSHTSVQATTTHTHKDVVSDSPSR--TPYK
                                                                                                                                     -KPNSQIEYTEDEVRIAQLADKYTTSDG----
                                                                                                                                                                               TETDNADNIEAPQALRPAMQENKROPEFEFDDLAPAAPITAPLRKAIAAEREEISADLTT
                                                                                                                                                                                                                                                                                                                       DFQALDKLLERLNDEST------
                                                                                                                                                                                                                                                                                                                                                                    ----LTAEAVLTNMPAPSMTATPSGKDQNALPTTSNVTQDTSNALIEAQSTTKTNIDTNT
                                                                                                                                                                                                                                                                                                                                                                                                                 SETVKNLESKLSKQESVSHTLT--AKKENVAPRDQEFYDKAYNLLTEAHKALFXNKGRNS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AQITSRTARGVAVPHGDHYHFIPYSQMSELEERIARIIPLRYRSNHWVPDS------
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Pred. No. 2
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ed. No. 2.5;
Mismatches 280;
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                                          ---DSLSDKEKVAAQAYTKEKGI--LPPSPDADV
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                                                                                                                                                                                                                                 -LAFLAPITHPERLG--
                                                                                                                                       ----YIFDEHDIISDEGDAYVTPHM
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rhoptry protein - Plasmodium yoelii (fragment)
(,Species: Plasmodium yoelii
(,Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_
(,Accession: T28676, A45521
(,Accession: T28676, A45521
R,Sinha, K.A., Keen, J.K., Ogun, S.A., Holder, A.A.
Mol. Biochem. Parasitol. 76, 329-332, 1996
A,Title: Comparison of two members of a multigene family
A,Reference number: Z20507; MUID:97077455; PMID:8920022
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Molecule type: DNA
A;Residues: 1-2401 <SIN>
A;Residues: 1-2401 <SIN>
A;Cross-references: EMBL:U36927; NID:g1041784; PID:g1041785; PIDN:AAB41263.1
A;Cross-references: EMBL:U36927; Lockyer, M.; Lewis, A.
Mol. Blochem. Parasitol. 42, 241-246, 1990
A;Title: Identification of the gene for a Plasmodium yoelii rhoptry protein. A;Reference number: A45521; MUID:91101660; PMID:2270106
A;Accession: A45521
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A;Molecule type: DNA
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KIKKIIDKVKEY-TDEIEKNNKKINAELSNSEKIITQLKENSSLKE-----CQSKIKST
                                                                                                                                                                                                                                                                                                                                                          YVIKVDGKYYVYLKDAAHADNVRTKEEINROKQEHSQHREGGTPRNDGAVALARSQGRYT
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                                                                 LFEKYEQEVTVLLNKYYAVELKNK-
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                                                                                                                                                 NFNNIEMADTKSQYILNIKKNNGTNNTDYNIKELKEHKKKSNVYKDEAGKNTQEIKKNKE 1146
                                                                                                                                                                                                                                                                        TDDGYIFNASDIJEDTGD--AYIVPHGDHYHYIPKNELSASELAAAEAFLSGRGNLSNSR
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                                                                                                                                                                                        TYRRONSDNTSRTNWVPSVSNPGTTNTNTS-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ^KEE>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3.6%;
18.9%;
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                                                                 FDKTKNYSEQIIKEIKDAHNTFTSQADK 1198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2;
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                                                                                                                                                                                                                                   AEEY----NQNVSL 1086
                                                                                                          RTARGVAVPHGDH 311
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A, Note: Clone PTP2E

A, Note: Clone PTP2E1>

A, Note: Clone PTP2E1>

A, Note: Clone PTP2E1

C, Superfamily: protei

C, Keywords: phosphoproter

F, 25-304/Domain: proter

F, 25-304/Domain: proter

F, 1115/Binding site: C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        protein-tyrosine-phosphatase (EC 3.1.3.48) 2E - rat C;Species: Rattus norvegicus (Norway rat) C;Date: 10-Apr-1996 #sequence revision 03-May-1996 #text_change 22-Jun-1999 C;Accession: $51005; S51161 R;L'Abbe, D.; Banville, D.; Tong, Y.; Stocco, R.; Masson, S.; Ma, S.; Fantus FEBS Lett. 356, 351-356, 1994 R;Title: Identification of a novel protein tyrosine phosphatase with sequenc A;Reference number: $51005; MUID:95104449; PMID:7805871 A;Accession: $51005.
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S51005
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A;Genetics: PTP2E1
C;Genetics: <PTP2E>
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A;Genetics: PTP2E
A;Accession: S51161
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A; Residues: 840-1175 < LAB >
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Query Match
Best Local S
Matches 138
                                                                                        ;Superfamily: protein-tyrosine-phosphatase, nonreceptor type 14; protein 4.1 membrane-b;Keywords: phosphoprotein; phosphoric monoester hydrolase; tyrosine-specific phosphatas;25-304/Domain: protein 4.1 membrane-binding domain homology <841>
;925-3104/Domain: protein-tyrosine-phosphatase homology <PTP2>
;9122-1157/Domain: protein-tyrosine-phosphatase homology <PTP2>
;1109/Active site: Cys (phosphocysteine intermediate) #status predicted
;1115/Binding site: substrate phosphate (Arg) #status predicted
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  Conservative
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Score 149.5; Description of the Score 149.5; Description of the Score 149.5; Description of the Score 149.5; Description of the Score 149.5; Description of the Score 149.5; Description of the Score 149.5; Description of the Score 149.5; Description of the Score 149.5; Description of the Score 149.5; Description of the Score 149.5; Description of the Score 149.5; Description of the Score 149.5; Description of the Score 149.5; Description of the Score 149.5; Description of the Score 149.5; Description of the Score 149.5; Description of the Score 149.5; Description of the Score 149.5; Description of the Score 149.5; Description of the Score 149.5; Description of the Score 149.5; Description of the Score 149.5; Description of the Score 149.5; Description of the Score 149.5; Description of the Score 149.5; Description of the Score 149.5; Description of the Score 149.5; Description of the Score 149.5; Description of the Score 149.5; Description of the Score 149.5; Description of the Score 149.5; Description of the Score 149.5; Description of the Score 149.5; Description of the Score 149.5; Description of the Score 149.5; Description of the Score 149.5; Description of the Score 149.5; Description of the Score 149.5; Description of the Score 149.5; Description of the Score 149.5; Description of the Score 149.5; Description of the Score 149.5; Description of the Score 149.5; Description of the Score 149.5; Description of the Score 149.5; Description of the Score 149.5; Description of the Score 149.5; Description of the Score 149.5; Description of the Score 149.5; Description of the Score 149.5; Description of the Score 149.5; Description of the Score 149.5; Description of the Score 149.5; Description of the Score 149.5; Description of the Score 149.5; Description of the Score 149.5; Description of the Score 149.5; Description of the Score 149.5; Description of the Score 149.5; Description of the Score 149.5; Description of the Score 149.5; Description of the Score 149.5; Description of the Score 149.5; Description of th
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R;Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; ma, A.; Mizutani-Ui, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K. Lancet 357, 125-1240, 2001

A;Title: Whole genome sequencing of meticillin-resistant Stapylococcus aureus. A;Reference number: A89758; MUID:21311952; PMID:11418146

A;Accession: A89959

A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-1274 <KUR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      hypothetical protein SA1562 [imported] - Staphyloco (;Species: Staphylococcus aureus C;Date: 10-May-2001 #sequence_revision 10-May-2001 C;Accession: A89959
                                                                                                                                          Cross-references: GB:BA000018; PID:g13701536; Experimental source: strain N315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   YLQPSPMSSNPSIPGSDVMRPDYIPSHRHSALIPPSYRPTPDYESVMKRLNRGMVHADRH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KALFXNKGRNSDFQAL---DKLLERLNDESTNKEKLVDDLL---
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A;Status pro---
A;Nolecule type: DNA
A;Residues: 1-2829 <GAL>
A;Residues: 1-2829 <GAL>
A;Experimental source: Belem strain, merozoites
A;Experimental source: Molecular merozoites
A;Experimental source: Belem strain, merozoites
                                                                                                                                                                                                                             RESULT 36
A42771
reticulocyte-binding protein 1 - Plasmodium vivax
c;Species: Plasmodium vivax
C;Species: Plasmodium vivax
C;Date: 04-Mar-1993 #sequence_revision 18-Nov-1994
C;Accession: A42771
R;Galinski, M.R.; Medina, C.C.; Ingravallo, P.; Bar
Cell 69, 1213-1226, 1992
                                                                                                                                                        Cell 69, 1213-1226, 1992
A;Title: A reticulocyte-binding protein complex of Plasmodium vivax merozoites. A;Reference number: A42771; MUID:92315338; PMID:1617731
A;Accession: A42771
                                                                                                                                   A; Status: preliminary
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|                                    | SO VANAE INDERHALIKYKOKKKIKHILDONOKVYLEKADVIKULIHKUHY  1108 V-INPLUNESKINKIASINGLDLKGNSKYSIKULYYLNDONOKVYLEKADVIKULIHKUHY  1108 V-INPLUNESKINKIASINGLDLKGNSKYSIKULYYLNDONOKVYLEKADVIKULIHKUHY  1108 V-INPLUNESKINKIASINGLDLKGNSKYSIKULYKLEKADKNGULIHKUHY  1108 V-NAME   | 9<br>5  |
|------------------------------------|---|---|
| PDAD 586<br>   <br>-DTD 1107       | 29 GYIFDEHD-IISDEGDAYVTPHMGHSHWIGKDS-LSDKEKVAAQAYTKEKGILPPS   | \$ \$ \$  |
| TSD 528<br>  :<br>TIN 1056         | 473 RLNDESTNKEKLVDDLLAPLAPITHPERLGKPNSQIEYTEDEVRIAQLADKYTTS   | Db<br>Db  |
| LLE 472<br> <br>ELL 1026           | 419 ESVSHTLTAKKENVAPRDQEFYDKAYNLLTEAHKALFXNKGRNSDFQALDKLLE  | Qy<br>Db  |
| 41<br>96                           | 361 PQPAPNLKIDSNSSLVSQLVRKVGEGYVFEEKGISRYVFAKDLPSETVKNLESKLSKQ  | Db<br>Db  |
| SPG 360                            |   | Qy<br>Db  |
| SRT 300                            | 241 VSNPGTTNTNTSNNSNTNSQASQSNDIDSLLKQLYKLPLSQRHVESDGLVFDPAQITSRT  | ДУ  |
| TPD 859                            | 181 GDAYIVPHGDHYHYIPKNELSASELAAAEAFLSGRGNLSNSRTYRRQNSDNTSRTNWVPS  | D Qy  |
| EDT 180                            | 147TPRNDGAVALARSQGRYTTDDGYIFNASDIIE   | Qy<br>Db  |
| 146<br>TIT 749                     | 109 VDGKYYVYLKDAAHADNVRT-KEEINRQKQEHSQHREGG   | Оy  |
| -IK 108<br> <br> <br> SID 689      | 62 HGDHYHYYNGKVPYDAIISEELLMKDPNYKLKDEDIVN-EVKGGYV635 HPDFTYDNDGNLEIHTQLANDLNDDLKQKALMNANVKGIVVDQDGIEHEIDVS  | Qy<br>Db  |
| VTS 61<br>:  <br>LDS 634           | 12 VKENNRVSYIDGKQATQKTENLTPDEVSKREGINAEQIVIKITDQGYVTS   | gg<br>Qy  |
| ps 52;                             | atch 3.6%; Score 149; DB 2; Length 4688;<br>cal Similarity 18.9%; Pred. No. 23;<br>186; Conservative 138; Mismatches 316; Indels 344; Gap   | Query M<br>Best Lo<br>Matches   |
| 2000<br>Cassell, G.<br>te views of | Ureaplasma urealyticum Ureaplasma urealyticum Aug-2000 #sequence_revision 20-Aug-2000 #text_change 20-Aug-2 1: F82885 1: Lefkowitz, B.J.; Glass, J.S.; Heiner, C.R.; Chen, E.Y.; CogenBank, February 2000 101: The complete sequence of Ureaplasma urealyticum: Alternate number: A82870 11: F82885 11: F82885 12: F82885 14688 | hypothetical p<br>C;Species: Ure<br>C;Species: Ure<br>C;Date: 18-Aug<br>C;Accession: F<br>R;Glass, J.I.;<br>submitted to G<br>A;Description: A;Description: F<br>A;Description: F<br>A;Description: F<br>A;Ccession: F<br>A;Status: prel<br>A;Residues: 1-<br>A;Cross-refere<br>A;Cross-refere<br>A;Cross-refere<br>A;Cross-refere<br>A;Cross-refere<br>A;Cross-refere<br>A;Cross-refere<br>A;Cross-refere<br>A;Cross-refere<br>A;Cross-refere<br>A;Cross-refere<br>A;Cross-refere<br>A;Cross-refere<br>A;Cross-refere<br>A;Cross-refere<br>A;Cross-refere<br>A;Cross-refere<br>A;Cross-refere<br>A;Cross-refere<br>A;Cross-refere<br>A;Cross-refere<br>A;Cross-refere<br>A;Cross-refere<br>A;Cross-refere<br>A;Cross-refere<br>A;Cross-refere<br>A;Cross-refere<br>A;Cross-refere<br>A;Cross-refere<br>A;Cross-refere<br>A;Cross-refere<br>A;Cross-refere<br>A;Cross-refere<br>A;Cross-refere<br>A;Cross-refere<br>A;Cross-refere<br>A;Cross-refere<br>A;Cross-refere<br>A;Cross-refere<br>A;Cross-refere<br>A;Cross-refere<br>A;Cross-refere<br>A;Cross-refere<br>A;Cross-refere<br>A;Cross-refere<br>A;Cross-refere<br>A;Cross-refere<br>A;Cross-refere<br>A;Cross-refere<br>A;Cross-refere<br>A;Cross-refere<br>A;Cross-refere<br>A;Cross-refere<br>A;Cross-refere<br>A;Cross-refere<br>A;Cross-refere<br>A;Cross-refere<br>A;Cross-refere<br>A;Cross-refere<br>A;Cross-refere<br>A;Cross-refere<br>A;Cross-refere<br>A;Cross-refere<br>A;Cross-refere<br>A;Cross-refere<br>A;Cross-refere<br>A;Cross-refere<br>A;Cross-refere<br>A;Cross-refere<br>A;Cross-refere<br>A;Cross-refere<br>A;Cross-refere<br>A;Cross-refere<br>A;Cross-refere<br>A;Cross-refere<br>A;Cross-refere<br>A;Cross-refere<br>A;Cross-refere<br>A;Cross-refere<br>A;Cross-refere<br>A;Cross-refere<br>A;Cross-refere<br>A;Cross-refere<br>A;Cross-refere<br>A;Cross-refere<br>A;Cross-refere<br>A;Cross-refere<br>A;Cross-refere<br>A;Cross-refere<br>A;Cross-refere<br>A;Cross-refere<br>A;Cross-refere<br>A;Cross-refere<br>A;Cross-refere<br>A;Cross-refere<br>A;Cross-refere<br>A;Cross-refere<br>A;Cross-refere<br>A;Cross-refere<br>A;Cross-refere<br>A;Cross-refere<br>A;Cross-refere<br>A;Cross-refere<br>A;Cross-refere<br>A;Cross-refere<br>A;Cross-refere<br>A;Cross-refere<br>A;Cross-refere<br>A;Cross-refere<br>A;Cross-refere<br>A;Cross-refere<br>A;Cross-refere<br>A;Cross-refere<br>A;Cross-refere<br>A;Cross-refere<br>A;Cross-refere<br>A;Cross-refere<br>A;Cross-refere<br>A;Cross-refere<br>A;Cross-refere<br>A;Cross-refere<br>A;Cross-refere<br>A |

5 5 B

160 K---VTNABHIISGTPTVVTTP------SEVTAAANQVNSAKQELNGDERL 201

유 성 유 성

|     | Qy 16 NRVSYIDGKQATQKTENLTDDEVSKREGINAEQIVIKITDQGYVTSHGDHYHYNN 70  |
|-----|---|
|     | Query Match 3.6%; Score 149; DB 2; Length 6713; Best Local Similarity 18.5%; Pred. No. 38; Matches 170; Conservative 127; Mismatches 373; Indels 250; Gaps 39;  |
|     | A;Status: preliminary A;Molecule type: DNA A;Molecule type: DNA A;Molecule type: DNA A;Cross-references: GB:BA000018; PID:g13701232; PIDN:BAB42527.1; GSPDB:GN00149 A;Experimental source: strain N315 C;Genetics: A;Gene: ebhA |
|     | A;Title: Whole genome sequencing of meticillin-resistant Stapylococcus aureus. A;Reference number: A89758; MUID:21311952; PMID:11418146 A;Accession: B89921   |
| Ogu | T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, tori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K. 40. 2001                                     |
|     | B89921 hypothetical protein ebhA [imported] - Staphylococcus aureus (strain N315) C;Species: Staphylococcus aureus C;Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 22-Oct-2001 C;Accession: B89921              |
|     | RESULT 38   |
|     | Qy 775 AEKLLALLKGSNPSSVSKEKI 795  |
|     | Qy 735 EVLLAKVTDSSLKANATETLAGLRNNLTLQIMDNNSIMAE 774   |
|     | Qy 701 KNFKA  |
|     | Qy 671 HPDERPHSNDGWGNASEHVLGKKDHSEDPN 700   |
|     | Db 1165 ITNPHKINLSFNKSAVEQDIFADHANLFIDYKDYDQKLRINEDVKIYYQN 1214   |

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R;Harris, B.
submitted to the EMBL Data Library,
submitted to the EMBL Data Library,
A;Reference number: Z19441
A;Accession: T21558
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 39
T21558
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           hypothetical protein F29G6.3b - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 18-Feb-2000
C;Accession: T21558
                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Cross-references: EMBL:278543; PIDN:CAB01754.1; GSPDB:GN00028; CESP:F29G6.3b
A;Experimental source: clone F29G6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Molecule type: DNA
A;Residues: 1-1785 <WIL>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Status: preliminary; translated
                                                                                                                                                                                                                                                                                                                                                         ;Map position: X
;Introns: 10/1; 43/3; 61/3; 88/3; 110/3; 144/2; 183/3; 218/3; 252/3;
                                                                                                                                                                                                                                                                                                                                                                                                                              Genetics:
                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                       Gene: CESP:F29G6.3b
                                                                               119
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                                                                                                                                                                                                   661 IAQSPQVQTIDYFKEINRAHHFVPSTPPSLFNNKRESFHHHSFIPNSLEAERKSRSVERA
                                                                                                                                                                                                                                                                                   134;
                                                                                                                                                             67
                                     LKVVHPEHHYVPLVRKTTEDHQQKVNHEHHFIPAEKKTEA--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     H---
ASDIIEDTGDAYIVPH--GDH-----YHYIP-KNE--LSASEL----
                                                                                                                                                                                                                                           VKENNRVSYIDGKQATQKTENLTPDEV----SKREGINAEQIVIKITDQGYVTSHGDHY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AKAILNKOTGSNSDKAAVDR 813
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DVKANPTGDSAAAIYNRVKGEKRIPLVRLPYMVEHTVEVKNGNLIIPHKDHYHNIKFAWF
                                                                             -DAAHADN-----VRTKEEINROKQEHSOHREGGTPRNDGAVALARSOGRYTTDDGYIFN
                                                                                                                                                           HYYNGKVPYDAIISEELLMKDPNYKLKDE-DIVNEVKGGYVIKVDGKYYVYLK-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AEKLLALLKGSNPSSVSKEK 794
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TSAQRVANVT-SIQQTANELNTAMGQLQHGIDDENATKQTQKYRDAEQSKKTAYDQAVAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TDSSLKANATETLAGLRNNLT-----LQ--IMDNNS------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TSNPNMDANAINQIATQVTSTKNALDGTHNLTQAKQTATNAIDGATNLNKAQKDALKAQV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEDPNKNFKA-----DEEPVEETPAEPEVPQVETEKVEAQLK----EAEVLLAKV 741
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           D--TVKS-SANTLNGAMGTLRNSIQDNTATKNGQNYLDATERNKTNYNNAVDSANGVINA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DDHTYKAPNGYTLEDLFATIKYYVE----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         --HDADSDKKTAYTQAVTNAENILNKNSGSNLDKAAVENALSQVTNAKGALNGNHNLEQA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DEHDIISDEGDAYVTPHMGHSHWIGKDSLSDKEKVAAQ----AYTKEKGILPPS---PDA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LTSINNAQKRDLTTKIDQATTVAGVEAVSNTGTQLNTAMANLQNGINDKANTLASENY--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LAPITHPERLGKPN-----SQIEYTEDEVRIAQ-----LADKYTT--SDGYIF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     - AYTNAVSRAETI LNKTQGANTSKQDVEAAI QNVTSAKNALNGDQNVTNAKNAAKNALNN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         KAY-NLLTEAHKALFXNKGRNSDFQALDKLLER-----LINDES--TINKEKLVDDLLAF
                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ----VSEVTAAKNAATELNAQMGNLEQAIHDQNTVKQGVNFTDADKAKRD-----
                                                                                                                                                                                                                                                                                                      3.6%;
17.3%;
                                                                                                                     -----LPDSPANVKDQRKIIRE----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -- INGLQHLTTAQKDKLKQQVQQAQN-----
                                                                                                                                                                                                                                                                                   126;
                                                                                                                                                                                                                                                                                                      Score 148.5;
Pred. No. 5.9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 from
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                                                                                                                                                                                                                                                                                 Mismatches
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                                                                                                                                                                                                                                                                                                                         DB 2;
                                                                                                                                                                                                                                                                                   305;
                                                                                                                     -----HHYVPLEKRSQSLD
                                                                                                                                                                                                                                                                                                                         Length
                                                                                                                                                                                                                                                                                   Indels
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                                                                                                                                                                                                                                                                                   211;
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---- AAA
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208
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                                                                                                                                                                                                                    A;Cross-references: GB:NC_003210; PIDN:CAC98301.1; A;Experimental source: strain EGD-e C;Genetics: A;Gene: lmo0086
                                                                                                                                                                                                                                                                                                                                                               Science 294, 849-852, 2001
A; Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; ok, C.; Schlueter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; A;Title: Comparative genomics of Listeria species.
A;Reference number: AB1077; MUID:21537279; PMID:11679669
A;Accession: AG1085
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              hypothetical protein lmo0086 [imported] - Listeria monocytogenes (strain EGD-C;Species: Listeria monocytogenes
C;Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 27-Nov-2001
C;Accession: AG1085
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A; Residues: 1-1959 <GLA>
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                                                             18
                                                                                                                                                             Similarity
                     --YVYLKD--
                                                             AIVSAFFLMRDDAYAIETEGFTYSPKGKVVDFSSEAKYNDTWINNEKTITDKKEMKPINL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  QKSTSHQSP-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 QPTPEPSPGP---QPAPNLKID-SNSSLVSQLVRKVGEGYVFEEKGISRYVFAKDLP---
                                                                                                  AIISEELLMKDPNYKLKDEDIVNEVKGGYV-IKVDGKY--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  --VHEHGYVPP--VKKSDLKTSVDHSKHEYLPSVVHTESKDDFKHSKHGYVPSLEH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AWFDDHTYKAPNGYTLEDLFATIKY-----YVEHPDERPHSNDGWGNASEH
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                                                                                                                                          Conservative
                                                                                                                                                             3.6%;
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                                                                                                                                          125;
                                                                                                                                        Score 148.5; I
Pred. No. 6.8;
25; Mismatches
  -AAHADNVRTKEEINRQKQEHSQHREGGTPRNDGAVALA 157
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urget, O.; Entian, K.D.; Fsihi, H.
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                                                                                                                                                                                    1959;
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                                                                                                                                        Gaps
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Voss, H.; Wehland,
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| RESULT 41 T38495 T38495 hypothetical protein SPAC29B12.07 - fission yeast (Schizosaccharomyces pombe) C;Species: Schizosaccharomyces pombe C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 03-Dec-1999 C;Accession: T38495 R;Gentles, S.; Churcher, C.M.; Barrell, B.G.; Rajandream, M.A.; Wood, V. submitted to the EMBL Data Library, September 1997 A;Reference number: 221797 A;Reference number: 221797 A;Reference number: T38495 A;Status: preliminary; translated from GB/EMBL/DDBJ A;Molecule type: DNA A;Residues: 1-1999 <gen' a;cross-references:="" embl:z99164;="" gspdb:gn00066;="" pidn:cab16252.1;="" spdb:spac29b12.07<="" th=""><th>Db 760 MVDELIGOSSVFRTTEITKVNASFSLDSVDTTKVAINVKLSDAAV-NLNDANLKIYEKKT 818  Qy 754 LAGLRNNLTLQIMDNNSIMAEAEKLLA 780   </th><th>Db 644SDYTFATPASSISVVOKKTKPTVEFSLKEAEQDKLTINYEVFDADNTLLFDNLTHP 699  Qy 673 DERPHSNDGWGNASEHVLGKKDHSEDPNKNF 703  Qy 673 DERPHSNDGWGNASEHVLGKKD</th><th>Db 538 DGWYFISSTLKAKPTIEGLNLSYSTDKGEFVASPVNLVDRDESITSIRYVA 588  Qy 584DADVKANPTGDSAAAIYNRVKGEKRIPLVRLPYMVEHTVEVKNGNLIIPHKDHYHNIK 641  Qy 589 YLEDDYKVNGSNAKEYA-YSVVDANQKKTAVKVGRTVDMNDGNYIFVGYISGNNGQ 643  Qy 642 FAWFDDITKAPNGYTLEDLFATIKYYV</th><th>462 SDFQALD</th><th>Qy 361 PQPAPNLKIDSNSSLVSQLVRKVGEGYVFEEKGISRYVFAKDLPSET 407   </th><th>Qy 241 VSNPGTTNTNTSNNSNTNSQASQSNDIDSLLKQLYKLPLSQRHVESDGLVFDPAQITSRT 300  ;   :   :   :   :   :   :   :   :   :  </th><th>Db 78 ARTLFLKDGRIQFLGKSVAVKSASDLIELPSKTSITESKGSYKAKSDSNKTLA 130  Qy 158 RSQGRY-TTDDGYIFNASDIIEDTG- 181    :   :   :   :   :   :   :   :   :  </th></gen'> | Db 760 MVDELIGOSSVFRTTEITKVNASFSLDSVDTTKVAINVKLSDAAV-NLNDANLKIYEKKT 818  Qy 754 LAGLRNNLTLQIMDNNSIMAEAEKLLA 780 | Db 644SDYTFATPASSISVVOKKTKPTVEFSLKEAEQDKLTINYEVFDADNTLLFDNLTHP 699  Qy 673 DERPHSNDGWGNASEHVLGKKDHSEDPNKNF 703  Qy 673 DERPHSNDGWGNASEHVLGKKD                   | Db 538 DGWYFISSTLKAKPTIEGLNLSYSTDKGEFVASPVNLVDRDESITSIRYVA 588  Qy 584DADVKANPTGDSAAAIYNRVKGEKRIPLVRLPYMVEHTVEVKNGNLIIPHKDHYHNIK 641  Qy 589 YLEDDYKVNGSNAKEYA-YSVVDANQKKTAVKVGRTVDMNDGNYIFVGYISGNNGQ 643  Qy 642 FAWFDDITKAPNGYTLEDLFATIKYYV | 462 SDFQALD  | Qy 361 PQPAPNLKIDSNSSLVSQLVRKVGEGYVFEEKGISRYVFAKDLPSET 407          | Qy 241 VSNPGTTNTNTSNNSNTNSQASQSNDIDSLLKQLYKLPLSQRHVESDGLVFDPAQITSRT 300  ;   :   :   :   :   :   :   :   :   : | Db 78 ARTLFLKDGRIQFLGKSVAVKSASDLIELPSKTSITESKGSYKAKSDSNKTLA 130  Qy 158 RSQGRY-TTDDGYIFNASDIIEDTG- 181    :   :   :   :   :   :   :   :   :  |
|--|---|---|---|--|---|--|--|
| QY       632 PHKDHYHNIKFAMFDDHTYKAPNGYTLEDLFATIKYYVEHPDERPHSNDGWGNASEH 688         Db       814QRTANLYKPMTTENAYNIK   | 709 PGPSLQVNAPYTPTSGELGNKVSNPTKEFVSTSSYAPAANTRNAIIREPGILSPLSP 587 VKANPTGDSAAAIYNRVKGEKRIPLVRLPYMVEHTVEVKNGNLII | Db 615 AQQKRSVSQNYNRQYSFQPRPATPSNPPRSLPPPSGQ 651  CY 508 IEYTEDEVRIAQLADKYTTSDGYIFDEHDIISDEGDAYVTPHMGH552  CY 508 IEYTEDEVRIAQLADKYTTSDGYIFDEHDIISDEGDAYVTPHMGH | OY  49 TDNQDSLLFSQLTNNALQAENATKVSENTINDEELIDDSEFTSLMSNFLESSTVQT 554  QY  413 SKLSKQESVSHTLTAKKENVAPRDQEF  | 244 PGTTNTNTSNNSNTNSQASQSNDIDSLLKQLYKLPLSQRHVESDGLVFDPAQITSRTARG    :: | Qy 134 RQKQEHSQHREGGTPRNDGAVALARSQGRYTTDDGYIFNASDIIEDTGDAYIVPH- 188 | QY  14 ENNRVSYIDGKQATQKTENLTPDEVSKREGINAEQIVIKITDQGYVTSHGDHYHYYNGKV 73.  | A;Experimental source: strain 972h-; cosmid c29B12 C;Genetics: A;Genetics: A;G |

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hypothetical protein PFB0765w - malaria parasite (Plasmodium falciparum)
C;Species: Plasmodium falciparum
C;Date: 13-Nov-1998 #sequence_revision 13-Nov-1998 #text_change 21-Jul-2000
C;Accession: E71606
R;Gardner, M.J.; Tettelin, H.; Carucci, D.J.; Cummings, L.M.; Aravind, L.; Koonin,
; Pertea, M.; Salzberg, S.; Zhou, L.; Sutton, G.G.; Clayton, R.; White, O.; Smith,
Science 282, 1126-1132, 1998
A;Title: Chromosome 2 sequence of the human malaria parasite Plasmodium falciparum.
A;Reference number: A71600; MUID:99021743; PMID:9804551
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C;Superfamily: h
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A;Experimental source: clone 3D7
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A;Status: preliminary; nucleic acid sequence
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                                                                                                                                                                                                                       SDEGDAYVTPHMGHSHWIGKDSLSDKEKVAAQAYTKEKGILPPSPDADVKANPTGDSAAA
                                                                                                                                                                                                                                                          IKNLEDDLL.
                                                                                                                                                                                                                                                                                          EK-LVDDLLAFLAPITHPERLGKPNSQIEYTEDE-VRI-AQLADKYTTSDGYIFDEHDII
                                                                                                                                                                                                                                                                                                                              LMEKONVIKUNEOLLKDIKDENEKMNEHVNKLONELIKRELONKCISKDIEFCKKEKEDK
                                                                                                                                                                                                                                                                                                                                                            TAKKENVAPRDQEFYD--KAYNLLTEAHKALFXNK--GRNSDFQALDKLLERLNDESTNK
                                                                                                                                                                                                                                                                                                                                                                                             ---YEENQKLNEEIKRR-----NSFIKNKDRKIDLLTNIENELLKKKEINNIK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SASELAAAEAFLSGRGNLSNSRTYRRONSDNTSRTNWVPSVSNPGT-----TNTNTS
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                                                   NKYDKEINMIIEQYNKKIQEEKDMLNNKIKSMDQTHKNQIEEMQEENKKELKRLKNVCDM
                                                                                   NGYTLEDLFATIKYYVEHPDERPHSNDGWGNASEHVLGKKDHSEDPNKN-----
                                                                                                                      --EFLKEEEKKKNIDMVYKIKEYEIQIKEKENEIDSLKKNEQNLHVLKNEELNEKEIILK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                KQNYYYLKKEYDLKNKELEKNIEHGKKLEHELSHC----
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----EKKKCIENLKDELINIKKKMEDKM-----HMTNEMDLL
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T22458
typothetical protein F49E2.5a - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Jate: 15-Oct-1999 #sequence_revision 15-Oct-1999 #te)
C;Accession: T22458
R;Sulston, J.
R;Sulston, J.
Submitted to the EMBL Data Library, October 1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Cross-references: EMBL:Z46267; PIDN:CAA86428.1; GSPDB:GN00028; A;Experimental source: clone F49E2 C;Genetics:
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A; Introns: 37/2;
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----SDGYIFDEHDIISDEGDAYVTPHMGHSHWIGKDSLSDKEKVAAQAYTKEKGILPPS 582
                                                                                                                                                SHTL----TAK---KENVAPRDQEFYDKAYNLLTEAHKALFXNKGRNSDFQALDKLLE 472
                                                                                                                                                                                                                                                          APVEEVVENVVENVVEKSTTPPATENKKKNKKDKKKSESEKVTEQPV-ESAPAPPQ----
                                                                                                                                                                                                                                                                                            --LEERIARIIPLRYRSNHWVP-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IIEDTGDAYIVPHGDHYHYIPKN----ELSASELAAAEAFL-------
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -----AEQERIQKEQEKKEADLKKLQAEKKKEKAVKAE-----
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                                                     PVQAAPTSKKPTADDSMDFLDFVTAKEERVEEVAPVQEQVKEQKNESPESEPVAKLITVS
                                                                                                                      DDSMDFLDFVTAKPDRSEVAAPVEVAKVDESTAVTSENRKKNKKDKKKSESEKAVE---E
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                                                                                    RLNDESTNKEKLVDDLLAFLAPIT---
                                                                                                                                                                                                                       KIDSNSSLVSQLVRKVGEGYVFEEKGISRYVFAKD-LPSETVKNLESKL-----SKQESV
                                                                                                                                                                                                                                                                                                                                                            KQLYKLPLSQRHVESDGLVFDPAQITS-RTARGVAVPHGDHYHFI-----PYSQMSE----
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                                                                                                                                                                                       -VEQVVETTPPASENKKKN-----KKDKKKSESEKAVEEPVQAAPSSKKPTA 451
                                                                                                                                                                                                                                                                                                                              DKKKSESEKVVEEPVQAEAPKSKKPTADDNMDFLDFVTAKEEPKDEPAETPA
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Mismatches 351;
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                                                                                    -HPERLGKPNSQIEYTEDEVRIAQLADKYTT---
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| A, Status: preliminary A, Molecule type: NA A; Residues: 1.1856 < KUR- A; Cross-references: GB.AE005672; PIDN:AAK74260.1; PID:g14971537; GSPDB:GN00164; TIGR:SP4 A; Cross-references: GB.AE005672; PIDN:AAK74260.1; PID:g14971537; GSPDB:GN00164; TIGR:SP4 A; Cross-references: GB.AE005672; PIDN:AAK74260.1; PID:g14971537; GSPDB:GN00164; TIGR:SP4 A; Experimental Source: Strain TIGR4 Cy | JSULT 44 JS008 JS008 JSpecies: JOACESSIC JACCESSIC JOACESSIC JOACESSIC JOACESSIC JOACESSIC JOACESSIC JOACESSIC JOACESSIC              | Db 569 NTEASAVNVMGFSDIVTPKADEVIT |
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| s: Staphylococcus aureu o3-Oct-1995 #sequence_r ion: A56976 , T.M.; Eaton, D.M.; Jol riol. 175, 4436-4447, 11 DNA sequence and units nce number: A36891; MUII ion: A56976 : preliminary le type: DNA es: 1-700 <mor> references: GB:L11998; 1 cs: treI amily: DNA topoisomeras: amily: DNA topoisomeras: 101; Conservative 388 VFEEKGISRYVFAKDLR; 96 IFKENKIDEVIIATD-P, 96 IFKENKIDEVIIATD-P, 155 LPKEKTYGFYKEGRARE; 155 LPKEKTYGFYKEGRARE; 199</mor>  | Db 718 DMTADEVSLGDKQTSYLTGAFTGSLIGSDGTKSYAIYDLKKPLFDTLNGAT 768  Qy 719 VPQVETEKVEAQLKEAEVLLAKVTDSSLKANATETLAGLRNNLTLQIMDNNS 770    :: | 370 DSNSSLVSQLV                  |

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R;Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.; M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; Vanaken, S.E.; Umayam, L.; Tallon, L. euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J. Nature 402, 761-768, 1999
A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A;Reference number: A84420; MUID:20083487; PMID:10617197
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A;Residues: 1-1269 <STO>
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;Map position: 2
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Similarity 18.4%;
                                                                                                                                                                                       ----NTSRTNWVPSVSNPGTTNTNTSNNSNTNSQASQSNDIDSLLKQLYKLPLSQRHVES 286
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                                                                           ESQKALEFSELLKSTKESAK--
                                                                                                                                                     GIELESSRKKLI-----SASHADS
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                                   DSRPEQPSPQPTPEPSPGPQPA------PNLKIDSNSSLVSQLVRKVGEGYV
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EKMSENEKVEAALKSSAGELAAVQEELALSKSRLLETEQKVSSTEALIDELTQELEQKKA
                                                                                                               D---GLVF-DPAQITSRTARGVAVPHGDHYHFIPYSQMSELEERIARIIPLRYRSNHWVP
                                                                                                                                                                                                                                                                   IEDT----GDAYIVPHGDHYHYIPKNELSASELAAAEAFLSGRGNLSNSRTYRRQNSD--
                                                                                                                                                                                                                                                                                                         EQKEVIERSSSGSQRELHESQEKAKELELELERVAGELKRYESENTHLKDE--LLSAKEK
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    %; Score 147; DB 2; Length 1269;
    %; Pred. No. 4.4;
    121; Mismatches 293; Indels 294;

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                                                                         EMEEKMASL - - - - QQEIKELN
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                                                                                                                                                                                                                                                                                           A;Gene: CESP:F29G6.3a
A;Map position: X
A;Introns: 10/1; 43/3; 61/3; 88/3; 110/3; 144/2; 183/3; 218/3; 252/3;
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T21559
                                                                                                                                                                                                                                                                                                                                                                                                                     A;Reference number: Z19441
A;Accession: T21559
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: T-1929 WILL
A;Residues: T-1929 WILL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         hypothetical protein F29G6.3a - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Datc: 15-Oct-1999 #sequence_revision 15-Oct-1999 #te
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LKVVHPEHHYVPLVRKTTEDHQQKVNHEHHFIPAEKKTEA-
                                     -DAAHADN----
                                                                                                                                                     IAQSPQVQTIDYFKEINRAHHFVPSTPPSLFNNKRESFHHHSFIPNSLEAERKSRSVERA 720
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                                                                                                               HYYNGKVPYDAIISEELLMKDPNYKLKDE-DIVNEVKGGYVIKVDGKYYVYLK-----
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17.6%; Pred. No. 8;
tive 125; Mismatches
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                                 VRTKEEINROKOEHSOHREGGTPRNDGAVALARSOGRYTTDDGYIFN 172
                                                                         -LPDSPANVKDQRKIIRE--
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immunoglobulin Al proteinase [imported] - Streptococcus pneumoniae (strain ?C.)Species: Streptococcus pneumoniae C.)Species: Streptococcus pneumoniae C.)Date: 03-Aug-201 #sequence_revision 03-Aug-2001 #text_change 14-Sep-2001 C;Accession: F95133

R.Tettelin, H.; Nelson, K.E.; Paulsen, I.T.; Eisen, J.A.; Read, T.D.; Peters on, J.D.; Umayam, L.A.; White, O.; Salzberg, S.L.; Lewis, M.R.; Radune, D.; nson, T.; Hickey, B.K.; Holt, I.E. Science 293, 498-506, 2001

A;Authors: Loftus, B.J.; Yang, F.; Smith, H.O.; Venter, J.C.; Dougherty, B.J. A;Title: Complete Genome Sequence of a virulent isolate of Streptococcus pne A;Reference number: A95000; MUID:21357209; PMID:11463916
                                                            A; Molecule type: DNA
A; Residues: 1-2004 «KUR»
A; Cross-references: GB: AE005672; PIDN: AAK75263.
A; Experimental source: strain TIGR4
                 A;Gene: SP1154
C;Superfamily:
                                                 A; Experimental C; Genetics:
                                                                                                                                           A;Reference number: A95000;
A;Accession: F95133
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RLPSEHNYIPIAIHDDSHQKVDLTNHQYLPPIVNA-----EQKEAVKLYEHQYVPLPP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          QPTPEPSPGP---QPAPNLKID-SNSSLVSQLVRKVGEGYVFEEKGISRYVFAKDLP---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ---QITSRTARGVAVPHGDHYHFIPYSQMSELEERIARIIPLRYRSNHWVPDSRPEQPSP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SDKEPISRHHNFVPLATKTVEETRHSND----LSHHHYMPLPAKREEGKTAAGDKVGYEH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  KSFDTGRSHSYIPLGGNVEQSKTEIFRQHNFVPVVDKKEKNVEEINQKHNYVPAHSNVAV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EAFLSGR-----GNLSNSRT--YRRQN------SDNTSRTNWVPSVSNPGT
                                                                                                                                                                                                                                                                                                                                                                                                                      PEVPQVETEKVEAQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     --VEHPDERPHS-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LDRQHGYIPVAAKHEAKKNVLYEH--QYIPPITRTEQTNGYDRRHNY----VPVGKTA-K 1184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FQALDKLLERLNDESTNKEKLVDDLLAFLAPITHPERLGKPNSQIEYTEDEVRIAQLADK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  KKDSFANYSSKAPQLPREHHYYPAPVRSVEHHQKHVHEQ-HNYIPAVH-----HHETNHQ
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                 Streptococcus
                   sanguis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -----NGY-----
                   IgA-specific
                                                                              .1;
                 metalloendopeptidase
                                                                            PID:g14972632;
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                                                                                                                                                                                                                                T.D.; Peterson, S.; Hei
Radune, D.; Holtzapple,
                                                                              GSPDB:GN00164;
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                                                                                                                                                                      B.A.; Morr:
pneumoniae
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                                                                                                                                                                                        Morrison
                                                                              TIGR:SP
hypothetical protein YOR195w - yeast (Saccharomyces W,Alternate names: hypothetical protein O4806 C;Species: Saccharomyces cerevisiae C;Date: 12-Jul-1996 #sequence_revision 12-Jul-1996;Accession: S67087 R;Hughes, B.; Pohl, T.M.
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Best Local Sim
Matches 173;
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19.7%;
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GTP--RNDGAVALARSQ------GRYTTDDGYIFNASDIIEDTGDAYIVPHGDHYHY
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LPFYNKATIVKYGNLVNENSLLYQKELLSAVMMKDN
                                                                                                          GTMLDASQIASKKAEINPLILPTVEPLSTSGK-KDSD--FSKVAYYQAKRNLTYKNIEKL
                                                                                                                                                              NFKADEEPVEETPAEPE----VPQVETEKVEAQLKEAEVLLAKVTDSSLKANAT---
                                                                                                                                                                                                                        VK--DTFSSKANRVYNV----TL--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     KKPLFENLSGATVEKLSLKNVAISGKDDIGSLANEAQNNTKIKQVHVDGVLA-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   QNPSGTYHLAASLNANEV---ELGPDERSYIKDTFTGRL--IGEKDGKNY-AIYNL----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             KDPNYKLKDEDIVNEVKGGYVIKVDGKYYVYLKDAAHADNVRTKEEINRQKQEHSQHREG
                                                   AGLRNNLTL----QIMDNNSIMAEAEKLLALLKGSN
                                                                                                                                                                                                                                                                         FAWFDDHTYKAPNGYTLEDLFATIKYYVEHPDERPHSNDGWGNASEHVLGKKDHSEDPNK 701
                                                                                                                                                                                                                                                                                                                                                                                   ----SAAAIYNRVKGEKRIPLVRLPYMVEHT------VEVKNGNLIIPHKDHYHNIK 641
                                                                                                                                                                                                                                                                                                                                                                                                                                          VGHLTGDKALLTKSKATVAISSNTNTSDQTVGGLAGLVDRDAQIQDSYAEGDINNVKHFG
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5; Mismatches
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1206
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#text\_change 19-Apr-2002

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submitted to the Protein Sequence Database, July 1996
A;Reference number: S66685
A;Accession: S67087
A;Molecule type: DNA
A;Residues: 1-821 <HUG>
A;Cross-references: EMBL:Z75103; NID:g1420464; PID:e252389; PID:g1420465; GSPDB:GN00015;
A;Kyperimental source: strain S288C
C;Genetics:
RESULT 50
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kinesin-related protein cut7 - fission yeast (Schiz kinesin-related protein cut7 - fission yeast (Schiz c; Species: Schizosaccharomyces pombe C; Date: 13-Uan-1995 #sequence_revision 13-Jan-1995 C; Accession: S14032
R;Hagan, I.; Yanagida, M.
Nature 347, 563-566, 1990
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Cross-references: SGD:S0005721
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                                                                                                                                       QKFEKTSLELESLQLKNSNIQAEHIKELENLHENLISLQNELKISSDRI
                                                                                                                                                                                             KWWQSKYETVEDEAKIRNAEVTELNGDIEDLKESKLHLEETITELENKVHKLENECELEK
                                                                                                                                                                                                                       ----PQVETEKVEAQLKEAEV--LLAKVTD-SSLKANATETLAGLRNNL------
                                                                                                                                                                                                                                                  NNLQQKMDDLNNLNDDNLKVVQDKLIKNEETLKLKEAEIDSLNSEMDELKKQITSKDDEF
                                                                                                                                                                                                                                                                          DERPHSNDGWGNASEHVLG-------KKDHSEDPNKNFKADEEPVEETPAEPEV
                                                                                                                                                                                                                                                                                                       LNDKIEST-----DIVLKSKENELDNLKLSL--KETLSISKDFNDSDLIGQINELISTK
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  - ADILHSHLNDTNSNIRKANEIMNNRSEEFLRNAASQAEIVGANKERIQKTVE - -
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A;Title: Novel potential mitotic motor protein encoded by the A;Reference number: S14032; MUID:91015362; PMID:2145514
A;Accession: S14032
A;Molecule type: DNA
A;Residues: 1-1073 <HAG>A;Cross-references: EMBL:X57513
A;Note: the authors translated the codon GCC for residue 2 as C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A,Description: probably involved in mitotic spindle body duplication (C,Superfamily: unassigned kinesin-related proteins; kinesin motor domain homology C,Keywords: ATP; microtubule binding; mitosis; nucleotide binding; P-loop F,61-415/Domain: kinesin motor domain homology <RWOT> F;147-154/Region: nucleotide-binding motif A (P-loop) F;153/Binding site: ATP (Lys) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         23 GKQATQKTENLTPDEVSKREGINAE-----QIVIKI--TDQGYVTSHGDHYHYYN
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                                                         VKTCTTSLNDADII-LSDYISDQKSKFESKQQDLIANIGKIVSNFLQEQNESLYTK----
                                                                                                                                                                   MSSQKLGNGISSELIELQKDMKESYRQLVQELRSLYNLQHTHEESQKELMYGVRNDIDAL
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                                                                                                                                                                                                                                                                             QLLISMTKITEHFQSLDEALQSARSSCAVPNSSLDLIVSELKDSKNSLLDALEHSLQDIS
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LPPSPDADVKANPTGDSAAAI--YNRVKGEKRIPLVR------LPYMVEHTVEVK
                                                                                                               ADKYTTS--DGYIFDEHDIISDEGDAYVTPHMGHSHWIGKDSLSDKEKVAAQAYTKEKGI
                                                                                                                                                                                                                       -HPERLGKPNS-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Saccharomyces cerevisiae.";
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Sasanuma S.-I., Sasanuma M., Tsuchiya Y.,
Yamazaki M., Tashiro H., Eki T.,
"Analysis of the nucleotide sequence of ch
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN-S288c
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01-NOV-1995 (Rel. 32, Last amotation update)
Hypothetical 137.7 kDa protein in UGS1-FAB1 i
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MEDLINE=95400292; PubMed=7670463;
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KDNLVLEDEAEAPTQENKPTEVVGEIDIPDAPRDD-----VEIVEAVEKNIIPEDLEVAK
                    --HWVPDSRPEQPSPQPTPEPSPGPQPAPNLKIDSNSSLVSQLVRKVGEGYVFEEKGISR
                                            QEAVRNNEVSGTEEESTSKGEEIMGGD
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1233 AA; 137697
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Pred. No. 0.12;
2; Mismatches 402;
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                                             KANATETLAGL-----RNNLTLQIMDNNSIMAEAEKLLALLKGSNPSSVSKEKIN
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APX XENLA Q01613; 01-JUN-1994 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial participates in amiloride-sensitive sodium channel a J. Cell Biol. 119:1497-1506(1992)

-i- FUNCTION: IS PART OF A MULTIMERIC COMPLEX WHICH AMILORIDE-SENSITIVE SODIUM CHANNEL ACTIVITY.

-i- SUBCELLULAR LOCATION: Membrane-associated Complex PROXIMAL INTESTINE, STON TISSUE SPECIFICITY: KIDNEY, PROXIMAL INTESTINE, STON TO A LESSER EXTENT IN THE DISTAL INTESTINE, STON TO A LESSER EXTENT IN THE DISTAL INTESTINE, STON TO A LESSER EXTENT IN THE DISTAL INTESTINE, STON TO A LESSER EXTENT IN THE DISTAL INTESTINE, STON TO A LESSER EXTENT IN THE DISTAL INTESTINE, STON TO A LESSER EXTENT IN THE DISTAL INTESTINE. Staub O., Verrey F., Kleyman T.R., Kraehenbuhl J.-P.; 01-JUN-1994 (Rel. 29, Creat 01-JUN-1994 (Rel. 29, Last 15-JUL-1998 (Rel. 36, Last Xenopus laevis (African clawed frog). Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae; -!- SIMILARITY: SOME, "Primary structure of an apical protein from Xenopus SEQUENCE FROM N.A. NCBI\_TaxID=8355 Xenopodinae; Apical protein (APX). Xenopus STANDARD; TO HUMAN APXL. Created) sequence update) annotation updat Benos D.J., 1420 update) ₿ Rossier B. STOMACH us laevis that activity."; OOCYTES, SI INVOLVED . . EYE. Ä

CAA78718.1;

(See http://www.isb-sib.ch/announce/

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LKGSNPSSVSK 792
                              RSAGASSSYDATVTWNDRFGKTSPLGRSAAEKTAGVQRK---TFSDQRTLDGSQEH----
                                                                                          QHNALVQYMERKTNQRPNSN----PQVQMERTSLGLPNYNEWSIYSSETSSSDASQKYLRR
                                                                                                                                                    HLGIOKSNFAWKEEPTFANRREMSDSDISANRIKYLE-SKERTNSS---SNLSKTELKOI
                                                                                                                                                                                  H--YHNIKFAWFDDHTYKAPNGYTLEDLFATIKYYVEHPDERPHSNDGWGNASEHVLGKK
                                                                                                                                                                                                                  SAYLQTKNSADSSYKKDDTEKVAVTRIGGRKRI-----
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01-FEB-1995 (Rel. 31, Last sequence update)
28-FEB-2093 (Rel. 41, Last annotation update)
Ubiquitin carboxyl-terminal hydrolase 8 (EC 3.1.2.15) (Ubiquitin thiolesterase 8) (Ubiquitin specific processing protease 8)
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-!- CATALTYIC ACTIVITY: Ubiquitin C-terminal ubiquitin + a thiol.
-!- SIMILARITY: Belongs to peptidase family (-!- SIMILARITY: Contains 1 rhodanese domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Nomura N., Nagase T., Miyajima N., Sazuka T., Tanaka A., Seki N., Kawarabayasi Y., Ishikawa K.-I., Tabata S., "Prediction of the coding sequences of unidentified human The coding sequences of 40 new genes (KIAA0041-KIAA080) analysis of cDNA clones from human cell line KG-1.";
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Homo sapiens (Hu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pfam; PF00581; Rhodanese; 1. Pfam; PF00443; UCH; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MIM; 603.58; -.
GO:0004197; F:cysteine-type endopeptidase
GO; GO:0004843; F:ubiquitin-specific protease
GO; GO:0008283; P:cell proliferation; TAS.
GO: GO:0007048; P:oncogenesis; TAS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEROPS; C19.011; -.
Genew; HGNC:12631; USP8.
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MEDLINE=96051398; PubMed=7584044;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SMART; SM00450; RHOD; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR001763; Rhodanese-like
InterPro; IPR001394; UCH-2.
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11
                                                                                                                                                                                                                                                                                3; PS00972; UCH 2_1; 1.

3; PS00973; UCH 2_2; 1.

3; PS50235; UCH 2_3; 1.

1) ugation pathway; Hydr

195

313

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                                                                                                                              Similarity
                                             LYQARTVKENNRVSYIDGKQATQKTENLTPDEVSKREGINAEQIVIKITDQGYVTSHGDH 65
                                                                                                                                                                                                                                                                                                                                                                                                                                          PS50206; RHODANESE
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19.0%;
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                                                                                                                                                                                                                                                                                                                                   Hydrolase; Thiol protease; Multigene family.
                                                                                                   143;
                                                                                                                                                                                               RHODANESE.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
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-KTE-VKPEKISTKSYVHSALKIFKTAEECRLDR--DE
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16-OCT-2001 (Rel. 40, Lass
16-OCT-2001 (Rel. 40) Lass
DNAJ-like protein MG200 h
MPNI19 OR MP035.
MYCOPOLASMA pneumoniae.
Bacteria; Firmicutes; Moll
NCBI_TaxID=2104;
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                                                                                                                                                                                                                                                          MYPPEMAPSSAPPSTPPTHKAKPQIPAERD---REPSKLKRSYSSPDITQAIQEEEKRKPT
                                                                                                                                                                                                                                                                                                                                                                        PSPDADVKA-----NPTGDSAAAIYNRVKGEKRIPLVRLPYMVEHTVEVKNGNL----
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                                                                                                                                                                  803
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                                                                                  Created)
              Mollicutes; Mycoplasmataceae; Mycoplasma
                                                homolog.
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Matches 161;
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SMART; SM00271; Dnau; 1.

PROSITE; PS00636; DNAJ 2; 1.

PROSITE; PS50076; DNAJ 2; 1.

Chaperone; Complete proteome.

J-DOMAIN.

TARNBERT COMPAIN.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pfam; PF00226; DnaJ;
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SEQUENCE FROM
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                                             LLAFL-----APITHPERLGKPNSQI-----EYTEDEVRIAQLA----
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FSSFVLSDQNPNPQTPTHHEEDAAAPEPTVDETSGESTAPEVTIAESTVELETAAEINNP
                                                                                                                                                                                                                                                         DSNSSLVSQLVRKVGEGYVFEEKGISRYVFAKDLPSETVKNLESKLSKQESVSHTLTAKK 429
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                                                                                                                                                ENVAPRDQEFYDKAYNLLTE--AHKALFXNKGRNSDFQALDKLLERLNDESTNKEKLVDD
                                                                                                                                                                                                      TTSAVEMDASVK----ADVSDEADATNEPTEQDTISEPEQ--ETDAAALEEINHT-TADL
                                                                                                                                                                                                                                                                                                                                                               IPLRYRSNHWVPDSRPE-----QPSPQPTP-----EPSPGP-----QPAPNLKI 369
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C 29342 / M129;
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R., Hilbert H., Plagens H.,
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Pred. No. 0.43;
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                                                                       Query Match
Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                          Pubmed = 2.00..., Pubmed = 2.00..., Lincoln Pubmed = 2.00..., Churcher C.M., Badcock K., Brown D., Charles S., Hamlin N., Hunt S., Connor R., Dedman K., Devlin K., Gentles S., Hamlin N., Hunt S., Jagels K., Lye G., Moule S., Odell C., Pearson D., Rajandream M.A. Rice P., Skelton J., Walsh S., Whitehead S., Barrell B.G.; "The nucleotide sequence of Saccharomyces cerevisiae chromosome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              YM67 YEAST STANDARD; PRT; 1658 AA. Q03661; Q04988; Q0. NOV-1997 (Rel. 35, Created) Q1-NOV-1997 (Rel. 35, Last sequence update) 15-SEP-2003 (Rel. 42, Last annotation update) Hypothetical 187.1 kDa protein in GUA1-ERG8 in YMR219W OR YM8261.13 OR YM9959, Q1.
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                                                                                                                                               EMBL; Z49809; CAA89934.1; -.
EMBL; Z49939; CAA90190.1; -.
PIR; S55101; S55101.
SGD; S0004832; ESC1.
GO; GO:0005634; C:nucleus; IDA.
GO; GO:0006548; P:chromatin silencing at telomere;
                                                                                                                       Hypothetical SEQUENCE 1
                                                                                                                                                                                                                                                                          entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email.to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through a collab between the Swiss Institute of Bioinformatics and the EMBL outst the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for com
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN=S288c / AB972;
PubMed=9169872;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                             Nature 387:90-93(1997).
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RESULT 6
SC16 YEAST STANDARD; PRT; 2195
ID SC16 YEAST STANDARD; PRT; 2195
AC P46415; Q02822;
DT 01-FEB-1996 (Rel. 33, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence upda
DT 28-FEB-2003 (Rel. 41, Last annotation up
DE Multidomain vesicle coat protein.
GN SEC16 OR YPL085W OR LPF1W.
OS Saccharomyces cerevisiae (Baker's yeast)
OC Eukaryota; Fungi; Ascomycota; Saccharomy
OC Saccharomycetales; Saccharomycetaceae; S
OX NCBI TaxID=4932;
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Saccharomycetales; Saccharomycetaceae; Saccharomyces.
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EMBL; U41849; AAB68254.1; -.
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                                                                                               KKASRYKPIIEE---EAGMRQEQVHFTNTT
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Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
Adams M.D., Celniker S.E., Holt R.A., Hoskins R.A., Galle R.F.,
George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MAPX DROME STANDARD; PRT; 1185 AA. P232Z6; Q9V9S1; 01-NOV-1991 (Rel. 20, Created) 01-MAR-1992 (Rel. 21, Last sequence update) 15-SEP-2003 (Rel. 42, Last annotation update) 205 kDa microtubule-associated protein.
                                                                                                                                                                                                                                                                                           MEDIINE=91115949; PubMed=1703540; Irminger-Finger I., Laymon R.A., ("Analysis of the primary sequence the Drosophila 205K MAP.";
                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Arthropoda; Hexapoda; Inso
Neoptera; Endopterygota; Diptera; Brachycera;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                MEDLINE=20196006; PubMed=10731132;
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Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W., RA Fosler C., Gabrielian A.E., Gary N.S., Gelbart W.M., Glasser K., RA Glodek A., Gong F., Gorrell J.H., Gu Z., Gunn P., Harris M., RA Glodek A., Gong F., Gorrell J.H., Gu Z., Gunn P., Harris M., RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J., RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C., RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C., RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A., RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A., Li J., Li Z., Liang Y., Lin X., RA Liu X., Mattei B., McIntosh T.C., McLeodd M.P., McPherson D., RA Lisko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X., RA Lisko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X., RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A., Na Melson K., Nusoka M.P., McPherson D.L., RA Meison D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M., RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G., RA Reinett K., Remington K., Saunders R.D.C., Scheeler F., Shen H., Spier E., Spradling A.C., Stapleton M., Skupski M.P., Smith T., RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T., RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T., RA Shue B.C., Siden-Kiamos I., Weinstock G.M., Weissenbach J., Wang X., Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J., Vang S., Yao Q.A., Shue B.C., Scheeler F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L., RA Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J., Zhan M., Zhang G., Zhao Q., Zheng L., RA Wang Z.-Y., Zhong F.N., Zhong W., Zhou X., Smith H.O., RA Wang Z.-Y., Rabin G.M., Weinstock G.M., Weissenbach J., Ra Wang Z.-Y., Shue Y., Shuh M., Shuh M., Zhang G., Zhao Q., Zheng L., Ra Wang Z.-Y., Shuh M., Shuh
Query Match
Best Local Sim
Matches 163;
                                                                                                                        SEQUENCE
                                                                                                                                                                                                                                           VARSPLIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; AE003780;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; X54061; CAA37996.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              use by non-profit institutions as long as modified and this statement is not removed. It entitles requires a license agreement (See htt or send an email to license@isb-sib.ch).
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Durbin K.J., Evangelista C.C., Ferraz C.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FlyBase;
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                                                                                                                                                                                                                                                                                                                                                                                AE003780; AAF5, Map205.

Base; FBgn0002645; Map205.

GO:0005875; C:microtubule associated complex; ID/
GO:0005875; Alternative splicing; Phosphorylation.

ASP/GIU-RICH (ACIDIC).
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A REGULATORY ROLE. THE BASIC DOMAIN C
THAT MATCH KNOWN CONSENSUS SEQUENCES
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een the Swiss Institute of Bioinformatics and the EMBL outst
European Bioinformatics Institute. There are no restrictions
by non-profit institutions as long as its content is in
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ISOIDEP23226-3; Sequence=VSP_004319;
ISOIDEP23226-3; Sequence=VSP_004319;
ISOELLANEOUS: PHOSPHORYLATION OF VARIOUS SERINE RESIDUES MAY PLAY
ISCELLANEOUS: PHOSPHORYLATION OF VARIOUS NUMEROUS SEQUENCES
REGULATORY ROLE. THE BASIC DOMAIN CONTAINS NUMEROUS SEQUENCES
OF SEVERAL DIFFERENT PROTEIN
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                                  Similarity
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8%; Score 156.5; D
1%; Pred. No. 0.66;
111; Mismatches
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D -> N (in isofor
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(in isoform
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(See http://www.isb-sib.
                                                                                                                                                    n isoform C2)
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      304;
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                                 NNSIMAEAEKLLALLKGSNP-SSVSKEKI
                                                                                                    KVEA-----QLKEAEVLLAKVTDSS----LKANATETLAGLRNNLTLQIMD------
                                                                                                                                      RVASEQNDE---ENAVFESVSGYETQNFDEISSPPEGINPFAQPF--TPAHLVIEQANTM
                                                                                                                                                                                                         TAEKHLVEDTKELVEEYTLDP-ESHFFGVV-----SSQAPLQLFGKHTLPSIIHSCKH
                                                                                                                                                                                                                                          ---PYMVEHTVEVKNGNLIIPHKDHYHNIKFAWFDDHTYKAP----NGYTLEDLFATIKY
                                                                                                                                                                                                                                                                            QMQL-PAECSDIFADQSLLLDTSAP--
                                                                                                                                                                                                                                                                                                             KGILPPSPDADVKANPT--GDSAAAIYNRVKGEKRIPLVRL---
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                                                                   MEDVGGMPIPASEDFAICDKVASKSSNEVEDHRSEQQAFVKEELLHPVGDVVAQVENLGT
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RESULT
ANK2_HU
 RRACOCOSCIDATO
                                                                             ANK2_HUMAN STANDARD; pj
Q01484; Q01485;
01-APR-1993 (Rel. 25, Created)
01-OCT-1996 (Rel. 34, Last seque
28-FEB-2003 (Rel. 41, Last annotation)
Ankyrin 2 (Brain ankyrin) (Anky
                                                                                                                                                      HUMAN
                                                                       ANK2
SEQUENCE FROM N.A.
                                 Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                        Homo sapiens (Human)
(ISOFORMS
                                 Chordata;
Primates;
                                                                               Last sequence update)
Last annotation updat
rin) (Ankyrin B) (Anky
                                 Craniata; Vertebrata;
Catarrhini; Hominidae
2 AND
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                                                                                             update)
                                                                                                                                          ₿
                                   Hominidae;
                                                                                nonerythroid).
                                             Euteleostomi;
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PRINTS; PRO1415; ANKYRIN.
SMART; SM00248; ANK; 22.
SMART; SM00205; DEATH; 1.
SMART; SM00218; ZUS; 1.
PROSITE; PS50089; ANK REPE R
PROSITE; PS500297; ANK REP R
PROSITE; PS50017; DEATH DOM
                                                                                                                                                                                            3MBL; X56957; CAA40278.1; -.
2MBL; X56958; CAA40279.2; -.
EMBL; Z56634; CAB42644.1; -.
EMBL; M37123; AAA62828.1; -.
PIR; S37431; S37431.
                                                                                 InterPro; IPR000488; Death.
InterPro; IPR000906; ZUS.
Pfam; PF0023; ank; 23.
Pfam; PF00531; death; 1.
Pfam; PF00791; ZUS; 1.
                                                                                                                                                                                                                                                                                                                                          This
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE OF 463-495 FROM N.A.

MEDLINE=92009921; PubMed=1833308;

TSE M.T., Menninger J.C., Yang-Reng T.L.

Lux S.E., Ward D.C., Forget B.G.;

"Isolation and chromosomal localization ankyrin gene.";
                                                                                                                                                            MIM; 106410;
                                                                                                                                                                       Genew; HGNC:493; ANK2.
                                                                                                                                                                                     HSSP; P42771;
                                                                                                                                                                                                                                                                      or send an email to license@isb-sib.ch)
                                                                                                                                                                                                                                                                                  entities requires a
                                                                                                                                                                                                                                                                                              modified
                                                                                                                                                                                                                                                                                                          use
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Submitted
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MEDLINE=91302466;
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                                                                                                                                                                                                                                                                                                                                                                                                                                          TISSUE SPECIFICITY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Event=Alternative splicing; Named isoforms=3;
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                                                                                                                                                                                                                                                                                                                              SWISS-PROT entry is copyright. It is produced through a collaboration een the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            W., Kordeli E., Bennett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IsoId=Q01484-2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     [soId=Q01484-1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        soId=Q01484-3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Kunimoto M., McLaughlin T., Bennett V.; ion and characterization of cDNAs encoding s reveal a family of alternatively spliced Biol. 114:241-253(1991).
                                                                                                                                                                                                                                                                                                                                                                                                    EACH PHOSPHORYLATION EVENT REGULAT
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                                                                                                                                                                                                                                                                                                                    Bioinformatics Institute.
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ANK_REP_REGION;
DEATH_DOMAIN; 1.
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                                                        HYYNGKVPYDAIISEELLMKDPNYKLKDEDIVNEVKGGYVIKVDGKYYVYLKDAAHADNV
                                                                     FEARVKEEEQK---IFGLMVDRQSQGTTPDTTPARTP---
           DTGDAYIVPHGDHYHYIPKNELSASELAAAEAFLSGRGNLSNSRTYRRQNSDN-----
                                 RTKEEINRQKQEHS---QHREGGT----
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Pred. No. 4.4
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QY -> HA (IN REF.
I -> Y (IN REF. 1)
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Q9TUZ3;
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16-OCT-2001
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                                                                                                                                                                                      Eukaryota; Metazoa; Ch
Mammalia; Eutheria; Ce
Bovidae; Bovinae; Bos.
NCBI_TaxID=9913;
                                                                                          JOVOV B., Ripoil P.J., Benos D.J.;
Submitted (AUG-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                        Hypothetical KIAA0373.
                                                                                                                                                                                                                                                                      Bos taurus (Bovine).
                                                                                                                                   TISSUE=Trachea;
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(Rel. 40, Last sequence update)
(Rel. 40, Last annotation updat)
1 protein KIAA0373.
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Cetartiodactyla; Ruminantia;
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Matches 171
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Similarity 18.5%; Pred. No. 1.2;
71; Conservative 124; Mismatches 329; Indels 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NQKEEVLKKYQHLLEKAREEQREIVKKHEEELHTLHRKLELQA---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IISMTSQKEANLNVQQIVDRHTKELKSQI--------EDL-NENILK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -LKQL--
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                     EKAEVERKLGRVRGSGRSGKTIPELEKTIGLMKKVVEKVQRENEQLKKASGILTSEKMAN
                                                          EKVEAQLKEAEV --
                                                                                              TSGIDSDDHYQREQELQRENLKLSSENIELKFQLEQANKDLPRLKNQVRDLKEMCEFLKK
                                                                                                                                 EHVLGKKDH----SEDPNKNFKADEEPVE----ETPAEPEVPQVET---
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                                                                                                                                                                                                         LIIPHKDHYHNIKFAWFDDHTYKAPNGYTLEDLFATIKYYVE--HPDERPHSNDGWGNAS
                                                                                                                                                                                                                                                LQRKLKTTGL------TVDQVMAA-RVLESEKELE
                                                                                                                                                                                                                                                                                    AQAYTKEKGILPPSPDADVKANPTGDSAAAIYNRVKGEKRIPLVRLPYMVEHTVEVKNGN
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COILED COIL (POTENTIAL).
MW; 03CBA02A64CF4139 CRC64;
                                                                                                                                                                      -LPRDSVIEDLHLQNKYLQEKLHALEKQLSKDAYSRPS
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                                                          -----LLAKVTDSSLKAN-----
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_Y373_HUT
O15078;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Nagase T., Ishikawa K.-I., Nakajima D., Ohira M., Seki N., miyajima N., Tanaka A., Kotani H., Nomura N., Ohara O.; "Prediction of the coding sequences of unidentified human The complete sequences of 100 new cDNA clones from brain with the complete sequences of 100 new cDNA clones from brain with the complete sequences of 100 new cDNA clones from brain with the code for large proteins in vitro.";
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Mammalia; Eutheria;
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IVKKHEEDLHILHHRLELQADSSLN-----KFKQTAW--DLMKQSPTPVPTNKHFIRLAE
                                   VAVPHGDHYHFIPYSQMSELEERIARIIPLRYRSNHWVPDSRPEQPSPQPT---
                                                                        KSHHTLKIAHQTIANMQA-RLNQKEEVLKKYQRLLEKAREEQ
                                                                                                              GTTNT-NTSNNSNTNSQASQSNDIDSLLKQLYKLPLSQRHVESDGLVFDPAQITSRTARG
                                                                                                                                                   ATCKSLEEKLKEKESALRLAEQNILSRDKVINE--LRLRLPATAEREKLIAELGRKEMEP
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                                                                                                                                                                                                                                                               QGRYTTDDGYIFNASDIIED-TGDAYIVPHGDHYHYIPKNEL-----
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                                                                                                                                                                                                                                                                                                                                                                                                                 QGYVTSHGDHYHYYNGKVPYDAIIS--EELL--MKDP-----NYKLKDEDI-VNEVKG
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LNENLL-KLKEALKTSKNRENSLTDNLNDLNNELOKKOKAYNKILREKEEIDOENDELKR
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NIEQENEKLKAELEKLKAHL
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                                                                                                                                                                                             SGIESDDHCQREQELQKENLKLSSENIELKFQLEQANKDLPRLKNQVRDLKEMCEFLKKE
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                                             ---- DNNSIMAEAEKLLALL
                                                                                             KAEVQRKLGHVRGSGRSGKTIPELEKTIGLMKKVVEKVQREN--EQLKKASGILTSEKMA 1224
                                                                                                                                             KVEAQLKEAEV----
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Tzermia M., Katsoulou C., Alexandraki D.;
"Sequence analysis of a 33.2 kb segment from the left arm chromosome XV reveals eight known genes and ten new open frames including homologues of ABC transporters, inositol phosphatases and human expressed sequence tags.";
Yeast 13:583-589(1997)
                                                                                                                                                                                                                                                                                                                                                                                                                Saccharomycetales;
NCBI_TaxID=4932;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
                     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                              MEDLINE=97321807; PubMed=9178509;
                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                   -!- SIMILARITY: BELONGS TO THE SINI FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (Rel. 40, Created)
(Rel. 40, Last sequence update)
(Rel. 40, Last annotation update)
l 131.4 kDa protein in REX4-ATP19
Bioinformatics Institute.
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EMBL; Z74819; CAA99088.1; -.
PIR; S66771; S66771; S66771; S66771; S60771; S60771; SGD; S0005438; YOLO78W.
GO; GO:0005737; C:cytoplasm; IPI.
GO; GO:0001558; P:regulation of cell growth;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                use by non-profit modified and this st entities requires a
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GYVIKVDGKYYVYLKDAAHADNVRTKEEINRQKQEHSQHREGGTPRNDGAVA---LARSQ
                             KVTDSSLKANATETLAGLRNNLTLQIMDNNSIMAEAEKL----LALLKGSNPSSVSKEK
                                                                     LGKNYILDLNDTVLRLDGINKVELISKKDARELHLEKMKPDLKKPVLPTIQSNDLTPLTL
                                                                                                                                                  NVNPKFNYTTISVLVT
                                                                                                                                                                                    N-----GYTLEDLFATIKYYVEHPDERPHSNDGWGNASEHVLGK--KDHSEDPN-----
                                                                                                                                                                                                                                                                                                       ---FGKLDRKSTIQSISDSEVVLCKVDDAEKSQNEIETPLPFETGGGLMDASTLDANSSH
                                                                                                                                                                                                                                                                                                                                         SHWIGK-----DSLSDKEKVAAQAYTKEKG---ILPPSP-----DAD-VKANPTG
                                                                                                                                                                                                                                                                                                                                                                                                                    ERLGKPNSQIEYTEDEVRIAQLAD-----KYTTSDGYIFDEHDIISDEGDAYVTPHMGH
                                                                                                                                                                                                                                                                                                                                                                                                                                                        DVLEYFSFVCGDKVPNYESMGLEIYIQASKKYKRNSFTTKVRKSSTIFEVIGFALFLYST
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SNLTSTRSPLLRGHGR-----
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EPLNSYLKADAGGAVAA----
                                                                                                                                                                                                                            DTTDGTINQLSFYK--PIIG----NEDDIDKTNGSKII-
                                                                                                                                                                                                                                                              DSAAAI YNRVKGEKRI PLVRLPYMVEHTVEVKNGNLI I PHKDHYHNI KFAWFDDHTYKAP
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Pred. No. 1.4;
18; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -LE-----RLNDEST--NKEKLVDDLLAFLAPITHP
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    IPENTKVTSKAKKISTKYKLGLAKQHSSSVASGS

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InterPro; IPR000299; Band_4.1.
InterPro; IPR000387; TYR_phosphatase.
InterPro; IPR000242; Tyr_pp.
Pfam; PF00373; Band_41; I.
Pfam; PF00102; Y_phosphatase; 1.
PFINTS; PR00935; BAND41.
PRINTS; PR00935; BAND41.
SMART; SM00295; B41; I.
SMART; SM00294; PTPC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PTNL RAT STANDARD; PRT; 1175 AA. 062728; 062732; 01-NOV-1997 (Rel. 35, Created) 01-NOV-1997 (Rel. 35, Last sequence update) 28-FEB-2003 (Rel. 41, Last annotation update) Protein tyrosine phosphatase, non-receptor tyrosine phosphatase
DOMAIN
DOMAIN
ACT_SITE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN-Sprague-Dawley;

MEDLINE-95.104449; PubMed=7805871;

L'Abbe D., Banville D., Tong Y., Stocco R.,

Fantus G., Shen S.H.;

"Identification of a novel protein tyrosine homology to the cytoskeletal proteins of the FEBS Lett. 356:351-356(1994).
                                        PROSITE; PS00660; FERM 1; 1.

PROSITE; PS00661; FERM 2; 1.

PROSITE; PS00067; FERM 3; 1.

PROSITE; PS00383; TYR_PHOSPHATASE 1; 1.

PROSITE; PS00383; TYR_PHOSPHATASE_PTP; 1.

PROSITE; PS50056; TYR_PHOSPHATASE_2; 1.

Structural protein; Cytoskeleton; Hydrolase; Alternative splicing.
                                                                                                                                                                                                                                                                                       EMBL; U17971; AAA62153.1; -.
EMBL; U18293; AAA62154.1; -.
PIR; S51005; S51005.
                                                                                                                                                                                                                                                                                                                                               use by non-profit institutions as long as its content modified and this statement is not removed. Usage by an entities requires a license agreement (See http://www.isborsend an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EN the European Bioinformatics Institute. There are no resti
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ISOId=Q62728-2; Sequence-VSP 000498;
-i- TISSUE SPECIFICITY: PARTICULARLY ABUNDANTLY IN ADRENAL-
-i- SIMILARITY: CONTAINS 1 FERM domain.
-i- SIMILARITY: BELONGS TO THE NON-RECEPTOR CLASS OF THE PR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (Protein-tyrosine phosphatase PTPN21 OR PTP2E.

    -!- CATALYTIC ACTIVITY: Protein tyrosine phosphate
tyrosine + phosphate.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ALTERNATIVE PRODUCTS: Event=Alternative splicing; Named isoforms=2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYROSINE PHOSPHATASE FAMILY.
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  PROTEIN-TYROSINE BY SIMILARITY.
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Sciurognathi;
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Q00798;
Q1-APR-1993
01-APR-1993
01-OCT-1996
SEQUENCE FROM N.A.
MEDLINE=92315338; PubMed=1617731;
Galinski M.R., Medina C.C., Ingra
                                                                                          Plasmodium vivax (str
Eukaryota; Alveolata;
NCBI_TaxID=31273;
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                                                                                                                                                                                                                     25, Created)
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Pred. No. 1.5;
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  Barnwell
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                                                                                                                           Plasmodium
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HUMAN RETICULOCYTE C
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    -!- SUBCELLULAR LOCATION: Membrane-bound.

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               RA WOOD V., Gwilliam R., Rajandream M.A., Lyne M., Lyne R., Stewart A.,
RA Sgouros J., Peat N., Hayles J., Baker S., Basham D., Bowman S.,
RA Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M.,
RA Gollins M., Connor R., Cronin A., Davis P., Felwell T., Fraser A.,
RA Gontles S., Goble A., Hamiin N., Harris D., Hidalgo J., Hodgson G.,
RA Gentles S., Goble A., Hamiin N., Harris D., Hidalgo J., Hodgson G.,
RA Gontles S., Goble A., Hamiin N., Harris D., Hidalgo J., Hodgson G.,
RA Gontles S., Jones M., Leather S., McDonald S., McLean J.,
RA Mooney P., Moule S., Mungall K., Murphy L., Niblett D., Odell C.,
RA James K., Jones M., Leather S., McDonald S., McLean J.,
RA Mooney P., Moule S., Mungall K., Murphy L., Niblett D., Odell C.,
RA RA Rutherford K., Rutter S., Saunders D., Seeger K., Sharp S.,
RA Rutherford K., Rutter S., Saunders D., Seeger K., Sharp S.,
RA Rutherford K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S.,
RA Woodward J., Volckaert G., Aert R., Robben J., Grymonprez B.,
RA Woltyens I., Vanstreels E., Rieger M., Schaefer M., Mueller-Auer S.,
RA Weltjens I., Vanstreels E., Rieger M., Schaefer M., Mueller-Auer S.,
RA Gabel C., Fuchs M., Fritzc C., Holzer E., Moestl D., Hilbert H.,
RA Borzym K., Langer I., Beck A., Lehrach H., Reinhardt R., Pohl T.M.,
RA Goffeau A., Cadieu E., Dreano S., Gloux S., Lelaure V., Mottier S.,
RA Galibert F., Aves S.C., Xiang Z., Hunt C., Moore K., Hurst S.M.,
RA Lucas M., Rochet M., Gaillardin C., Tallada V.A., Garzon A., Thode G.,
RA Lucas M., Rochet M., Gaillardin C., Tallada V.A., Garzon A., Thode G.,
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Nature 347:563-566(1990)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Schizosaccharomyces pombe (Fission yeast).
Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
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CUT7 OR SPAC25G10.07C.
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(Rel. 41, Last annotation update)
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Sanchez M.,
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Best Local :
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PRINTS; PR00129; KISC; 1.

PROSITE; PS00411; KINESIN MOTOR DOMAIN1; 1.

PROSITE; PS50067; KINESIN MOTOR DOMAIN2; 1.

PROSITE; PS50067; KINESIN MOTOR DOMAIN2; 1.

MOTOR protein; Cell division; Microtubules; ATP-binding;

Motor protein; Cell division; Microtubules; ATP-binding;
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REPEAT
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GeneDB SPombe; SPAC25G10.07c; -.
InterPro; IPP001752; kinesin_motor.
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EMBL; Z70691; CAA94636.1; -.
EDIR; T38378; T38378.
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                                        MEDLINE-96367601; PubMed-8771715;
Garcia-Cantalejo J.M., Boskovic J., Jimenez A.;
"Sequence analysis of a 14.2 kb fragment of Sacc chromosome XIV that includes the ypt53, tRNALeu four new open reading frames.";
Yeast 12:599-608(1996).
-i- SIMILARITY: TO S.POMBE SPAC29E6.10C.
             This
                                                                                                                                                                                                         Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Sacci
Saccharomycetales; Saccharomycetaceae; Saccharomyces
                                                                                                                                                                                                                                                                   01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
01-OCT-1996 (Rel. 34, Last annotation update)
Hypothetical 141.5 kDa protein in YPT53-RHO2
                                                                                                                                                                 SEQUENCE FROM N.A
                                                                                                                                                                                                                                                         YNL091W OR N2231.
                                                                                                                                                                                           _TaxID=4932;
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SWISS-PROT entry is copyright. It is produced through a sen the Swiss Institute of Bioinformatics and the EMBL
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Saccharomyces cerevisiae
VALeu and gsr m2 genes and
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Best Local
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SGD; S0005035; YNL091W.
GO; GO:0009651; P:salinity response;
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NRL---
                           NSIMAEAEKLLALLKGSNPSSVSKEK
                                                     EGDDEEDTYDSGLDETDRLEEGRKLIQIAITKLLQSRIMASYHEKQA
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                                                                                                            -HPHHHYHST---STHSEDELSEEEYISDIELPHDPHKHFHRDDDILDGDEDEPEEEDEN
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                                                                                ETEKVEAQLKEAEVLLAKVTDSSLKANATETLAGLRNNLTLQIMDN
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RA RABA VILLAL
RA FABEY
RA FAB
RX MEDLINE=22388257; PubMed=12477932;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Klausner R.D., Collins F.S., Wagner L., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Stapleton M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Brownstein M.J., Usdin T.B., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Mahamson R.D., Mullahy S.J.,
RA RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SPECIFICITY, SUBSCILULAR LOCATION, PHOSPHORYLATION, IN
ARG-205; PRO-206; THR-207; SER-208; LEU-209; THR-266, M
THR-287, AND INTERACTION WITH MAPK8IP2; MAPK8; MAPK9;
AND MAP3K11.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=99455010; PubMed=10523642;
Ito M., Yoshioka K., Akechi M., Yamashita S.,
Sugiyama K., Hibi M., Nakabeppu Y., Shiba T.,
"JSAP1, a novel jun N-terminal protein kinase
that functions as a scaffold factor in the JNK
Mol. Cell. Biol. 19:7539-7548(1999).
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28-FEB-2003 (Rel. 41, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
15-SEP-2003 (Rel. 42, Last annotation update)
C-jun-amino-terminal kinase interacting protein 3 (JNK-interacting protein 3) (JIP-3) (JNK MAP kinase scaffold protein 3) (Mitogenactivated protein kinase 8-interacting protein 3) (JNK/SAPK-associated protein 1) (JSAPI) (Sunday driver 2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gindhart J.G., Goldstein L.S.B.;
"Kinesin-dependent axonal transport
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=20560743; PubMed=11106729; Bowman A.B., Kamal A., Ritchings B Gindhart J.G., Goldstein L.S.B.;
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28-FEB-2003
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Kelkar N., Gupta S., Dickens M., D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN=C57BL/6; TISSUE=Brain,
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Gene 255:229-234(2000).
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Makabeppu Y., Tadayoshi S., Yamamoto K.-I., Yoshioka K.;
"Isoforms of JSAP1 scaffold protein generated through alternative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN=C57BL/6; TISSUE=Brain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Interaction of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ito M., Akechi M., Hirose
Nakabeppu Y., Tadayoshi S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=20480689; PubMed=11024282;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TISSUE=Brain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MAPK8IP3 OR JSAP1 OR JIP3 OR SYD2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NTERACTION WITH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SSUE=Brain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 eraction of a mitogen-activated the neuronal protein JIP3."; Cell. Biol. 20:1030-1043(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                       protein.";
103:583-594(2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Q99KU7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FROM N.A.
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; Q9EQD8; Q9ESN7;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (ISOFORM 1A), FUNCTORAPK9; MAPK10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (ISOFORM 1C), SUBCELLULAR LOCATION,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (ISOFORMS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Chordata;
Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1A; 1B;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          and Heart;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Craniata; Vertebrata;
Sciurognathi; Muridae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           B.W.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Davis R.J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FUNCTION, PHOSPHORYLATION, APK10; MAP2K4 AND MAP3K1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             is mediated
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Philp
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A.V.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Takamatsu N.,
Yamamoto K.-I.;
(JNK)-binding pr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     signaling
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I, MUTAGENESIS
266; THR-276 AN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 McGrail M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     signaling module
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; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sunday
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AND INTERACTION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TISSUE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MAP2K7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Driver
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EMBL; EMBL; EMBL;

AB005662; BAA85874.1; AB043124; BAB16675.1; AB043125; BAB16676.1; AB043123; BAB16674.1; AB043129; BAB16685.1; AB043129; BAB16685.1; AB043126; BAB16685.1;

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"Cargo or Allessia accounts.";
associated signaling molecules.";
J. Cell Biol. 152:959-970(2001).
-!- FUNCTION: The JNK-interacting protein (JIP) group of scafiproteins selectively mediates JNK-signaling by aggregating specific components of the MAPK cascade to form a function specific components of the MAPK cascade to form a function signaling module. May function as a regulator of vesicle transport, through interactions with the JNK-signaling com and motor proteins
-!- SUBUNIT: Forms homo- or heterooligomeric complexes. The cascade of Mapk!
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Whiting M., Madan A., Young A..., Green E.D., Dickson Blakesley R.W., Touchman J.W., Green E.D., Dickson Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M. Butterfield Y.S.N., Krzywinski M.I., Skalska U., Sm. Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.; "Generation and initial analysis of more than 15,00 human and mouse cDNA sequences."; Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the El the European Bioinformatics Institute. There are no resti
                                                                                                                                                                                                                                                                                                                                                                                       -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Rapoport
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Verhey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=21135887; PubMed=11238452;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TISSUE=Brain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INTERACTION
                                                                                                                                                                                                                                                                         and kidney. All isotorms have been and lung. Mapk8ip3A is also expressed in the spleen and lung. INDUCTION. Expressed in neurities 5 days following initiation of nerve growth factor Ngf induced differentiation. Ngf withdrawal nerve growth.
                                                                                                                                                                                                                                                  mediated cleavage.
SIMILARITY: BELONGS
                                                                                                                                                                                                                                                                                                                                                                                   TISSUE SPECIFICITY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    pathway namely Mapk8, Mapk9 and Mapk10 to the N-terminal region Map2k4 and Map2k7 to the central region and Map3k11 to the Cterminal region. Binds the TPR motif-containing C-terminal Ckinesin light chain, pre-assembled Mapk8ip1 scaffolding comple are then transported as a cargo of kinesin, to the required subcellular location.

SUBCELLULAR LOCATION: Cytoplasmic; localised in the soma and growth comes of differentiated neurites and the Golgi and vesion the early secretory compartment of epithelial cells.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         region of Mapk8ip3 interacts with the C-terminal of Mapk8ip2 not Mapk8ip1 Binds specific components of the UNK signaling pathway namely Mapk8, Mapk9 and Mapk10 to the N-terminal reg. Map2k4 and Map2k7 to the central region and Map3k11 to the C
                                                                                                                                                                                                                                                                                                                                                  the brain and at lower levels in the heart, liver, lu and kidney. All isoforms have been identified in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ALTERNATIVE PRODUCTS: Event=Alternative splicing; Named isoforms=6;
                                                                                                                                                                                                                                                                                                                                                                                                                      Name=1e
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Name=1b
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Name=1c; Synonyms=3b;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IsoId=Q9ESN9-4;
                                                                                                                                                                                                                                                                                                                                                                                                     IsoId=Q9ESN9-6; Sequence=VSP_002776;
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kinesin identified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       [d=Q9ESN9-2;
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C
                                                                                                                                                                                                                                                                                                                                                TY: Highly expressed throughout many regions lower levels in the heart, liver, lung, test isoforms have been identified in the brain,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence=VSP_002776,
                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence=VSP_002778,
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form a functional JNK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AB043127; BAB16685.1; CAB043128; BAB16685.1; CAB178637; AAF26843.1; AF178636; AAF26842.1; AF262046; AAG36931.1; AG362046; AAG369886;                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GO:0046328;
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                                                                                                                                                                                                                                                 Similarity
 TSRTNWVPSVSNPGTTNTNTSNNSNTNSQASQSNDIDSLLKQLYKL--
                                   LADGMVRAQMGGKLVPAGDHWH---
                                                                 NASDII EDTGDAYI VPHGDHYHYI PKNELSASELAAAEAFLSGRGNLSNSRTYRRQNSDN
                                                                                                   SEMKKEYNALHQRHTEMIQTYVEHIERSKMQQVGGSGQTESSLP-GRSRKERPTSLNVFP
                                                                                                                                NROKQE----HSQHRE-----
                                                                                                                                                                EELLMKDPNYK-LKDEDIVNEVKGGYVIKVDGKYYVY----LKDAAHADNV-RTKEEI
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PHOSPHORYLATION (BY MAPK).
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Missing (in isoform la and i
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                                                                                                                                                                                                                             Score 144; DB Pred. No. 3.6; .2; Mismatches
                                                                                                                                                                                                                                                                                             AND A-287. DOES NOT EFFECT BII
COMPONENTS OF THE JNK PATHWAY
K -> R (IN REF: 4).
F -> L (IN REF: 3; AAF26843).
E -> K (IN REF: 4).
                                                                                                                                                                                                                                                                                                                                                                                            AND A-287. DOES NOT EFFECT BINDING OF COMPONENTS OF THE JNK PATHWAY.
T->A: RESULTS IN LOSS OF PHOSPHORYLATION
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                                                                                                                                                                                                                                                                                                                                                             OF MAPK81P3; WHEN ASSOCIATED WITH AND A-287. DOES NOT EFFECT BINDING
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A: RESULTS IN LOSS OF PHOSPHORYLATION
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Alanyl-tRNA syl
ALAS OR MG292
SEQUENCE FROM N.A.

STRAIN-ATCC 33530 / G-37;

MEDLINE=96026346; PubMed=7569993;

Fraser C.M., Gocayne J.D., White O., Adams M.D., Clayton R.A.,

Fleischmann R.D., Bult C.J., Kerlavage A.R., Sutton G., Kelley J.

Fritchman J.L., Weidman J.F., Small K.V., Sandusky M., Fuhrmann J

Nguyen D.T., Utterback T.R., Saudek D.M., Phillips C.A., Merrick

Tomb J.-F., Dougherty B.A., Bott K.F., Hu P.-C., Lucier T.S.,

Peterson S.N., Smith H.O., Hutchison C.A. III, Venter J.C.;

"The minimal gene complement of Mycoplasma genitalium.";

Science 270:397-403(1995).

-i- CATALYTIC ACTIVITY: ATP + L-alanine + tRNA(Ala) = AMP +
                                                                                                                                                                                                                                                                                                                                                SYA MYCGE
P47534;
                                                                                                                                                                                                              NCBI_TaxID=2097;
                                                                                                                                                                                                                                Mycoplasma genitalium 
Bacteria; Firmicutes;
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annotation update)
6.1.1.7) (Alanine--tRNA
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694 667

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612 600 574 559 518 521 458 467

Kelley J.M.,

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(AlaRS)

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Query Match
Best Local S
Matches 127
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PROSITE; PS50860; AA_TRNA_LIGASE_II_ALA; 1.

Aminoacyl-tRNA synthetase; ProteIn biosynthesis; Ligase;
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InterPro; IPR002318; tRNA-synt_2c.
InterPro; IPR006193; tRNA_synt_Ala.
Pfam; PF01411; tRNA-synt_2c; 1.
PRINTS; PR00980; TRNASYNTHALA.
PRINTS; PR00980; TRNASYNTHALA.
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PIR; C64232; C64232.
TIGR; MG292; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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SUBCELLULAR LOCATION: Cytoplasmic.
SIMILARITY: Belongs to class-II aminoacyl-tRNA synthetase family.
                                                                                                                                          699
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127; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           QLYKLPLSQRHVESDGLVFDPAQITSRTARG----VAVPHGDHYHFIPYSQMSELEERIA
SDTLLALKNDINQLKTKNYKVSQQALALSIKKQLLSLVDENKSYV
                                            TETLAGLRUNLTLQIMDNNSIMAEA----EKLLALLKGSNPSSV
                                                                                         INNYLKAENOKLIOLKSELEKVLSLIDSSIFKVELKELOORLDKFILPEKITO---LRDA
                                                                                                                                          PNKNFKADEEPVEETPAEPE---VPQVETEKVEAQLKEAE------VLLAKVTDSSLKANA
                                                                                                                                                                                         FGDYSVELCGGTHVANTASIEDCFITDFYSL-----
                                                                                                                                                                                                                                 FDDHTYK-----APNGYTLEDLFATIKYYVEHPDERPHSNDGWGNASEHVLGKKDHSED
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Pred. No. 2.2
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P31111;
01-JUL-1993
01-OCT-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Johnston M., Andrews S., Brinkman R., Cooper J., Ding H., Du Z., Favello A., Fulton L., Gattung S., Greco T., Kirsten J., Kucaba T., Hallsworth K., Hawkins J., Hillier L., Jier M., Johnson D., Johnston L., Langston Y., Latreille P., Le T., Johnson D., Johnston L., Langston Y., Latreille P., Le T., Mardis E., Menezes S., Miller N., Nann M., Pauley A., Peluso D., Rifken L., Riles L., Trevaskis E., Vignati D., Wilcox L., Wohldman P., Vaudin M., Wilson R., Waterston R., Submitted (MAR-1996) to the EMBL/GenBank/DDBJ databases.
--- FUNCTION: REQUIRED FOR MEIOTIC CHROMOSOME SYNAPSIS AND CELL CYCL PROGRESSION. MAY ACT AS A MOLECULAR ZIPPER TO BRING HOMOLOGOUS CHROMOSOMES IN CLOSE APPOSITION. ZIPI MAY ENCODE THE TRANSVERSE FILAMENTS OF THE SYNAPTONEMAL COMPLEX.
                                                                                                                                                                                                                                                                                                                                                                                                    use by non-profit institutions as long modified and this statement is not removed entities requires a license agreement (See
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=93161412; PubMed=7916652;
MEDLINE=93161412; PubMed=7916652;
                                                                                                                                                                                                                                    Nuclear protein; Meiosis;
DOMAIN 177 333
                                                                                                                                                                                                                                                                                                                                         EMBL; L06487; AAA35239.1; -. EMBL; U51031; AAB64474.1; -.
                                                                                                                                                                                                                                                                                                                                                                                      or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sym M., Engebrecht J.A., Roeder G.S.;
"ZIP1 is a synaptonemal complex protein required chromosome synapsis.";
Cell 72:365-378(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Synaptonemal complex protein ZIP1. ZIP1 OR YDR285W OR D9819.9.
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01-OCT-1996 (Rel.
15-JUL-1998 (Rel.
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                                                                                                                                                                                                                                                                GO:0005716; C:synaptonemal complex; GO:0007126; P:meiosis; IMP. GO:0007129; P:synapsis; IMP.
                                                                                                                                                                                                                                                                                                            $70115; $70115.
$0002693; ZIP1.
 138
                           62
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                                                                                                                                 Similarity
                                                                                     ELGLYQART-VKENNRVSYIDGKQATQKTENLTPDEVSKREGINAEQIVIKITDQGYVTS
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HGDPNDSETTLKDSKMHEYTMTNGKAPLHTSINNSSTSSNDVLLEAFTNTQRICSNLKQE
                             HGD-----
                                                          EIGSPKKTTSTDQYNRIL---
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875 1
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34, Last sequence up
36, Last annotation
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752
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COILED COIL (POTENTIAL).
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COILED COIL (POTENTIAL).
COILED COIL (POTENTIAL).
T -> A (IN REF. 1).
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16-OCT-2001 (Rel. 40, 0
16-OCT-2001 (Rel. 40, 0
28-FEB-2003 (Rel. 41, 1
                                                                                                                                                                                    SCHPO
                                           Schizosaccharomyces pombe (Fission yeast).
Eukaryota; Fungi; Ascomycota; Schizosaccharomycete
Schizosaccharomycetales; Schizosaccharomycetaceae;
                                                                                          Protein sts5.
STS5 OR SPCC16C4.09.
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                                                                                                                                                                                                                                                                 KIKKGSNCMKPPISSRKKLLLVEDEDQSLK
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RA Bgouros J., Peat N., Hayles J., Baker S., Basham D., Bowman S.,
RA Brown S., Cronin R., Davis P., Feltwell T., Fraser A.,
RA Collins M., Connor R., Cronin A., Davis P., Feltwell T., Fraser A.,
RA Gontles S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgson G.,
RA Holroyd S., Hornsby T., Howarth S., Hucke E.J., Hunt S., Jagels K.,
RA Holroyd S., Hornsby T., Howarth S., Hucke E.J., Hunt S., Jagels K.,
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RA Holroyd S., Hornsby T., Howarth S., Hucke E.J., Hunt S., Jagels K.,
RA Holroyd S., Hornsby T., Howarth S., Hucke E.J., Hunt S., Jagels K.,
RA Holroyd S., Moule S., Mungall K., Murphy L., Niblett D., Odell C.,
RA James K., Jones M., Leather S., McLean J.,
RA Mooney P., Moule S., Mungall K., Murphy L., Niblett D., Odell C.,
RA Rutherford K., Rutter S., Saunders D., Seeger K., Sharp S.,
RA Rutherford K., Rutter S., Squares R., Squares S., Stevens K.,
RA Ratherford K., Rutter S., Squares R., Squares S., Stevens K.,
RA Weltjens I., Volckaert G., Aert R., Robben J., Grymonprez B.,
RA Gabel C., Fuchs M., Fritzc C., Holzer E., Moest D., Hilbert H.,
RA Gabel C., Fuchs M., Fritzc C., Holzer E., Moest D., Hilbert H.,
RA Goffeau A., Cadieu E., Dreano S., Gloux S., Lehaure V., Wottier S.,
RA Goffeau A., Rochet M., Gaillardin C., Tallada V.A., Garzon A., Thode G.,
RA Daga R.R., Cruzado L., Jimenez J., Sanchez M., del Rey F., Benito J.,
RA Daga R.R., Cruzado L., Jimenez J., Sanchez M., del Rey F., Benito J.,
RA Dominguez A., Revuelta J.L., Moreno S., Armstrong J., Forsburg S.L.,
RA Spakovski G.V., Ussery D., Barrell B.G., Nurse P.;
"The genome sequence of Schizosaccharomyces pombe.";
RL Jager P., Fills Herors M., Schizosaccharomyces pombe.";
RL Jager P., Fills Herors M., Forsburg S., Letaure V., Metter P., 
                                                                       Matches
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                                                                                                                                                                                                                                                         Hydrolase; Nuclease; Exonuclease.
CONFLICT 5 5 F ->
CONFLICT 794 794 V ->
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J. Cell Sci. 109:2331-2342(1996).
                                                                                                                                                                                                                       SEQUENCE
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InterPro; IPR001900; Ribonuclease_II.
Pfam; PF00773; RNB; 1.
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PIR; T45283; T45283.
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                                                                                                                                                                                                                                                                                                                                                                   PROSITE;
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SUBUNIT: INTERACTS WITH SERINE/THREONINE PHOSPHATASE KINASE C AND AN OSMOSENSING MAP KINASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SIMILARITY: Belongs to the ribonuclease II (RNB) family.
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186 VPHGDHYHYIPKNELSASELAAAE-AFLSGR--
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                                                                                                             Similarity
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                                                                                                                                                                                                                       1066 AA;
                                                                           Conservative
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94 V -> G (IN REF. 1).
117602 MW; 077187800B330C15
                                                                                                             21.9%;
                                                                                                                                           3.4%;
                                                                       69;
                                                                                                             Score 142.5;
Pred. No. 3.2
                                                                           Mismatches
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   GNLSNSRTYRRONSDNTSR 234
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D8-D1-D2-D1996 (Rel. 34, Created)
D1-OCT-1996 (Rel. 34, Last sequence update)
D1-NOV-1997 (Rel. 35, Last annotation updat
           SIGNAL
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                                                                       This SWISS-PROT entry is copyright. It is produced through a cobetween the Swiss Institute of Bioinformatics and the EMBL the European Bioinformatics Institute. There are no restrict use by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and foentities requires a license agreement (See http://www.isb-sib.or send an email to license@isb-sib.ch).
                                                                                                                                                                  regulation.";
Differentiation 57:151-162(1994).
Differentiation 57:151-162(1994).
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Agarwal A., Sloger M.S., Oyama M., Blumberg D.D.;
Panalysis of a novel cyclic Amp inducible prespore
Dictyostelium discoideum: evidence for different po
                                                                                                                                                                                                                                                                               Dictyostelium discoideum Eukaryota; Mycetozoa; Dic NCBI TaxID=44689;
                                                                                                                                                                                                                                                     STRAIN-AX3
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                                                    EMBL; U25143; AAA73514.1;
                               Sporulation;
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   LQEVED
                              LAKVTDSSLKANATETLAGLRNNLTLQIMDNNSIMAEAEKLLALLKGSNPSSVSKEKI
                                                                                                  SNDGWGNASEHVLGKKDHSEDPNKNFKADEEPVEETPAEPEVPQVETEKVEAQLKEAEVL
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                                                                    LNDANDNFEQVNNNNNNINNNNNNNNFKVDKS
                                                                                                                                        CNHLNO
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                                                                                                                                                                                                       ----QQPQKVSNKQQLQEQQINSPED----
                                                                                                                                                                                                                                         KDSLSDKEKVAAQAYTKEKGILPPSPDADVKANPTGDSAAAIYNRVKGEKRIPLVRLPYM 617
                                                                                                                                                                                                                                                                                                              PERLGKPNSQIEYTEDEVRIAQLADKYTTSDGYIFDEHDIISDEGDAYVTPHMGHSHWIG
                                                                                                                                                                                                                                                                                                                                                --DKEQLIDLQNREPGLYKNQ---QDLK-----QEKRANQQELI---
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16.7%;
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- APERLYEETHNSNL-----NKAVQEAEETERQQNGNGSPAVNSHKT
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                                                                                                                                      PFODDYHNDOTEELKD
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Pred. No. 2
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the European Bioinformatics Institute. The
use by non-profit institutions as long
modified and this statement is not removed.
entities requires a license agreement (See
or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Neuron 9:417-428(1992).
-!- TISSUE SPECIFICITY: GROWTH CONES OF EMBRYONIC VERTEBRATE NEURONS
-!- DEVELOPMENTAL STAGE: IS EXPRESSED IN THE NEURULA AND PERSIST DURING EMBRYOGENESIS IN THE BRAIN, CRANIAL NERVES, AND SPINAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TISSUE=Tadpole head;
MEDLINE=92398961; PubMed=1524825;
Hemmati-Brivanlou A., Mann R.W., Harland R.M.;
"A protein expressed in the growth cones of em
"A protein expressed in the growth cones of em
neurons defines a new class of intermediate fi
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
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-- INEQECLKSDQIREAFDTEEV-
                              KLPLSQRHVESDGL--VFDPAQITSRTARGVAVPHGDHYHFIPYSQMSELEERIARIIPL
                                                                                            GNLSNSRTYRRONSDNTSRTNWVPSVSNPGTTNTNTSNNSNTNSOASQSNDIDSLLKQLY
                                                                                                                                                            LARSQGRYTTDDGYIFNASDIIEDTGDAYIVPHGDHYHYIPKNELSASELAAAEAFLSGR 215
                                                                                                                                                                                                                            EVKGGYVIKVDGKYYVYLKDAAHADNVRTKEEI----NRQKQEHSQHREGGTPRNDGAVA
                                                                                                                                                                                                                                                            NIFQSNQEHLE----NLEFDSVVPDTVKFMYPQENNLLEEENVYGDGELVQMATDENIIN
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                                                                                                                                IPVEISENVSVEEIIHEISDVEEDTKQAF-
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IPR001664; IF.
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COIL 1B.
LINKER 12.
COIL 2A.
                                                                                                                                                                                                                                                                                                                                                                                                       Score 142;
Pred. No. 6.
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filament protein.";
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                                                                                                                            Bowman S., Churcher C.M., Badcock K., Brown D., Chill Bowman R., Churcher K., Devlin K., Gentles S., Hamlin N. Jagels K., Lye G., Moule S., Odell C., Pearson D., Ra Rice P., Skelton J., Walsh S., Whitehead S., Barrell "The nucleotide sequence of Saccharomyces cerevisiae"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   YEAST
                                                                                                                                                                                                                                                              STRAIN=S288c;
Madison J., Winston F.;
Submitted (APR-1995) to
                                                                                                                                                                                                                                                                                                                                                Saccharomyces cerevisiae (Baker's yeast).

Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                            Zinc finger protein MOT3/HMS1.
MOT3 OR HMS1 OR YMR070W OR YM9916.09
                                                                                                                                                                                                                                                                                                                                                                                                                        01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation updat
          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                   PubMed=9169872;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      P54785;
01-OCT-1996
                                                                     -!- SUBCELLULAR LOCATION: Nuclear
-!- SIMILARITY: Contains 2 C2H2-ty
                                                                                                    Nature 387:90-93(1997)
                                                                                                                                                                                                                    STRAIN=S288c
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Vains 2 C2H2-type zinc fingers.
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(See http://www.isb-sib.ch/announce/

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GO; GO:0005634; C:nucleus; IDA.

GO; GO:0005677; F:DNA binding activity; IPI.

GO; GO:0003677; F:DNA binding activity; IPI.

GO; GO:0016564; F:transcriptional repressor activity; IDA

GO; GO:0016560; P:transcription; IGI.

InterPro; IPRO07087; Znf C2H2.

Pfam; PF00096; zf-C2H2; 2.

Pfam; PF00096; zf-C2H2; 2.

SMART; SM00355; ZhF C2H2; 2.

PROSITE; PS00128; ZINC_FINGER C2H2_1; 1.

PROSITE; PS0157; ZINC_FINGER_C2H2_2; 1.

Nuclear protein; Zinc_Finger; Metal-binding; Repeat.

Nuclear protein; Zinc_Finger; Metal-binding; Repeat.
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Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccl
Saccharomycetales; Saccharomycetaceae; Saccharomyces
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                         Myosin-1 isoform (Type MYO1 OR YHR023W.
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PIR; S52830; S52830.
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Similarity 19.3%;
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C2H2-TYPE 2.
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Johnston M., Andrews S., Brinkman R., Cooper J., Ding H. Du Z., Favello A., Fulton L., Gattung S., Geisel C., Kitt Kucaba T., Hillier L., Jier M., Johnston L., Langston Y., Latteille P., Louis E.J., Macri C., Mardis E., Menezes S. Nhan M., Rifkin L., Riles L., St Peter H., Trevaskis E., Vignati D., Wilcox L., Wohldman P., Waterston R., Wilson Vaudin M.;
MOD_RES
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                                                                                                                                                                                                                                                 InterPro; IPR001048; IQ_region.
InterPro; IPR001609; myosin head.
Pfam; PF00063; myosin head; 1.
PRINTS; PR00193; MYOSINHEAVY.
PRODOM; PD000355; myosin_head; 1.
                                                                                                                                                                                                                                                                                                                                          GO; GO:00065; MYO1.
GO; GO:0000142; C:contractile ring (se GO; GO:0007120; P:caxial budding; IMP.
GO; GO:00016288; P:cytokinesis; IMP.
GO; GO:0006970; P:response to osmotic
                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; X53947; CAA37894.1; -.
EMBL; X06187; CAA29550.1; -.
EMBL; U10399; AAB68872.1; -.
PIR; S46773; S46773.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN=S288c;
MEDLINE=9108308; PubMed=2263482;
Sweeney F.P., Watts F.Z., Pocklington M.J., Orr E.
"The MYO1 gene from Saccharomyces cerevisiae: its
sequence.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -!- FUNCTION: REQUIRED FOR CELL DIVISION.
-!- SIMILARITY: Contains 1 myosin-like globular head
-!- SIMILARITY: Contains 1 IQ domain.
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EMBO J. 6:3
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"The yeast MYO1 gene e
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MEDLINE=94378003; PubMed=8091229;
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SM00242; MYSC;
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ACTIN-BINDING (BY SIMILARITY)

K -> I (IN REF. 1).

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V -> S (IN REF. 1).
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EYTVEGWLSKNK -> NTLMKAGYPKT (IN REI
MISSING (IN REF. 3).
EKSSSA -> GKNLLVC (IN REF. 1 AND 3).
R -> S (IN REF. 1 AND 3).
ENSTITT -> RKFNHHD (IN REF. 3).
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01-JUL-1993
28-FEB-2003
TISSUE=Brain;
MEDLINE=92366472; PubMed=1323835;
Krueger N.X., Saito H.;
                                                                  PTPRZ1 OR PTPRZ OR PTPZ.
Homo sapiens (Human). ,
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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P23471;
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                                                                                                                          Protein-tyrosine
                                                       NCBI_TaxID=9606
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EMBL; M93426; AAA60225.1; -
EMBL; X54135; CAA38070.1; -
PIR; A46151; A46151.
HSSP; P18052; 1YFO.
Genew; HGNC:9685; PTPRZ1.
MIM; 176891; --
GO; GO:0005887; C:integral
GO; GO:0005001; F:transmemb
GO; GO:0007417; P:central n
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TISSUE=Brain stem;
MEDLINE=93252948; PubMed=8387522;
MEDLINE=93252948; PubMed=8387522;
Levy J.B., Cannoll P.D., Silvennoinen O.
Levy J.B., Mang J.-T., Cannizzaro
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Ricca G., Jaye M., Schlessinger J.;
"Cloning of three human tyrosine phosphatases reveals a
family of receptor-linked protein-tyrosine-phosphatases
brain.":
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J. Biol. Chem. 268:10573-10581(1993).
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; 176891; -.
GO:0005887; C:integral to plasma membrane; TAS.
GO:0005001; F:transmembrane receptor protein tyrosine
GO:0007417; P:central nervous system development; TAS
                                                                                                                                                                                                    s SWISS-PROT entry is copyright. It is produced through a collaboration ween the Swiss Institute of Bioinformatics and the EMBL outstation - European Bioinformatics Institute. There are no restrictions on its by non-profit institutions as long as its content is in no way
                                                                                                                                                                                                                                                                              ANTERIOR HORN OF THE LATERAL VENTRICLE. DEVELOP
IN THE BRAIN.
SIMILARITY: IN THE N-TERMINAL SECTION; BELONGS
TYPE CARBONIC ANHYDRASE FAMILY.
SIMILARITY: Contains 2 protein-tyrosine phospha
SIMILARITY: Contains 1 fibronectin type III dom
CAUTION: CALLED RPTPASE BETA IN REF.2 AND REF.4
                                                                                                                                                                                                                                                                                                                                                                                           ISOId=P23471-2; Sequence=VSP 005151;
TISSUE SPECIFICITY: SPECIFICALLY EXPRESSED IN THE CENTRAL SYSTEM, WHERE IT IS LOCALIZED IN THE PURKINJE CELL LAYER CEREBELLUM, THE DENTATE GYRUS, AND THE SUBEPENDYMAL LAYER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SIMILARITY).
SUBCELLULAR LOCATION: Type I membrane ALTERNATIVE PRODUCTS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DEVELOPMENTAL PROCESSES IN THE CNS.

CATALYTIC ACTIVITY: Protein tyrosine phosphate + H(2)O = protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     tyrosine + phosphate.
SUBUNIT: THE CARBONIC-ANHYDRASE LIKE DOMAIN BINDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Event=Alternative
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Natl. Acad. Sci. U.S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IsoId=P23471-1;
                                                                                                                                                         non-profit institutions as long as its content is and this statement is not removed. Usage by and for requires a license agreement (See http://www.isb-sib.an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence=Displayed;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      human receptor-like protein
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Pfam; PF001041; fn3; 1.
Pfam; PF00102; Y bhosphatase; 2.
PRINTS; PR00700; PRTYPHPHTASE.
ProDom; PD000865; Euk Coanhd; 1.
SMART; SM00060; FN3; 1.
SMART; SM00194; PTPC; 2.
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PROSITE; PS50056; TYR_PHOSPHATASE_2; 2.

PROSITE; PS50055; TYR_PHOSPHATASE_PTP; 2.

Signal; Glycoprotein; Transmembrane; Hydrolase;
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InterPro; IPR000387; TYR phosphatase.
InterPro; IPR000242; Tyr_PP.
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                                VGVTYQGSLFSGPSHI-
                                                IKITDQGYVTSHGDHYHYYNGKVPYDAIISEELLMKDPNYKLKDEDIVNEVKGGYVIKVD
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Pred. No. 10;
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NUM1 YEAST
Q00402;
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SEQUENCE FROM N.A.
STRAIR-ATCC 28383 / FL100;
MEDLINE=92079907; PubMed=1745235;
Kormanec J., Schaaff-Gerstenschlaeger I.,
Perecko D., Kuentzel H.;
                                                                                                Saccharomyces cerevisiae (Baker's yeas
Eukaryota; Fungi; Ascomycota; Saccharo
Saccharomycetales; Saccharomycetaceae;
                                                                                                                                               Nuclear migration protein NUM1.
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01-DEC-1992 (Rel.
01-OCT-1996 (Rel.
                                                                                    NCBI_TaxID=4932;
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24, Last sequence up
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Nuclear migration in Saccharomyces cerevisiae is controlled highly repetitive 313 kDa NUM1 protein."; mol. Gen. Genet. 230:277-287(1931).
-i- FUNCTION: CONTROLS NUCLEAR MIGRATION. NUM1 SPECIFICALLY CHE INTERACTION OF THE BUD NECK CYTOSKLEFTON WITH THE PRIDIVISIONAL G2 NUCLEUS PERHAPS BY RECOGNIZING G2-SPECIFIC CYTOPLASMIC MICROTUBULI OR OTHER COMPONENTS OF THE NUCLEB
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SMART; SM00233; PH; 1
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SGD; S0002557; NUM1.
InterPro; IPR001849; PH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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P39936;
01-FEB-1995
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01-FEB-1995 (Rel. 31, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Eukaryotic initiation factor 4F subunit pl30
binding protein complex subunit pl30)
TIF4632 OR YGL049C.
                                                                                                                                     Feuermann M., de Montigny J., Potier S., Souciet J.-L., "The characterization of two new clusters of duplicated suggests a 'Lego' organization of the yeast Saccharomyce
                                                                                                                                                                                                                SEQUENCE FROM
STRAIN=S288c;
                                                                                                                                                                                                                                                                Goyer C., Altmann M., Lee H.S., Blanc A., Deshmukh M., Woolford J.L., Trachsel H., Sonenberg N.; Woolford J.L., Trachsel H., Sonenberg N.; and TIF4632: two yeast genes encoding the high-molecular-weight subunits of the cap-binding protein confeukaryotic initiation factor 4F) contain an RNA recognition motif-like sequence and carry out an essential function."; Mol. Cell. Biol. 13:4860-4874(1993).
                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A. MEDLINE=93330281; PubMed=8336723;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Fungi; Ascomycota; Saccharo; Saccharo; Saccharomycetales; Saccharomycetaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Saccharomyces cerevisiae (Baker's yeast).
                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=4932;
                                                                                                                            chromosomes."
                                                                                                                                                                                            MEDLINE=97377993; PubMed=9234674;
                                                                                                          Yeast 13:861-869(1997)
                                  SUBUNIT: MAY FORM PART OF THE CAP-BINDING PROTEIN COMPLEX.
                                                     FUNCTION: INTERACTS WITH THE MRNA CAP STRUCTURE, M7GPPPX. INTERACTION IS REQUIRED FOR EFFICIENT RIBOSOME BINDING TO MRNA. TIF4632 IS PROBABLY ESSENTIAL WHEN TIF4631 IS MISSIN
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SMART; SM00543; MIF4G; 1.
Initiation factor; Protein biosynthesis;
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InterPro; IPR000504; RNA_rec_mot.
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S0003017; TIF40
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                                                               TSSSRVSSKRRSKRMGDDR-RSNRGY-----TSRKDRE-----
                                                                                           TLEDLFATIKYYVEHPDERPHSNDGWGNASEHVLGKKDHSEDPNKNFKADEEPVEETPAE
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19.7%; Pred. No.
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RESULT 27 SPT7\_YEAST

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SALA BERREAR B
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P35177;
01-FEB-1994
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                SGD; S0000285; SPT7.
GO; G0:000124; C:SAGA complex; IDA.
InterPro; IPR001487; Bromodomain.
Pfam; PF00439; bromodomain; 1.
Pfam; PF00439; bromodomain; 1.
SMART; SM00297; BROMODOMAIN.
SMART; SM00297; BROMODOMAIN_1; 1.
PROSITE; PS00633; BROMODOMAIN_1; 1.
PROSITE; PS01014; BROMODOMAIN_2; 1.
Transcription regulation; Nuclear protein; Activator; Bromodomain.
DOMAIN 458 528 BROMODOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                the European Bioinformatics Institute. The use by non-profit institutions as long modified and this statement is not removed. entitles requires a license agreement (See or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                  EMBL; X76294; CAA53940.1; -.
EMBL; Z35950; CAA85026.1; -.
EMBL; M87651; AAA35087.1; -.
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Gansheroff L.J., Dollard C., Tan P., Winston F.,
"The Saccharomyces cerevisiae SPT7 gene encodes
important for transcription in vivo.";
Genetics 139:523-536(1995).
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SPT7 OR YBR081C OR YBR0739.
Saccharomyces cerevisiae (Baker's yeast).

Bukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetales; Saccharomycetaceae; Saccharomyces
SEQUENCE
                                                                                                                                                                                                                                                                                     PIR; S41552; S41552.
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EMBL; X76294; CAA53940.1; -.
EMBL; Z35950; CAA85026.1; -.
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Saccharomyces cerevisiae chrom
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01-FEB-1994 (Rel.
01-OCT-1996 (Rel.
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85152; PubMed=1350857;
, Dollard C., Winston
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STANDARD;

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                                                                                                                                                                                                                                                                                                                                    NYTEHSTPFLNKVSKREAPNYHQIIKKSMDLNTVLKKLKSFQYDSKQEFVDDIMLIWKNC
KEQKALESYRQKIEQNSIMKNGFGTVLKQEDDDQLQFHNDHSL
                           KEAEVLLA--
                                                      DDLEISVWKTVTAKVRAEICLKRTEYFKNGKLNSDSEAFLKNPQRMK---
                                                                                   ED-----
                                                                                                             ----DADAAKKDTEDGLQDKTAENKEAGENNEEEEDDDDEDEDEDMVDSQSYLLEKDDDR
                                                                                                                                                                                                                        EEVAGSGRKGL--NMG-AHMLAKENGKVSEKDSSKTVKDEAPTNDDKLTSVIPEGEKEKD
                                                                                                                                                                                                                                                 DIISDEGDAYVTPHMGHSHWIGKDS--LSDKEK---VAAQAYTKEKGILPPSPDADVKAN
                                                                                                                                                                                                                                                                             LTYNSDPSHFLR--GHAIAMOKKSLOLIRMIPNITIRNRADLEKEIEDMEKDKDYELDEE
                                                                                                                                                                                                                                                                                                                                                              ---AHKALFXNKGRNSDFQALDKLLERLNDEST-----NKEKLVDDLLA----
                                                                                                                                                                                                                                                                                                                                                                                                                    KGISRYVFAKDLPSETVKNLESKLSKQESVSHTLTAKKENVAPRDQEFYDKAYNLLTE--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ---ESDKMIEKGKKKRSRSDLEAATDEQD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   QNSDNTSRTNWVPSVSNPGTTNTNTSN----NSNTNS-QASQSNDIDSLLKQLYKLPLSQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         YIFNASDIIEDTGDAYIVPHGDHYHYIPKN--ELSASELAAAEAFLSGRGNLSNSRTYRR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  KDAAHAD------NVRTKEEINRQKQEHSQHREGGTPRNDGAVALARSQGRYTTDDG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ARTVKENNRVSYIDGKQATQKTENLTPDEVSKREGINAEQIVIKITDQGYVTSHGDHYHY
                                                                                                                                       FAWFDDHTYKAPNGYTLEDLFATIKYYVEHPDERPHSND-----GWGNASEHVLGKKDHS
                                                                                                                                                                  KTASSTVTVHENVNKNEIKENGKNEEQ------DMVEESSKTEDSSK--
                                                                                                                                                                                              PTGDSAAAI YNRV-----
                                                                                                                                                                                                                                                                                                                                                                                         LGISDYEL-KHLIMDVRKN-RSKWTSDERIG------QEELYEACEKVVLELR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PDSRPEQPSPQPTPEPSPGPQPAPNLKID------
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -EIDDERRLVLNISISKETLSKLKINNVEEIMGNWNKIYHSFEYDKETMIKRL-KLE---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               YDDEDENYDEDSTDVKNVDDP----PKNLDSISSSNI-
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                                                                                                                                                                                                                                                                                                     FLAPITHPERLGKPNSQIEYTEDEVRIAQLAD-----KYTTSDGYIFDEH
                                                                                -----PNKNFKADEEPVEETPAEPEVPQVETEKVEAQL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -VEEDL----FKLDLEDLKQQISGTRFIGNLSLKIRYVLWQCAIDYIYC
                           -KVTDSSLKANATETLAGLRNNLTLQIMDNNSI
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                                                                                                                                                                                           KGEKRIPLVRLPYMVEHTVEVKNGNLIIPHKDHYHNIK
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Best Local S
Matches 88
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ACT SITE
SEQUENCE
 LMG1_HUMAN
P11047;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Signal; Cell wall.
SIGNAL 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.

MEDLINE=89385998; PubMed=2780297;

Fuerst P., Mesch H.-U., Solioz M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; X16421; CAA34442.1; ALT_INIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "A protein of unusual composition from Enterococcus Nucleic Acids Res. 17:6724-6724(1989).
-i- SUBCELULAR LOCATION: Attached to the cell wall.
-i- SIMILARITY: BELONGS TO PEPTIDASE FAMILY C40.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Enterococcus faecium Bacteria, Firmicutes,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEROPS; C40.UPW; -
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                                                                                                                                                                                     ALMINNINI .
                                                                                                                                                                                                                      RYRSNHWVPDSRPEQPSPQPTPEPSPGPQPAPNLKIDSN-SSLVSQLVRKVGEGYV----
                                                                                                                                                                                                                                                                                                                                 SSSTESSTEESTVPESSTQESTPANTESSSSSSNTNVNNNTNNSTNNSTNNSTTN----
                                                                                                                                                                                                                                                                                                                                                                                                                                             NASDIIEDTGDAYIVPHGDHYHYIPKNELSASELAAAEAFLSGRGNLSNSRTYRRQNSDN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NRKKAEAEAEOARIREOARLAEOAROOAAOEKAEKEAREOAAAOAAOTOA-----LS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       YLKDA-AHADNVRTKEE----INROKOEHSOHREGGTPRINDGAVALARSOGRYTTDDGYIF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           KQAVEAKKAENEAKQKELADNQAALESQKGDLLAKQADLNVLKTSLAAEQATAEDKKADL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   QARETQVKNTSSNYIDAV-----LNADSLADAVGRIQAMSTIVK-ANQDLVQQQKED
                                                                                                           DPSGFDCSGFTRYVYLQVTGRDIGGWTVPQESAGTKISVSQA
                                                                                                                                                ----FEEKGISRYVF----AKDLPSETV--KNLESKLSKQES
                                                                                                                                                                                                                                                                                               LYKLPLSQRHVESDGLVFDPAQITSRTARGVAVPHGDHYHFIPYSQMSELEERIARIIPL
                                                                                                                                                                                                                                                                                                                                                                        TSRT-----NWVP----
                                                                                                                                                                                                                                                                                                                                                                                                             SASTTTESSSAA----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IPR000064; NLPC
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429
516
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                   STANDARD;
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429
54596
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19.0%;
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                                                                                                                                                                                   -TPAPTPTPTPAPAPAPNPSGSVNGAAIVAEAYKYIGTPYVWGGK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 140.5;
Pred. No. 1.5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        POTENTIAL.
P54 PROTEIN.
                   PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   402ECAA439846D26 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches 151;
                                                                                                                                                                                                                                                                                                                                                                    SVSNPGTTNTNTSNNSNTNSQASQSNDIDSLLKQ
                   1609
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                   B
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                                                                                                             464
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            153;
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EMBL; M55210;
EMBL; M55217;
EMBL; M55201;
EMBL; M55211;
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01-NOV-1991
15-SEP-2003
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Fukushima Y., Pikkarainen T., Kallunki T., Edd
Haley L.L., Henry W.M., Tryggvason K., Shows T
"Isolation of a human laminin B2 (LAMB2) cDNA
the gene to chromosome region 1q25-->q31.";
Cytogenet. Cell Genet. 48:137-141(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.

MEDLINB=91093128; PubMed=1985895;

Kallunki T., Ikonen J., Chow L.T., Kallunki P.

Kalructure of the human laminin B2 chain gene divergence from the laminin B1 chain gene.";

J. Biol. Chem. 266:221-228(1991).
                                                                                                                                                                               entities requires a license agreement or send an email to license@isb-sib.cl
                                                                                                                                                                                                                                                    use by non-profit institutions as long modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                the
                                                                                                                                                                                                                                                                                                                                                                                                        This
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Santos C.L.S., Sabbaga J., Brentani R.;
"Differences in human laminin B2 sequences.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TISSUE=Endothelial
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MEDLINE=88198245; PubMed=3360804;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=9606;
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LAMC1 OR LAMB2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=92216129; PubMed=1806043;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE OF 1282-1609 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Seq. 1:275-277(1991).

FUNCTION: Binding to cells via a high affinity receptor, laminin is thought to mediate the attachment, migration, and organization of cells into tissues during embryonic development by interacting with other extracellular matrix components.

SUBUNIT: Laminin is a complex glycoprotein, consisting of three different polypeptide chains (alpha, beta, gamma), which are bour to each other by disulfide bonds into a cross-shaped molecule
                                                                                                                                                                                                                                                                                                             s SWISS-PROT entry is copyright. It is produced through ween the Swiss Institute of Bioinformatics and the EN Buropean Bioinformatics Institute. There are no restrained to the content of                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WITH OTHER LAMININ CHAINS TO FORM A COILED COIL S DOWAIN: DOWAINS VI AND IV ARE GLOBULAR. SIMILARITY: Contains 1 laminin N-terminal domain. SIMILARITY: Contains 11 laminin EGF-like domains. SIMILARITY: Contains 1 laminin IV domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LAMININ-2 (MEROSIN), LAMININ-3 (S-LAMININ), LAMININ-LAMININ-6 (K-LAMININ) AND LAMININ-7 (KS-LAMININ).
SUBCELLULAR LOCATION: Extracellular.
TISSUE SPECIFICITY: FOUND IN THE BASEMENT MEMBRANES COMPONENT).
DOMAIN: THE ALPHA-HELICAL DOMAINS I AND II ARE THOUG
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end.

THE GAMMA-1 CHAIN IS A SUBUNIT OF LAMININ-1 (EHS LAMININ)

THE GAMMA-1 (MEROSIN), LAMININ-3 (S-LAMININ), LAMININ-4 (S-LAMININ).
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Shows T.B.;
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GO; GO:0005604; C:basement membrane; TAS.
GO; GO:0007492; P:endoderm development; TAS.
GO; GO:0007461; P:protein complex assembly; TAS.
InterPro; IPR006209; EGF like.
InterPro; IPR0002049; Laminin EGF.
InterPro; IPR000034; Laminin EGF.
InterPro; IPR001886; LamNT.
2fam; PF00052; laminin EGF; 10.
2fam; PF00052; laminin EGF; 10.
2fam; PF00053; laminin Nterm; 1.
2fam; PF0002082; LamN; 1.
2fam; PF001166; EGF 1; 8.
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86; EGF 2; 2.

248; LAMININ TYPE EGF; 11.

Basement membrane; Extracellular matrix; Coiled cul-
Basement, Cell adhesion; Repeat; Signal; Polymorphism.

Anmain; Cell adhesion; Cepain.

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Nature 415:871-880(2002).
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Sporulation-specific protein 15.
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-!- FUNCTION: Has a role in the initiation
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01-AUG-1991 (Rel. 1
28-FEB-2003 (Rel. 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=91187857; PubMed=1901413; Laurent B.C., Treitel M.A., Carlson M.; "Functional interdependence of the yeast SNF2, SN proteins in transcriptional activation."; Proc. Natl. Acad. Sci. U.S.A. 88:2687-2691(1991).
  Saccharomyces cerevisiae 
Yeast 12:1059-1064(1996) [5]
                                             Cheret G., Bernardi A., Sor F.J.;
"DNA sequence analysis of the VPH1-SNF2
Saccharomyces cerevisiae.";
                                                                                                                                                                                                                   MEDLINE=9533226i; PubMed=7608126; Kodaki T., Hosaka K., Nikawa J., Yamashita "The SNF2/SWI2/GAMI/TYE3/RIC1 gene is invol regulation of phospholipid synthesis in Sac J. Biochem. 117:362-368(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SNF2 OR SWI2 OR GAM1 OR TYE3 OR RIC1 OR YOR290C. Saccharomyces cerevisiae (Baker's yeast). Eukaryota; Fungi; Ascomycota; Saccharomycotina;
                                                                                                                        MEDLINE=97051594;
                                                                                                                                               STRAIN=S288c;
                                                                                                                                                                                                                                                                                                                                              STRAIN=X2180-1B;
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"The GAM1/SNF2 gene of Sacc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE
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28-FEB-2003 (Rel. 41, Last annotation update)
Transcription regulatory protein SNF2 (SWI/SNF complex component SI
(Regulatory protein SWI2) (Regulatory protein GAM1) (Transcription
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                                                                                                  PubMed=8896271;
di A., Sor F.J.;
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PRINTS; PR00503; BROMODOMAIN.
SMART; SM00384; AT hook; 2.
SMART; SM00297; BROMO; 1.
SMART; SM00287; DEXDC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     end), CPA1, SLY41, a putative transport ATPase, protein and an SNF2 homologue.";
Yeast 13:479-482(1997).
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Jauniaux J.-C.;
"Sequence and analysis of a 36.2 kb fragment from the right arm of yeast chromosome XV reveals 19 open reading frames including SNF2 (5 yeast chromosome XV reveals 19 open reading frames including SNF2 (5 yeast chromosome XV reveals 19 open reading frames including SNF2 (5 yeast chromosome XV reveals 19 open reading frames including SNF2 (5 yeast chromosome XV reveals 19 open reading frames including SNF2 (5 yeast chromosome XV reveals 19 open reading frames including SNF2 (5 years) which was a supplied to the state of 
                                                                                                                                                                                                                                                                                                                                                                                                                                    Pfam; PF00439; bromodomain; 1.
Pfam; PF00271; helicase C; 1.
Pfam; PF00176; SNF2_N; 1.
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                                                                                                                                                                                               Bromodomain;
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PROSITE; PS50014; BROMODOMAIN_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pfam; PF02178; AT_hook; 2.
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TRANSFAC; T02401
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=97025355; PubMed=8871545;
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                                                                                                                                                                        DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR001650;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SUBCELLULAR LOCATION: Nuclear.
SIMILARITY: STRONG, TO DROSOPHILA BRAHMA.
SIMILARITY: Contains 1 bromodomain.
SIMILARITY: Contains 3 A.T book DNA-binding repeats.
SIMILARITY: BELONGS TO THE SNF2/RAD54 HELICASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FUNCTION: INVOLVED IN TRANSCRIPTIONAL ACTIVATION. THE SWI/SNF COMPLEX IS REQUIRED FOR THE INDUCED EXPRESSION OF A LARGE NUMBER OF GENES. THIS COMPLEX ALTERS CHROMATIN STRUCTURE TO FACILITATE BINDING OF GENE-SPECIFIC DEDICATED TRANSCRIPTION FACTORS.

SUBUNIT: COMPONENT OF THE SWI/SNF GLOBAL TRANSCRIPTION ACTIVATOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                M61703; AAA35059.1;
X57837; CAAA0969.1;
D90459; BAA14423.1;
X89633; CAA61793.1;
X89633; CAA61793.1;
Z75198; CAA99517.1;
Z75199; CAA99519.1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 S0005816; SNF2.
                                                                                                                                                                                                                                                                                              SM00490; HELICC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IPR000330;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IPR001410;
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     1446
1502
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                                   87 (Rel. 05, Created)
96 (Rel. 33, Last sequence update)
03 (Rel. 42, Last annotation update)
surface protein 1 precursor (Merozoite
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Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
NCBI_TaxID=5848;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REVISIONS.
Holder A.A.
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MEDLINE=86014355; PubMed=2995820;
Holder A.A., Lockyer M.J., Odink
Nicholls S.C., Hillman Y., Davey
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P25386;
01-MAY-1992
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                                                                                                                                                                                                                                                                                  SEQUENCE OF 782-1790 FROM N.A. Hostetter M.K., Herman D.J., B
                                                                                                                                                                                                                                                                                                                                     "A cytoskeleton-related gene, uso1, is required protein transport in Saccharomyces cerevisiae.", J. Cell Biol. 113:245-260(1991).
                                                                                                                                                                                                                                                                                                                                                                                       Nakajima H., Hirata A.,
Yamasaki M.;
                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=91185402; PubMed=2010462;
Nakaiima H., Hirata A., Ogawa Y.,
                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN=X2180-1A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Fungi; F
Saccharomycetales;
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16-OCT-2001 (Rel. 40, Le
Intracellular protein to
USO1 OR INT1 OR YDL058W
                                                                                                                                                                                                                  SEQUENCE OF 1-8 FROM N.A.
                                                                                                                                                                                                                                                                    Kendrick K.E.;
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                                             MEMBRANES. PROBABLY PRESENT ON VESICLES OPERATIONAL BETWEEN THE ER AND THE GOLGI COMPLEX.

ER AND THE GOLGI COMPLEX.

DOMAIN: THE RODLIKE TAIL SEQUENCE IS HIGHLY REPETITIVE, COMPOSED OF AN HEPTAPEPTIDE REPEAT PATTERN CHARACTERISTIC OF ALPHA-HELICAL COILED COILS. MAY FORM FILAMENTOUS STRUCTURES IN THE CELL.
                               SIMILARITY: BELONGS TO THE VDP/USO1/YBL047C
                                                                                                                                  SUBCELLULAR LOCATION: CYTOPLASMIC.
                                                                                                                                                                 FUNCTION: REQUIRED FOR
                                                                                                                                                   COMPLEX.
SWISS-PROT entry is copyright. It is produced through a collaboration
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InterPro; IRR006953; Usol_p115_C.
Pfam; PF04871; Usol_p115_C; 1.
Pfam; PF04897; Usol_p115_C; 1.
Transport; Protein Franchised; 1.
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S0002216; USO1.
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22; Mismatches
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G-> E (IN REF. 2).
E-> K (IN REF. 2).
V-> I (IN REF. 2).
V-> V (IN REF. 2).
N-> S (IN REF. 2).
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RA Adams M.D., Celniker S.E., Richards S., Ashburner M., Henderson S.N.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA George R.A., Lewis S.E., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Beason K.M., Basu A., Baxerdale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Dodson K., Doup L.E., Gary N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Hostin D., Houston K.A., Howland T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Liu K., Mattei B., McIntosh T.C., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Liu K., Mattei B., McIntosh T.C., Kravitz S., Kulp D., Lai Z.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Melson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT
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Eukaryota, Metazoa, Arthropoda, Hexapoda, Inse
Neoptera, Endopterygota, Diptera, Brachycera,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-MAR-1989 (Rel. 10, Created)
01-MAR-1989 (Rel. 10, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN=Berkeley;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=88232956; PubMed=2897632;
Blochlinger K., Bodmer R., Jack J., Jan L.Y., Jan Y.N.;
"Primary structure and expression of a product from cut, a loc
involved in specifying sensory organ identity in Drosophila.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
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01-MAR-1989 (Re
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era; Muscomorpha;
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Siden-Kiamos I., Simpson M., Skupski M.P., Smith T., Spier E., Spradling A.C., Stapleton M., Strong R., Sun E., Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X., Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J., Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A., Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng I. Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H. Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.; "The genome sequence of Drosophila melanogaster."; Science 287:2185-2195 (2000).
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Pfam; PF00046; homeobox; 1.
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GO; GO:0005634; C:nucleus; IDA.
GO; GO:0008587; P:wing margin morphogenesis; NAS
InterPro; IPR007108; Cut_homeo.
InterPro; IPR003350; Hmoeo CUT.
InterPro; IPR001356; Homeobox.
                                                                                                                                                                                                                                                                                                                                                                                                                                               PIR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; X07985; CAA30794.1; -. EMBL; AE003441; AAF46264.2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            use by non-profit institutions as long modified and this statement is not removed.
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                                                                                                                                                                                                                                    Developmental
                                                                                                                                                                                                                                                  Transcription
                                                                                                                                                                                                                                                                PROSITE; PS50071;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DEVELOPMENTAL STAGE: CELL-SPECIFIC PATTERN OF E EXPRESSED DURING EMBRYONIC DEVELOPMENT.

DOMAIN: ASN AT POSITION 47 OF THE HONEOBOX MAY REGULATING DNA-BINDING ACTIVITY BY PROMOTING HO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       European
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SIMILARITY: Contains 3 CUT SIMILARITY: BELONGS TO THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SUBCELLULAR LOCATION: Nuclear (Probable).
TISSUB SPECIFICITY: Detected in many cells in the central nervous system, all external sensory organs, some peripheral neurons, and in the non-neural cells of the spiracles and the Malpighian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          cut gene external sensory organs are transformed into chordotonal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Specifically, functions as a determination factor
sensory organ identity in precursor cells. Probal
in cell type specification of Malpighian tubules
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FUNCTION: Regulator of cell fate decisions in multiple lineages Specifically, functions as a determination factor that specifies
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HETERODIMERIZATION
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                                                                                                                                                                                                                                                                                                    PD000010; Homeobox;
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pean Bioinformatics Institute.
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50071; HOMEOBOX 2; 1.
on regulation; Homeobox; DNA-binding; on regulation; Homeobox; DNA-binding; al protein; Repeat; Co 265
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COLLED COIL (POTENTIA)
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CUT 1.
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COLLED COIL (POTENTIA)
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ASP/GLU-RICH
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ALA/GLN-RICH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    of Bioinformatics
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             domains.
CUT HOMEOBOX FAMILY
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                                                                                                                                                    (POTENTIAL)
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               (OPA-REPEAT)
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P15205; Q62958; Q9ER21; Q9QW92;
D1-APR-1990 (Rel. 14, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
28-FCB-2004 (Rel. 41, Last annotation update)
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                                            SEQUENCE OF 1-142 FROM N.A.
STRAIN-Sprague-Dawley; TISSUE-Testis;
MEDLINE-96257242; PubMed-8666295;
                                                                                                                                                                         Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                             Rattus norvegicus (Rat)
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19.9%;
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Rodentia;
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Pred. No. 16
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ALA/PRO-RICH.
                                                                                                                                                                           Craniata; Ver
Sciurognathi;
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thi; Muridae; Murinae; Rat
  of.
  the
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Ma D., Nothias F., Boyne L.J., Fischer I.;
"Differential regulation of microtubule-associated protein 1B (MAP1B)
in rat CNS and PNS during development.";
J. Neurosci. Res. 49:319-332(1997).
-!- FUNCTION: The function of brain MAPS is essentially unknown.
Phosphorylated MAP1B may play a role in the Cytoskeletal changes
that accompany neurite extension. Possibly MAP1B Binds to at least
two tubulin subunits in the polymer, and this bridging of subunits
might be involved in nucleating microtubule polymerization and in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Rienitz A., Grenningloh G., Hermans-Borgmeyer I., Kirsch J.,
Littauer U.Z., Prior P., Gundelfinger E.D., Schmitt B., Betz H
"Neuraxin, a novel putative structural protein of the rat cent
nervous system that is immunologically related to microtubule-
associated protein 5.";
EMBO J. 8:2879-2888(1989).
                    PROSITE; PS00230; MAPIB NEURAXIN; 8.
Microtubules; Repeat; Phosphorylation.
CHAIN ? 2459
MAPI LIGHT
                                                                                                                                                               EMBL; U52950; AAB17068.1;
EMBL; X60370; CAC16162.1;
EMBL; X16623; CAA34620.1;
PIR; A56577; A56577.
                                                                                                       InterPro; IPR000102; MAP1B_neuraxin. Pfam; PF00414; MAP1B_neuraxin; 10.
                                                                                                                                                                                                                                                                                                                                                              use by non-profit institutions as long as modified and this statement is not removed. I
                                                                                                                                                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collab between the Swiss Institute of Bioinformatics and the EMBL outst the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               stabilizing microtubules.
-!- SUBUNIT: 3 different light chawith MAP1A and MAP1B proteins.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Zauner W., Kratz J., Stau "Identification of two di recombinant rat MAP 18."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN=Sprague-Dawley; TISSUE=Bra
MEDLINE=92347374; PubMed=1639092;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           associated protein (MAPIB) -encoding cDNA.";
Gene 172:307-308(1996).
                                                                                                                                                                                                                                                                                                               or send
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DEVELOPMENTAL STAGE, AND PHOSPHORYLATION MEDLINE=97405699; PubMed=9260743;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=90059871;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SIMILARITY: TO MAPIA
SIMILARITY: TO MAPIA
CAUTION: A C-terminal fragment of this protein (residual fragment)
2459) was originally described as neuraxin in Ref. 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           nerve levels are high early in development but decrease during postnatal development and are low in adults. In dorsal root ganglia levels remain high throughout development. INDUCTION: By nerve growth factor.

INDUCTION: By nerve growth factor.

IOMANN: Has a highly basic region with many copies of the sequence KKEE and KKEI/V, repeated but not at fixed intervals, which is responsible for the binding of MAP1B to microtubules.

PTM: LC1 is coexpressed with MAP1B. It is a polypeptide generated from MAP1B by proteolytic processing. It is free to associate with both MAP1A and MAP1B. It interacts with the amino-terminal region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PTM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TISSUE SPECIFICITY: Nervous system (spinal cerebellum and cerebrum). Not expressed in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      of MAP1B (By similarity).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      heart or muscle
                                                                                                                                                                                                                                                                                                            s requires a license agreement (S an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OF 96-2459 FROM N.A., DOMAII prague-Dawley; TISSUE=Brain,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Phosphorylated
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        NGYTLEDLFATIKYYVEHPDERPHSNDG------WGNASEHVLGKKDHSEDPNKNFK 704
                                                                                                                 PDSESPIEKV-----LSPLRSPPLIGSESAYEDFLSADDKALGRRSE---
                                                                                                                                                           TDEKSSHLPTEVTENAQAVPVSFEF-----
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                                                   DSAAAIYNRVKGEKRIPLVRLPYMVEHTVEVKNGNLIIPHKDHYHNIKFAWFDDHTYKAP
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L -> I (IN :
1 MW; 2E3F687
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Pred. No. 19;
01; Mismatches
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LYS-RICH (HIGHLY
KKEE AND KKEI/V I
LYS-RICH.
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InterPro; IPR000299; Band 4.1.
InterPro; IPR000299; Band 4.1.
InterPro; IPR000387; Tyr_Pp.
InterPro; IPR000242; Tyr_Pp.
Pfam; PF00102; Y phosphatase; 1.
Pfam; PF00102; Y phosphatase; 1.
PRINTS; PR00935; BAND41.
PRINTS; PR00935; BAND41.
SMART; SN00295; B41; 1.
SMART; SN00294; PTPC; 1.
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Q62136;
Q1-NOV-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Oncogene 10:407-414(1995).

-!- FUNCTION: MAY BE INVOLVED IN THE REGULATION
-!- DIFFERENTIATION OF LIVER CELLS.
-!- CATALYTIC ACTIVITY: Protein tyrosine phosphate.
-!- TISSUE SPECIFICITY: LIVER.
PROSITE; PS00660; FERM 1; 1.
PROSITE; PS00661; FERM 2; 1.
PROSITE; PS00061; FERM 3; 1.
PROSITE; PS00033; TYR_PHOSPHATASE_PTP; 1.
PROSITE; PS00055; TYR_PHOSPHATASE_PTP; 1.
PROSITE; PS00055; TYR_PHOSPHATASE_2; 1.
Structural protein; Cytoskeleton; Hydrolase
                                                                                                                                                                                                                                                 HSSP;
                                                                                                                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a collab between the Swiss Institute of Bioinformatics and the EMBL outst the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for comentities requires a license agreement (See http://www.isb-sib.ch/anor send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDIINE=95140431; PubMed=7838537;
Higashitsuji H., Arii S., Furutani M., Imamura M., Kaneko Y.,
Takenawa J., Nakayama H., Fujita J.;
"Enhanced expression of multiple protein tyrosine phosphatases in the
regenerating mouse liver: isolation of PTP-RLIO, a novel cytoplasmic-
type phosphatase with sequence homology to cytoskeletal protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      [1]
SEQUENCE FROM N.A.
TISSUE=Liver;
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Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOUSE
                                                                                                                                                                                                                                                              EMBL; D37801; BAA07053.1; PIR; I58345; I58345.
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                                                                                                                                                                                                                                                                                                                                                                                                                                           SIMILARITY: Contains 1 FERM domain. SIMILARITY: BELONGS TO THE NON-RECEPTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                TYROSINE PHOSPHATASE FAMILY.
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Sciurognathi;
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thi; Muridae;
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DT Hypot
GN YIROS
OC Sacch
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Best Local Similarity
Matches 137; Conserv
                                                       01-FEB-1995 (Rel. 31, 0
01-FEB-1995 (Rel. 31, 1
15-SEP-2003 (Rel. 42, 1
Hypothetical 74.8 kDa F
YIROJOW OR YIB3W.
                                                                                        P40563;
01-FEB-1995
01-FEB-1995
15-SEP-2003
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ACT SITE
DOMAIN
DOMAIN
SEQUENCE
            Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomyco
Saccharomycetales; Saccharomycetaceae; Sa
                                                                                                                                                                   YEAST
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                                                                                                                                                                                                                                                                                                                     AFLAPITHPERLGKPNSQIEYTEDEVRIAQLADKYTTSDGYIFDEHDIISDEGDAYVTPH
                                                                                                                                                                                                                                                                                                                                                    GGRYSHKKSLSDATMLIDSSEEDEDLE----EDSSREQAISAVSEPRLTAAFSQELNYPC
                                                                                                                                                                                                                                                                                                                                                                                ----AHKALFXNKGRNSDFQALDKLLERLNDESTNKEKLVDDL-------L
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                                                                                                                                                                                                                                                                                                                                                                                                                                            LSKQESV------SHTLTAKKENVAPR-----DQEFYDKAYNLLTE---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SLQTQAATLNSVRRDSSSR----MSLPKPQPYAMPPPPQLHYNGHYT-----EPF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EAELLYMQEVERMDGYGEESYPAK-DSQGSDISIGACLDGIFVKHKNGRPPVVFRWHDIA
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Last sequence up
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PROTEIN-TYROSINE PHOSPHATASE.
BY SIMILARITY.

POLY-PRO.
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                               Saccharomycotina;
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                                                                      ation update)
BET1-PAN1 in
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                 Saccharomyces
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                               Saccharomycetes;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; X79743; -; NOT ANNOTATED_CDS.
EMBL; Z38062; CAA86205.1; -.
PIR; S48437; S48437.
SGD; S0001442; YIR003W.
Hypothetical protein.
SEQUENCE 679 AA; 74763 MW; 9DE7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Churcher C.M., Bowman S., Badcock K., Bankier A., Brown D., Chillingworth T., Connor R., Devlin K., Gentles S., Hamlin N., Harris D.E., Horsnell T., Hunt S., Jagels K., Jones M., Lye G., Moule S., Odell C., Pearson D., Rajandream M.A., Rice P., Rowley Skelton J., Smith V., Walsh S., Whitehead S., Barrell B.G.; "The nucleotide sequence of Saccharomyces cerevisiae chromosome I Nature 387:84-87(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Schwager C., Zimmermann J., Sander C., Ansorge W.; "Nucleotide sequence and analysis of the centromeric region of yeast
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=95282515; PubMed=7762303;
Voss H., Tamames J., Teodoru C., Valencia A.,
Schwager C., Zimmermann J., Sander C., Ansorge
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        [1]
SEQUENCE FROM N.A.
STRAIN=S288C;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AHADNVRTKEEINROKQEHSQHREGGTPRNDGAVALARSQGRYTTDD--GYIFNASDIIE 178
   ---DIISDEGDAYVTPHMGHSHWIGKDSLSDKEKVAAQAYTKEKGILPP---
                                                                                                                                                                                                                                                                                                                                                                                                                              DTGDAYIVPHGDHYHYIPKNELSASELAAAEAFLSGRGNLSNSRTYRRQNSDNTSRTNWV 238
                                                             LAFLAPITHPERLG-----KPNSQIEYTEDEVRIAQLADKY----
                                                                                                                                                                                LVRKVGEGYVFEEKGISRYVFAKDLP----SETVKNLESKLSKQESVSHTLTAKKENVAP
                                                                                                                                                                                                                H--QEQQEEKIFQNPTDEESTTSLNEKQEGKDNMEVNSQPQGPSDTETVIAATSSNVPSQ
                                                                                                                                                                                                                                                                            DRSHFEEKLIPGDMKVQVDVSKDVEEGSLNALPPSGITESDDKAEKFTKHPESSLEELQK 263
                                                                                                                                                                                                                                                                                                                                                               PSVSN-----PGTTNTNTSNN--SNTNSQASQSNDIDSLLKQLYKLPLSQRHVESDGLVF 291
                                                                                                                                                                                                                                                                                                                                                                                                  EI-ESLISKHNIHNVSRKKSPTSVEEGKVAAIHONG-
                                                                                                                                                                                                                                                                                                                                                                                                                                                           AGTPNVPTRRPILKAKTMTS-FESGMDQESLPKVPLQRPVRRSTTEELNNVMNNTSKELE
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                                 ----PSERPKRRAPPPVPKKPSSRIAAFQEMLQKQQQQDLHNNGNSSATTASADIAKKH
                                                                                                                    RDOEFYDKAYNLLTEAHKALFXNKGRNSDFOALDKLLERLNDE-----STNKEKLVDDL 488
                                                                                                                                                                                                                                              HWVPDSRPEQPSPQPTPEPS---------PGPQPAPNLKIDSNSSLVSQ
                                                                                                                                                                                                                                                                                                        DPAQITSRTARGVAVPHGD------HYHFIPYSQMSELEERIARII-----PLRYRSN
                                                                                                                                                                                                                                                                                                                                      PLEKNEHEGAEGNESAISPSNLVNKSNNEVTEHSDSEDLTEK-----QKVHAALDNEAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  74763 MW; 9DF79500375339E7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; Pred. No. 3.6;
97; Mismatches 260;
                                                                                                                                                     ----NDVPVIPRSRPKKDFEAHVQKEE
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                                                                                           -----KRVSEECDSTLISTEEESKIPKI
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RESULT 38
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                                                                                                                                                aureus adhesin.";
Nat. Struct. Biol.
                                                                                                                                                                       Moore D., Jin L., Schneider A., Del
Narayana S.V.L.;
"Structure of the collagen-binding
                                                                                                                                                                                                                   MEDLINE=97475225; PubMed=9334749; Symersky J., Patti J.M., Carson M
                                                                                                                                                                                                                                                                        MEDLINE=94032261; PubMed=8218209; Patti J.M., Boles J.O., Hoeook M.; Patti J.M., Boles J.O., Hoeook M.; "Identification and biochemical characterization of the ligand binding domain of the collagen adhesin from Staphylococcus aury Biochemistry 32:11428-11435(1993).
                                                                                                                                                                                                                                                                                                                                                                                        J. Biol.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Staphylococcus
J. Biol. Chem.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN=FDA 574;
MEDLINE=92165839; PubMed=1311320;
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15-DEC-1998
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15-SEP-2003
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"Molecular characterization and expression of a "Molecular characterization and expression of a Staphylococcus aureus collagen adhesin.";
J. Biol. Chem. 267:4766-4772(1992).
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B SWISS-PROT entry is copyright. It is prove
ween the Swiss Institute of Bioinformatics
European Bioinformatics Institute. There a
by non-profit institutions as long as j
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                                                                                                                  Struct. Biol. 4:833-838(1997).
FUNCTION: MEDIATES ATTACHMENT O
COLLAGEN-CONTAINING SUBSTRATA.
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(Rel. 37, Last sequence update)
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InterPro; IPR006192; LPXTG.
TIGRRAMS; TIGR01167; LPXTG anchor; 1
PROSITE; PS50847; GRAM_POS_ANCHORING; FALSE NEG.
Cell wall; Peptidoglycan-anchor; Repeat; Signal;
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or send an email to license@isb-sib.ch).
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                                                             "Polymorphism of the precursor for the Plasmodium falciparum merozoites: studiEMBO J. 4:3823-3829(1985).
                                                                                                          Mackay M., Goman M., Bone N., Stunnenberg H., Bujard H.;
                                                                                                                                         SEQUENCE FROM N.A.
MEDLINE=86136024; PubMed=3004972;
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Eukaryota; Alveolata;
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lle R., Bujard H.;
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Best Local Similarity 19.
Matches 132; Conservative
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Pfam; PF00008; EGF; 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            entities requires a license agreement (S or send an email to license@isb-sib.ch).
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Submitted (JUN-1995) to the EMBL/GenBank/DDBJ databases -!- SUBCELLULAR LOCATION: Attached to the membrane by a
                ဝှု
                                                 GPI-anchor
ANTIGENS
                83
                kDa,
   Q
                42
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REPEAT. PROTEIN Glycoprotein; CRC64; (POTENTIAL).
(POTENTIAL).
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(POTENTIAL).
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| Matches | 13. | 132; CONSERVATIVE 90; NISMATCHES 229; Indels 216; Gaps 29        | 29; |
|---------|-----|--|-----|
| Ü       | 20  | VTHESYQELVKKLEALEDAVLTGYSLFHKEKMILNEEEITTKGASAQSGTSGTSGTSGTS;    | 79  |
|         | 239 | -PSVSNPGTTNTNTSNNSNTNSQASQSNDI-DSLLKQLYKLPLSQRHVESD 2            | 287 |
| J       | 80  | GPSGTSP-SSRSNTLPRSNTSSGASPPADASDSDAKSYADLKHRVRNYLLTIKELKYPQ- 137 | 37  |
|         | 288 | GLVFDPAQITSRTARGVAVPHGDHYHFIPYSQMSELEERIARIIP-LRYRSNHWVPDSRP     | 346 |
| J       | 138 | LFDLTNHMLTLCDNIHGFKYLIDGYEEINELLYKLNFYFDLLRAKLNDVCANDYC 1        | 192 |
| `       | 347 | EQPSPQPTPEPSPGPQPAPNLKIDSNS-SLVSQLVRKVGEGYVFEEK 392              | 92  |
| Ū       | 193 | QIPFNLKIRANELDVLKKLVFGYRKPLDNIKDNVGKMEDYIKKNK                    | 237 |
|         | 393 | ESKLSKQESVSHTLTAKKENVAPRDQEFYDK                                  | 442 |
| Ü       | 238 | KTIENINELIEESKKTIDKNKNATKEEEKKKLYQAQYDLSIYNKQLE                  | 284 |
|         | 443 | LLAFLAPITHPERL   | 501 |
| Ū       | 285 | EAHNLISVLEKRIDTLKKNENIKELLDKINEIKNPPPPANSGNTPNTL                 | 331 |
|         | 502 | GKPNSQIEYTEDEVRIAQLADKYTTSDGYIFDEHDIISDEGDAYVTPHMGHSHWIGKDSL 5   | 561 |
| Ü       | 332 | LDKNKKIEBHEKEIKHIKFNIDSL 3                                       | 359 |
| `       | 562 | SDKEKVAAQAYTKEKGILPPSPDADVKANPTGDSAAAIYNRVKGEKRIPLVRLPYMVEHT 621 | 21  |

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RESULT 40
BUD3 YEAST
ID BUD3 YEAST
ID TO1-MAY-1992 (Rel. 22, Created)
DT 01-MAY-1995 (Rel. 32, Last sequence updat
DT 01-MAY-1995 (Rel. 32, Last sequence updat
DT 28-FEB-2003 (Rel. 41, Last annotation upo
DE Bud site selection protein BUD3.
GN BUD3 OR YCL014W OR YCL14W/YCL13W.
OS Saccharomyces cerevisiae (Baker's yeast).
OC EUKARYOCLA; Pungi; Ascomycota; Saccharomyce
OC Saccharomycetales; Saccharomycetaceae; Sa
OX NCB1_TaxID=4932;
RN GLI
RN SEQUENCE FROM N.A.
RN SEQUENCE FROM N.A.
CHANT J., Mischke M., Mitchell E., Herskc
RI J. Cell Biol. 129:767-778(1995).
RN SEQUENCE FROM N.A.
Oliver S.G., Anwar R., Brown A., Gent M.E.
RA Stateva L.I.;
RN CJI
RN SEQUENCE FROM N.A.
RA Oliver S.G., Anwar R., Brown A., Gent M.E.
RA Stateva L.I.;
RN REVISIONS.
RA STATEVAL S.G.;
RA Gromadka R.;
Submitted (JAN-1996) to the EMBL/GenBank/
RN YALLES G., Volckaerts G.;
RA SUBmitted (JUN-2001) to the EMBL/GenBank/
RL Submitted (JUN-2001) to the EMBL/GenBank/
RP REVISIONS.
RA GROMAGRATE TO RECOGNIZE A SPATIAL LAND
CC ENTABLISHING THE AXIAL BUDDING PATTER
CC COPERATE TO RECOGNIZE A SPATIAL LAND
CC LINE SWISS-PROT entry is copyright. It is
CC DEVWeen the Swiss Institute of Bioinform
CC the European Bioinformatics Institute.
CC ESTABLISHING THE AXIAL BUDDING PATTER
CC ESTABLISHING THE AXIAL BUDDING PATTER
CC Coperate and this statement is not remove
CC entities requires a license agreement (Se
CC or send an email to license@isb-sib.ch).
CC C SEMBL; U17580; AAAA6315.1; -.

DR EMBL; U17580; AAAA6315.1; -.

EMBL; N39720; CAAA2346.2; -.

DR EMBL; SOUNDS SPANOSEP.
SGD SCOUNCE 1636 AA; 184717 MW; 9E4E46BF
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                                                                                                                                                                                       the European Bioinformatics Institute. There are no rest
use by non-profit institutions as long as its content
modified and this statement is not removed. Usage by ar
entities requires a license agreement (See http://www.isb-
or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                  Valles G., Volckaerts G.;
Submitted (JUN-2001) to the EMBL/GenBank/DDBJ databases.
-:- FUNCTION: CO-ASSEMBLES WITH BUD4 AT BUD SITES. BUD4 AND BUD3 M
-:- COOPERATE TO RECOGNIZE A SPATIAL LANDMARK (THE NECK FILAMENTS)
DURING MITOSIS AND THEY SUBSEQUENTLY BECOME A LANDMARK FOR
ESTABLISHING THE AXIAL BUDDING PATTERN IN G1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.

MEDLINE=95247824; PubMed=7730410;

Chant J., Mischke M., Mitchell B., Herskowitz I., Pring Proceeding the axial budding pattern J. Cell Biol. 129:767-778 (1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Saccharomyces cerevisiae (Baker's yeast).

Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WGNASEHVLGKKDHSEDPNKNFKADEEPVEETPAEPEVPQVETEKVEAQ-----
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(Rel. 06, Created)
(Rel. 12, Last sequence update)
(Rel. 41, Last annotation updat
wall protein precursor (MWP).

update)

STANDARD;

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EMBL; M15364; AAAB7321.1; -.
EMBL; M14238; AAA22372.1; -.
EMBL; M19115; AAA22760.1; -.
EMBL; M31828; AAA22619.1; -.
PIR; A28555; A28555.
InterPro; IPR001119; SLH.
Pfam; PF00395; SLH; 2.
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                                                                                                                                                                                                      This SWI
between
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Tsuboi A., Uchihi R., Adachi T., Sasaki T., Hayakawa S., Yam Tsukagoshi N., Udaka S.;
Tsukagoshi N., Udaka S.;
"Characterization of the genes for the hexagonally arranged layer proteins in protein-producing Bacillus brevis 47: comp nucleotide sequence of the middle wall protein gene.";
J. Bacteriol. 170:935-945(1988).
                                                                                                                                                                                                                                                                            protein gene from Bacillus brevis 47.";

J. Bacteriol. 171:6747-6752(1989).

-!- FUNCTION: THE MIDDLE WALL PROTEIN BINDS TO PEPTIDOGLYCAN AND THE OUTER CELL WALL PROTEIN.

-!- SUBUNIT: THE MIDDLE CELL WALL LAYER IS COMPOSED OF SUBUNITS THE MIDDLE CELL WALL PROTEIN. THESE PROTEINS FORM A HEXAGONZ ARRAY WITH A LATTICE CONSTANT OF 14.5 NM IN THE MIDDLE CELL ARRAY WITH A LATTICE CONSTANT OF 14.5 NM IN THE MIDDLE CELL
                                 SIGNAL
                                                                                                                                                  use by non-profit institutions as long modified and this statement is not removed. entities requires a license agreement (See or send an email to license@isb-sib.ch).
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Tsukagoshi N., Udaka S.;
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Tsukagoshi N.,
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Bacteria; Firmicutes; Bacillales; Paenibacillaceae;
MCBI_TaxID=1393;
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                                                                                                                                                                                                                                    HEXAGONAL S-LAYER.
SIMILARITY: Contains 3 S-layer homology (SLH) domains.
                                                                                                                                                                                            European
                                                                                                                                                                                                                                                         SUBCELLULAR LOCATION: CELL WALL. THIS BACTERIUM IS
                                                                                                                                                                                                                                                                      WALL LAYERS.
                                                                                                                                                                                                      SWISS-PROT entry is copyright. It is produsen the Swiss Institute of Bioinformatics
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                                                      PS01072;
                                          S-layer;
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                                                                                                                                                                                      Swiss Institute or Brown.
Bioinformatics Institute.
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R., Engelhardt H.,
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PVKLYRATVELNSKVKAE-DVDAIEFYFNGKKVEPSLLNFKDGVITIGYNTEDKVTSSKI
                                                                                                                                                                                SDVRKDT--ITYKDADDNKKKASIKSATVYFDLYDDFGEADGVNEGDYVVMIDSGDISGT
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                                            PNKNFKADEEPVEETPAEPEVPQVE----TEKVEAQL---KEAEVLLA----
                                                                                                                                                                                                                             -EVKNGNLIIPHKDHYHNIKFA-----WFD-----
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Pred. No. 7.
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Pfam; PF01576; Myosin_N; 1.
Pfam; PF01576; Myosin_tail; 1.
PRINTS; PR00193; MYOSINHEAVY.
ProDom; PD000355; myosin_head; 1.
SMART; SM00015; IQ; 11.
SMART; SM00242; MYSC; 1.
PROSITE; PS50096. TO:
             NP_BIND
MOD_RES
MOD_RES
                                                                                                                                                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                         EMBL; AB022023; BAA36494.1; -. EMBL; U15716; AAA87715.1; -. HSSP; P10587; 1BR2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             J. Biol. Chem. 270:14533-14540(1995).

-!- FUNCTION: CELLULAR MYOSIN APPEARS TO PLAY A ROLE IN CYTOKIN CELL SHAPE, AND SPECIALIZED FUNCTIONS SUCH AS SECRETION AND CAPPING (BY SIMILARITY).

-!- SUBUNIT: MYOSIN IS A HEXAMERIC PROTEIN THAT CONSISTS OF 2 H CHAIN SUBUNITS (MHC), 2 ALKALI LIGHT CHAIN SUBUNITS (MLC) A REGULATORY LIGHT CHAIN SUBUNITS (MLC-2).

-!- DOMAIN: THE RODLIKE TAIL SEQUENCE IS HIGHLY REPETITIVE, SHO CYCLES OF A 28-RESIDUE REPEAT PATTERN COMPOSED OF 4 HEPTAPE CHARACTERISTIC FOR ALPHA-HELICAL COILED COILS.
-!- SIMILARITY: Contains 1 myosin-like globular head domain.
-!- SIMILARITY: Contains 1 IQ domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ohāra M., Ishiguro N., Shinagawa M.;
"Bos taurus nonmuscle myosin heavy chain B mRN
Submitted (JAN-1999) to the EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BOVIN
                                                                   DOMAIN
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                entities requires a license agreement (s or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Neuronal cell expression of inserted isoforms myosin heavy Chain II-B.";
                                                                                                                                                                                                                                                                InterPro; IPR001609; myosin_head.
InterPro; IPR004009; Myosin_N.
InterPro; IPR002928; Myosin_tail.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bovidae; Bovinae; Bos.
NCBI_TaxID=9913;
 SEQUENCE
                                                                                                                                                                                                                                        Pfam; PF00612; IQ; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=95301542; PubMed=7782316;
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16-OCT-2001
                                                                                                                                                                                                                                                                                                            nterPro; IPR000048;
                                                                                                                                                                                                                                                         nterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Biol.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 B) (Nonmuscle myosin
                                                                                                                                                                                                         PF00063; myosin_head; 1.
PF02736; Myosin_N; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BOVIN
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-2001 (Rel. 40, Last sequence update)
-2001 (Rel. 40, Last annotation update)
-2001 (Rel. 40, Last annotation update)
1 heavy chain, nonmuscle type B (Cellular )
                                                                                                          ; PS50096; IQ; 1.
ATP-binding; Calmodulin-binding;
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Eutheria; Cetartiodactyla; Ruminantia; Pecora;
786
845
178
701
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1976
                                                                                               Alkylation;
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Α,
              815
1976
185
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Best Local Sim
Matches 152;
MOUSE STANDARD; PKI; J...

PGCV MOUSE STANDARD; PKI; J...

Q62059; Q62058; Q9CUUU;

Q1-NOV-1997 (Rel. 35, Created)

Q1-NOV-1997 (Rel. 35, Last sequence update)

15-SEP-2003 (Rel. 42, Last annotation update)

Versican core protein precursor (Large fibroblast proteoglycan)

Verndroitin sulfate proteoglycan core protein 2) (PG-M).
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18.5%; Pred. No. 18;
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Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
A Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
A Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
A Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
A Kadota K., Matsuda H.A., Ashburner M., Batalov S., Cochiwa H.,
A Kuchi P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
A Kuchi P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
A Schriml L. M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
A Schriml L. M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
A Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
A Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
A Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
A Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
A Gustincich S., Ringwald M., Rodriguez I., Sakamoto N.,
A Sasaki H., Sato K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
A Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
Hayashizaki Y.,
Functional annotation of a full length moves CNN Collection ".
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J. Biol.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A. (ISOFORMS V0; V1 AND V2).
STRAIN=C57BL/6, and Swiss Webster; TISSUE=Brain;
MEDLINE=95122551; PubMed=7822336;
TIO. K., Shinomura T., Zako M., Ujita M., Kimata
                                                                                                                                                                                                                                                                                                                                                                                                                                  Aspberg A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                     PubMed=10400671;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Functional annotation of Nature 409:685-690(2001).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE OF 1-1692 FROM N.A. STRAIN=C57BL/6J; TISSUE=Skin;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=95181355; PubMed=7876137; Zako M., Shinomura T., Ujita M., Ito "Expression of PG-M(V3), an alternati
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N
STRAIN=C57BL/6;
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Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                  "Fibulin-1 is a ligand
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INTERACTION WITH FBLN1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=10090;
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Biol.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Biol.
                                                                                                                                                                                                                                                             SUBUNIT: Interacts with FBLN1.
SUBCELLULAR LOCATION: Secreted; extracellular matrix.
ALTERNATIVE PRODUCTS:
                                                                                                                                                                                                                                                                                                                              FUNCTION: May play a role in intercellular signaling and in connecting cells with the extracellular matrix. May take part the regulation of cell motility, growth and differentiation.
                                                                                                                                                                                                                               Event=Alternative splicing; Named isoforms=4;
Comment=Additional isoforms seem to exist;
                                                                                                                                                                                                                                                                                                                hyaluronic acid
                                                                                                                                                             [soId=Q62059-2;
                                                                                                                                                                                              [soId=Q62059-1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           മ
                                                                                                                                                                                                                                                                                                                                                                                  Chem.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           on of PG-M(V3), an alternatively chondroitin sulfate attachment i
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               hinomura T., Zako M., Ujita M., Kimata K., forms of mouse PG-M, a large chondroitin can generated by alternative splicing.";
                                                                                                                                                                                                                                                                                                                                                                                                                  Adam S., Kostka G., is a ligand for the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               N.A. (ISOFORM V3).
                                                                                                                                                                                                                                                                                                                                                                                    274:20444-20449(1999).
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                                                                                                                                                         Sequence=VSP_003087,
                                                                                                                                                                                              Sequence=Displayed;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    a full-length mouse cDNA collection.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (ISOFORM
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C-type
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lectin domains
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Y spliced f
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           in region in mouse and human
                                                                                                                                                         VSP_003088;
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PROSITE; PS00010; ASX HYDROXYL; 1.
PROSITE; PS00615; C TYPE LECTIN 1; 1.
PROSITE; PS00614; C TYPE LECTIN 2; 1.
PROSITE; PS00022; EGP 1; 2.
PROSITE; PS001186; EGF 2; 1.
PROSITE; PS01187; EGF CA; 1.
PROSITE; PS01184; LINK; 2.
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SMART; SM00034; CLECT; 1.
SMART; SM00179; EGF_CA; 1.
SMART; SM00409; IG; 1.
SMART; SM00445; LINK; 2.
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InterPro; IPR001881; EGF Ca.
InterPro; IPR006209; EGF like.
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PRINTS; PR01265; LINKMODULE.
ProDom; PD000918; Link; 2.
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Pfam; PF00059; lectin_c; 1.
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EMBL; D32040; BAA06802
EMBL; AK014525; BAB294
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MGD; MGI:102889; Cspg2
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-!- SIMILARITY: Contains 1 Sushi (SCR) domain.
-!- SIMILARITY: BELONGS TO THE AGGRECAN/VERSICAN PROTEOGLYCAN FAMILY.
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SIMILARITY: BELONGS TO PEPTIDASE FAMILY S6.
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use by non-profit institutions as long as its cont
modified and this statement is not removed. Usage by an
entitles requires a license agreement (See http://www.isb-
or send an email to license@isb-sib.ch).
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01-NOV-1997 (Rel. 35, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Hypothetical 105.9 kDa protein in ADH3-RCA1 intergenic
YMR086W OR YM9582.10.
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SGD; S0004692; YMR086W.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes; Saccharomycetales; Saccharomycetaceae; Saccharomyces.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PEMEQADPTAVAAAASIGKLLMKKGNQSDNEQRPTYRSASMTNLRKPSAPKRMSSISSIS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          960 AA; 105873 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
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  -QALDKLLERLNDESTNKEKLVDDLLAFLAPITHPERLGKPNSQIEYTED
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                                                                                                                                                                                                                                                                                              -QRQKSKTHQRISYDEAQRTFKDFGGPQARGILTGQHRTENPS
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Pred. No. 7.
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(See http://www.isb-sib.ch/announce/
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Science 254:1791-1794(1991)
                                                                                                                                                                                                                                                                                                                                        MEDITINE-92108424; PubMed=1840704; MEDITINE-92108424; PubMed=1840704; Williams T.M., Moolten D., Burlein J., Romano J., Bhaerman F. Godillot A., Mellon M., Rauscher F.J. III, Kant J.A.; "Identification of a zinc finger protein that inhibits IL-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bachman N.J., Scarpulla R.C.;
"A human zinc finger homeodomain protein homologous to delta-crystallin enhancer binding protein, delta EF1.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A. MEDLINE=94186507; PubMed=8138542;
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Mammalia; Eutheria;
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15-JUL-1999 (Rel. 38, Last sequence up
15-SEP-2003 (Rel. 42, Last annotation
Transcription factor 8 (NIL-2-A zinc f
regulator of IL2).
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                                                             between
                                                                                                                                   FUNCTION: INHIBITS INTERLEUKIN-2 (IL-2) GENE EXPRESSION. MAY RESPONSIBLE FOR TRANSCRIPTIONAL REPRESSION OF THE IL-2 GENE. ENHANCES OR REPRESSES THE PROMOTER ACTIVITY OF THE ATELAI GEN DEPENDING ON THE QUANTITY OF CDNA AND ON THE CELL TYPE. SUBCELLULAR LOCATION: Nuclear.
TISSUE SPECIFICITY: EXPRESSED IN HEART AND SKELETAL MUSCLE, B NOT IN LIVER, SPLEEN, OR PANCREAS.
SIMILARITY: BELONGS TO DELTA-EF1/ZFH-1 FAMILY OF TWO-HANDED Z
  European Bioinformatics Institute. The by non-profit institutions as long ified and this statement is not remove.
                                                                                                                        FINGER/HOMEODOMAIN PROTEINS.
                                                         SWISS-PROT entry is copyright. It is produced through en the Swiss Institute of Bioinformatics and the E
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Catarrhini;
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GO; GO:0003714; F:transcription co-repressor act:
GO; GO:0003700; F:transcription factor activity;
GO; GO:0008270; F:zinc ion binding activity; TAS
GO; GO:0008283; P:cell proliferation; TAS.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ProDom; PD000010; Homeobox; 1. 
ProDom; PD000003; Znf C2H2; 2. 
SMART; SM00389; HOX; 1. 
SMART; SM00355; ZnF_C2H2; 7.
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InterPro; IPR007087; Znf_C2H2.
Pfam; PF00096; zf-C2H2; 7.
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TRANSFAC; T00625; -
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EMBL; U12170;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               domeobox;
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SPGPQPAPNLKIDSNSSLVSQLVRKVGEGYVFEEKGISRYVFAK----DLPSETVKNLE-
                     DQPQSANANE - - -
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                                        SRTARGVAVPHGDHYHFIPYSQMSELEERIARIIPLRYRSNHWVPDSRPEQPSPQPTPEP
                                                               YALNAQPSAEELSKIADSVNLPLDVVKKWFEKMQAGQISVQSSEPSSPEPGKVNIPAKNN
                                                                                    GTTNTNTSNNSNTNSQASQSNDIDSLLKQLYKLPLSQRHVESD-----
                                                                                                         DL--KQPTQPPPLPAAEAEKPESSV$SATGDGNLSPSQPPLK-
                                                                                                                              HYIPKNELSASELAAAEA-----FLSGRGNLSNSRTYRRQNSDNTSRTNWVPSVSNP
                                                                                                                                                     LTVKSEKDKSFEGGV--NDSTCLLC-----DD------CPGDINALPELKHY
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19.0%;
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V -> I (IN REF. 2).

E -> Q (IN REF. 3).

I -> T (TN PET. 3).
                    PQDSTVNLQS-----PLKMTNSPVLPVGSTTNGSRSSTPSP
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C2H2-TYPE.
C2H2-TYPE
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Pred. No. 9.7
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Q9JKI1; Q9JK10; Q9ROD9; Q9WUE9; Q9WUF0;
28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Reticulon 4 (Neurite outgrowth inhibitor) (Nogo (Glutt vesicle 20 kDa protein).
"Cloning of a member of the reticulon minor splice variants.";
Submitted (FEB-1999) to the EMBL/GenBa
                                                                                                                                                                                                                                                     Morris N.J., Ross S.A., Neveu J.M., Lane W.S., Lie "Cloning and characterization of a 22 kDa protein a new member of the reticulon family.", Biochim. Biophys. Acta 1450:68-76(1999).
                                                                   STRAIN=Wistar Kyoto;
                                                                                                                                                                    Chen M.S., Huber A.B., Van der Haar M.E., Spillmann A.A., Christ F., Schwab M.E.;
                                                                                                                                                                                                    SEQUENCE FROM N.A. (ISOFORMS 1; 2 AND 3). MEDLINE=20129258; PubMed=10667796;
                                                                                                                                                                                                                                                                                                                        STRAIN=Sprague-Dawley;
MEDLINE=99249816; PubMo
                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A. (ISOFORM 3),
                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rat
                                                                                                                                                                                                                                                                                                                                                                                                                                             Rattus norvegicus (Rat).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                RTN4 OR NOGO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RTN4_RAT
                                                 Ito T., Schwartz S.M.
                                                                                    SEQUENCE
                                                                                                                    Nature 403:434-439(2000)
                                                                                                                                  "Nogo-A is a myelin-associated neurite outgrowth inhibitor and antigen for monoclonal antibody IN-1.";
                                                                                                                                                                                                                                                                                                                                                                                         _TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1089
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Q9JK10; Q9ROD9; Q9WUE9; Q9WUF0;
                                                                                                                                                                                                                   FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ----VKNGNLIIPH---
                                                                                                                                                                                                                                                                                                                          wley; TISSUE=Adipocyte;
PubMed=10231557;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -TEGLMKDDRAESQASS-LGQKVGESSEQVSEEKTN 1122
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                                                                 (ISOFORMS 2 AND 4)
); TISSUE=Vascular
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -SYCKREAEERDSTEQEEAGPEILSNEHVGARASPSQGDSDERESLTREED
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 EMBL/GenBank/DDBJ databases
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                                                                                                                                                                                                                                                                                                                                                           AND PARTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1163
                                                                 smooth muscle;
                              gene family in rat:
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                                                                                                                                                                                    Frank M.,
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ein from rat adipocytes:
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   EMBL; AF051335; AAF01564.1; -.

EMBL; AJ242961; CAB71027.1; -.

EMBL; AJ242962; CAB71029.1; -.

EMBL; AJ242963; CAB71029.1; -.

EMBL; AF132045; AAD31019.1; -.

EMBL; AF132046; AAD31020.1; -.

EMBL; AF132045; C:endoplasmic reticulum membrane, into GO; GO:0030176; C:endoplasmic retivity ISS.

GO; GO:0005615; F:protein binding activity; ISS.

GO; GO:0019987; P:negative regulation of axon extens:
                                                                                                                                                                                                     TRANSMEM
DOMAIN
                                                                                                                                                                                                                                       TRANSMEM
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EM the European Bioinformatics Institute. There are no restruse by non-profit institutions as long as its content modified and this statement is not removed. Usage by and entities requires a license agreement (See http://www.isb-sor send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GrandPre T., Li S., Strittmatter S.M. "Nogo-66 receptor antagonist peptide Nature 417:547-551(2002).
 VARSPLIC
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                                                                                                                                                                                                                                                                                        Endoplasmic
                                                                                                                                                                                                                                                                                                            PROSITE;
                                                                                                                                                                                                                                                                                                                          Pfam; PF02453;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -!- SUBCELLULAR LOCATION: Integral membrane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=22033691; PubMed=12037567; GrandPre T., Li S., Strittmatter S.M.;
                                                                                                                                                      DOMAIN
                                                                                                                                                                                                                                                                                                                                             InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FUNCTION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TISSUE SPECIFICITY: Isoforms 1, 2 and 3 are present in optic nerve, spinal cord and cerebral cortex. Isoforms 1 and 2 are present in dorsal root ganglion, sciattic nerve and PC12 cells after longer exposure. Isoforms 2 and 3 are detected in kidney, cartilage, skin, lung and spleen. Isoform 3 is expressed at high level in skeletal muscle. In adult animals isoform 1 is expressed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Name=1; Synonyms=Nogo-A, NI-220-250; IsoId=09JK11-1; Sequence=Displayed; Name=2; Synonyms=Nogo-B, Foocen-M1; IsoId=09JK11-2; Sequence=VSP 005658;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Name=3; Synonyms=Nogo-C, VP20;
IsoId=Q9JK11-3; Sequence=VSP_005656,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SIMILARITY: Contains 1 reticulon domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SUBUNIT: Binds to RTN4R. Interacts with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FUNCTION: Potent neurite outgrowth inhibitor which may also block the regeneration of the nervous central system in adul
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    mainly in the nervous system.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Event=Alternative splicing; Named isoforms=4; Name=1; Synonyms=Nogo-A, NI-220-250;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ALTERNATIVE PRODUCTS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              membrane of the endoplasmic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ame=4; Synonyms=Foocen-M2;
IsoId=Q9JK11-4; Sequence=VSP_005659;
                                                                                                                                                                                                                                                                                                            PS50845;
                                                                                                                                                                                                                                                                                                                                          IPR003388; Reticulon.
                                                                                                                                                                                     990
1011
1105
1126
976
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1010
1104
1125
1163
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   975
                               975
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                                                                                                                                                                                                                                                                       Alternative splicing; Transme CYTOPLASMIC (Potential)
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              /FTId=VSP_005657.
Missing (in isoform
/FTId=VSP_005658.
                                                                                 /FTId=VSP_005656
AVLSAELSKTS -> M
                                                                                                    Missing (:
/FTId=VSP
                                                                                                                                                                      POLY-GLU
                                                                                                                                                                                       RETICULON.
                                                                                                                                                                                                     POTENTIAL.
CYTOPLASMIC (Potential).
                                                                                                                                                                                                                                         LUMENAL
                                                                                                                                                                                                                                                         POTENTIAL
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                                                                                                                                                                                                                                         (Potential)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                           anti-apoptosis;
axon extension;
   isoform 4)
                                                                                                                    isoform 3).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VSP_005657;
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RESULT 48

OSH1 YEAST STANDARD; PRT; 1188

AC P35845; P39555; P80234;

DT 01-UN-1994 (Rel. 29, Created)

DT 28-FEB-2003 (Rel. 41, Last sequence upda

DT 28-FEB-2003 (Rel. 41, Last annotation up

DE Oxysterol-binding protein homology
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Best Local S
Matches 170
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                      HMGHSHWIGKDSLSDKEKVAAQAYTKEKGILPPSPDA------DVKANPTGDSAA-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VAPRDQEFYDKAYNLLTEAHKALFXNKG--RNSDFQALDKLLERLNDESTNKEKLVDDLL
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                                                                                                                                              KEAEKKL---
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 EMBL; L28920; AAC09497.1; A:
EMBL; L28920; AAC09496.1; A:
EMBL; X74552; CAA52646.1; -
SGD; S0000082; OSH1.
GO; GO:0005799; C:early end
GO; GO:0000138; C:Golgi tra
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Storms R.
               Pfam;
SMART;
                                                       InterPro;
Pfam; PFOC
                                                                                                                                                                                                                                                                                                                                                                                                                                 Genetics 157:1117-1140(2001).
-!- FUNCTION: PLAYS A ROLE IN ERGOSTEROL
-!- SUBCELLULAR LOCATION: Found in Golgi
                                                             SGD; S0000082; OSH1.
GO; GO:0005769; C:early endosome; IDA.
GO; GO:0000138; C:Golgi trans cisterna;
GO; GO:0000138; C:Golgi trans cisterna;
GO; GO:0005545; F:phosphatidylinositol transcripto; IPR002110; ANK.
InterPro; IPR002110; ANK.
InterPro; IPR000648; Oxysterol_BP.
InterPro; IPR001649; PH.
                                                                                                                                                                                                                            the European Bioinformatics Institute. There are no rest
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or send an email to license@isb-sib.ch).
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SEQUENCE FROM N.A.
AB972;
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[1]
                           Pfam; PF01237; Oxysterol_BP; Pfam; PF00169; PH; 1.
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MEDLINE=21301806; PubMed=11408574;
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Eukaryota; Fungi; Ascomycota; Saccharomycotina;
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"Dual targeting of Oshlp, a yeast homologue of ox
protein, to both the Golgi and the nucleus-vacuol
Mol. Biol. Cell 12:1633-1644(2001).
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een the Swiss Institute of Bioinformatics and the EMBL outst
European Bioinformatics Institute. There are no restrictions
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Quellette B.F.F., Keng T.,
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, Phillips J., Rine J.;
tions of the yeast oxysterol-binding
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18.7%;
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                                         -SDADEFFDAEEAASDKKANDSEDLTTNKETPANAKPQEEAPED
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POLY-ASN.
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Pred. No. 11;
3; Mismatches 256;
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TP -> AS (IN REF. 2).
MW; 872952DFD2330207 CRC64;
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RESULT 49
UN89_CAEEL
 Waterston R.;
Submitted (APR-2002) to the EMBL/GenBank/DDBJ databases.
Submitted (APR-2002) to the EMBL/GenBank/DDBJ databases.
-i- FUNCTION: Structural component of the muscle M-line. Myofilament lattice assembly begins with positional cues laid down in the basement membrane and muscle cell membrane. UNC-89 responds to these signals, localizes, and then participates in assembling an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ON89 CAEEL STANDARD; PRT; 6632 AA.

001761; 017362;
15-SEP-2003 (Rel. 42, Created)
15-SEP-2003 (Rel. 42, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Muscle M-line assembly protein unc-89 (Uncoordinated UNC-89 OR COSD1.1.

Caenorhabditis elegans.
                                                                                                                                                                                                                                                     EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                    M-line.

"ITSSUE SPECIFICITY: Localizes to the middle of A-ban in ITSSUE SPECIFICITY: Localizes to the middle of A-ban SIMILARITY: Contains 1 DBL-homology (DH) domain.

"SIMILARITY: Contains 1 fibronectin type III domain.

"SIMILARITY: Contains 49 immunoglobulin-like C2-type

"SIMILARITY: Contains 1 PH domain.

"SIMILARITY: Contains 5 RCSD domains.

"SIMILARITY: Contains 1 SH3 domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN-Bristol N2;
MEDLINE=96180278; PubMed=8603916;
Benian G.M., Tinley T.L., Tang X., Borodovsky M.;
Benian G.M., Tinley T.L., Tang X., Borodovsky M.;
"The Caenorhabditis elegans gene unc-89, required assembly, encodes a giant modular protein composed transduction domains.";
                                        Pfam;
                                                                    Pfam;
Pfam;
                                                                                                Pfam;
                                                                                                                                                       InterPro;
InterPro;
                                                                                                                                                                                                                                         PDB;
                                                                                                                                                                                                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through a collab between the Swiss Institute of Bioinformatics and the EMBL outst the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN=Bristol N2;
Du Z., Le T.T., Wilson
Submitted (MAY-1997) to
                                                                                                                                                                                                                                                                                               entities requires a license agreement (S or send an email to license@isb-sib.ch).
                                                        Pfam;
                                                                                                                                                                                                                            WormPep;
                                                                                                                                                                                                                                                                   EMBL; U33058; AAB00542.1;
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Rhabditidae; Peloderinae;
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InterPro; IPR003598;
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i; PR00047; ig; 47.
i; PF00169; PH; 1.
i; PF0017; RCSD; 5.
i; PF00621; RhoGEF; 1.
i; PF00018; SH3; 1.
i; PF00018; SH3; 1.
i; SM00408; TGC2; 23.
i; SM00325; RhoGEF; 1.
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C09D1.1; CE
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IPR001849;
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IG_c2.
IG_MHC.
PH.
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PROSITE; PS50035; IG_LIKE; 4
PROSITE; PS50003; PH_DOMAIN;
PROSITE; PS50002; SH3; 1.
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                                                                        ADVKANPTGDSAAAIYNRVKGEKRIPLVRLPYMVEH-----TVEVKNGNL-IIPHKDHYH
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13; Mismatches
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RESULT
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P02468;
                                                                                                       MEDLINE=96196435; PubMed=8648631;
Baumgartner R., Czisch M., Mayer U.,
Timpl R., Holak T.A.;
"Structure of the nidogen binding LE
chain in solution.";
J. Mol. Biol. 257:658-668(1996).
                                                                                                                                                                                                                                                                                          X-RAY CRYSTALLOGRAPHY (2.1 ANGSTROMS)
MEDLINE=96196434; PubMed=8648630;
Stetefeld J., Mayer U., Timpl R., Hub
                                                                                                                                                                                                                                                                                                                                                                 Barlow D.P., Green N.M., Kurkinen M., Hogan E "Sequencing of laminin B chain cDNAs reveals coiled-coil alpha-helix.";
                                 <del>-</del>
                                                                                                                                                                                                                               factor-like (LE) modules of laminin
nidogen binding site.";
J. Mol. Biol. 257:644-657(1996).
                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=85051302; PubMed=6209134; Barlow D.P., Green N.M., Kurkinen
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Durkin M.E., Barto
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=88059118; PubMed=3680290;
Sasaki M., Yamada Y.;
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Mammalia; Eutheria; Rodentia;
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LAMC1 OR LAMC-1 OR LAMB-2.
Mus musculus (Mouse).
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01-JUL-1989
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Durkin M.E., Bartos B.B., Liu S.-H., Phillips S.L., "Primary structure of the mouse laminin B2 chain an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=10090;
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15-SEP-2003 (Rel. 42, Last annotation update)
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Biol. (
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SUBUNIT: Laminin is a complex glycoprotein, different polypeptide chains (alpha, beta, to each other by disulfide bonds into a cro
                                          Mol. Biol. 257:658-668(1996).

FUNCTION: Binding to cells via a high affinity receive thought to mediate the attachment, migration, are of cells into tissues during embryonic development with other extracellular matrix components.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           INE=88228071; PubMed=2836421;
a K., Burbelo P.D., Sasaki M., Yamada Y.;
laminin B2 chain promoter contains unique repeat sequences ctive in transient transfection.";
iol. Chem. 263:8384-8389(1988).
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consecutive laminin-type epidermal
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                 gamma),
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                 consisting of three
gamma), which are bo
                                                                                                                                                                      Huber
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                                                         receptor, laminin
n, and organization
ment by interacting
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PROSITE; PS01186; EGF 2; 2.
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Pfam; PF00055; laminin_Nterm; 1.
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GO; GO:0005604; C:basement membrane;
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DOMAIN: DOMAINS VI AND IV ARE GLOBULAR.
SIMILARITY: Contains 1 laminin N-terminal domain.
SIMILARITY: Contains 11 laminin EGF-like domains.
SIMILARITY: Contains 1 laminin IV domain.
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THE GAMMA-1 CHAIN IS A SUBUNIT OF LAMININ-1 (EHS LAMIN LAMININ-2 (MEROSIN), LAMININ-3 (S-LAMININ), LAMININ-4 LAMININ-6 (K-LAMININ) AND LAMININ-7 (KS-LAMININ).
SUBCELLULAR LOCATION: Extracellular TISSUE SPECIFICITY: FOUND IN THE BASEMENT MEMBRANES (MCOMPONENT).
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1KLO; 20-AUG-97.
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0052; laminin_B; 1.
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|      | 1439 TSTKADAER 1447   | рь |
|      | 762 TLQIMDNNSIMAEAEK 777  | Qy |
| 1438 | 1383 EEALRRIPAINRTIAEANEKTREAQLALGNAAADATEAKNKAHEAERIASAVQKNA     | рь |
| 761  | 707 EEPVEETPAEPEVPQVETEKVEAQLKEAEVLLAKVTDSSLKANATETLA-GLRNNL      | νQ |
| 1382 | 1332TADQLLARADAAKALAEEAAKKGRSTLQEANDILNNLKDFDRRVNDNKTAA           | рЬ |
| 706  | 650 YKAPNGYTLEDLFATIKYYVEHPDERPHSNDGWGNASEHVLGKKDHSEDPNKNFKAD     | Qy |
| 1331 | 1289 KEAADLDRLIDQKLKDYEDLREDMRGKEHEVKNLLEKGKAEQQ                  | Ъ  |
| 649  | 605 GEKRIPLVRLPYMVEHTVEVKNGNLIIPHKDHYHNIKFAWFDDHT                 | γQ |
| 1288 | 1243 DLEKQAARVHEBAKKAGDKAVEIYASVAQLTPVDSEALENEANKIK               | Ф  |
| 604  | 563 DKEKVAAQAYTKEKGILPPSPDADVKANPTGDSAAAIYNRVK                    | 8  |
| 1242 | 1184 LAERHKQEADDIVRVAKTANE-TSAEAYNLLLRTLAGENQTALEIEELNRKYEQAKNISQ | дь |
| 562  | QLADKYTTSDGYIFDEHDIISDEGDAYVTPHMGHSHWIGKDSLS                      | γQ |
| 1183 | 1124 ETGILAERARSRVESTEQLIEIASRELEKAKMAAANVSITQPESTGEPNNMTLLAEEARR | ф  |
| 508  | JVDDLLAFLAPITHPERLGKPNSQI   | Ş  |
| 1123 | 1065 -TDQAFEDRLKEAEREVTDLLREAQEVKDVDQNLMDRLQRVNSSLHSQISRLQNIRNTIE | Дb |
| 465  | 406 ETVKNLESKLSKQESVSHTLTAKKENVAPRDQEFYDKAYNLLTEAHKALFXNKGRNSDFQ  | Ş. |
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Search completed: November 14, 2003, 10:35:07 Job time : 53 secs

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Minimum DB
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Tettelin H., Nelson K.E., Paulsen I.T., Eisen J.A., Read T.D.,

Peterson S., Heidelberg J., DeBoy R.T., Haft D.H., Dodson R.J.,

Durkin A.S., Gwinn M., Kolonay J.F., Nelson W.C., Peterson J.D.,

Umayam L.A., White O., Salzberg S.L., Lewis M.R., Radune D.,

Umayam L.A., Khouri H., Wolf A.M., Utterback T.R., Hansen C.L.,

Holtzapple E., Khouri H., Wolf A.M., Utterback T.R., Hansen C.L.,

McDonald L.A., Feldblyum T.V., Angiuoli S., Dickinson T., Hickey I

Holt I.E., Loftus B.J., Yang F., Smith H.O., Venter J.C.,

Dougherty B.A., Morrison D.A., Hollingshead S.K., Fraser C.M.;

"Complete genome sequence of a virulent isolate of Streptococcus
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01-OCT-2001 (TrEMBLrel 18,
01-MAR-2003 (TrEMBLrel 23,
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SEQUENCE
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EMBL; AE007418; AAK75284.1;
TIGR; SP1175; -.
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TIGRFAMs; TIGR01363; strep_his_triad;
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VSNPGTTNTNTSNNSNTNSQASQSNDIDSLLKQLYKLPLSQRHVESDGLVFDPAQITSRT
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                                                                                            GDAYIVPHGDHYHYIPKNELSASELAAAEAFLSGRGNLSNSRTYRRQNSDNTSRTNWVPS
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EMBL; AF291695; AAK19155.1.
InterPro; IPR006270; Strep_his_triad.
TIGRRAMs; TIGR01363; strep_his_triad; 2.
SEQUENCE 816 AA; 91519 MW; 5359126A611D27ED CRC64;
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Choi G.H., Barash S.C., Rosen C.A., Masure H.
Gayle A., Brewah Y.A., Walsh W., Barren P., L
Langermann S., Johnson S., Koenig S.;
"Use of a Whole Genome Approach To Identify V
Affording Protection against Streptococcus pn
Infect. Immun. 69:1593-1598(2001).
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DT 01-MAR-2003 (TrEMBLrel. 23, Created)
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DT 01-MAR-2003 (TrEMBLrel. 23, Last annota
DE Pneumococcal histidine triad protein A.
GN PHTA OR SPR1061.
OS Streptococcus pneumoniae (strain ATCC B
OC Bacteria; Firmicutes; Lactobacillales;
OX NCBI TaxID=171101;
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RX MEDLINE=21429245; PubMed=11544234;
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REMBL, AE008479; AAK99865.1; -.
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ilarity 99.7%;
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Q9AG74;
01-JUN-2001
01-JUN-2001
01-MAR-2003
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MEDLINE=21246685; PubMed=11349048;
Zhang Y., Masi A.W., Barniak V., Mountzouros
Green B.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    from Streptococcus pneumoniae, Protects Mice aga-
Pneumococcal Challenge.";
Infect. Immun. 69:3827-3836(2001).

EMBL; AF340221; AAK26629.1; -
InterPro; IPR006270; Strep_his triad.
InterPro; IPR001633; Strep_his triad.
ITGRFAMMs; TUGRO1183; Strep_his triad; 2.
SEQUENCE 844 AA; 94769 MW; D738A55290FF8902
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NCBI_TaxID=1313;
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Bacteria; Firmicutes; Lactobacillales;
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ITSDEGDAYVTPHMTHSHWIKKDSLSEAERAAAQAYAKEKGLTPPSTDHQDSGNTEAKGA
                                IISDEGDAYVTPHMGHSHWIGKDSLSDKEKVAAQAYTKEKGILPPSPDADVKANPTGDSA
                                                                                                                    ESTNKEKLVDDLLAFLAFITHPERLGKPNSQIEYTEDEVRIAQLADKYTTSDGYIFDEHD
                                                                                                                                                                                       KQESLSHKLGAKKTDLPSSDREFYNKAYDLLARIHQDLLDNKGRQVDFEALDNLLERLKD
                                                                                                                                                                                                                              KQESVSHTLTAKKENVAPRDQEFYDKAYNLLTEAHKALFXNKGRNSDFQALDKLLERLND
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Q8CWR4;
01-MAR-2003
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01-MAR-2003 (TrEMBirel. 23, Last sequence up
01-MAR-2003 (TrEMBirel. 23, Last annotation
Histidine motif-containing protein.
PHPA OR SPR1060.
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MEDILINE=21429245; PubMed=11544234;

Hoskins J., Alborn W.E. Jr., Arnold J., Blaszczak L.C., Burgett & Hoskins J., Alborn W.E. Jr., Arnold J., Fuller W., Geringes DeHoff B.S., Estrem S.T., Fritz L., Fu D.-J., Fuller W., Geringes Gilmour R., Glass J.S., Khoja H., Kraft A.R., Lagace R.E., Gilmour R., Glass J.S., Khoja H., Kraft A.R., Lagace R.E., LeBlanc D.J., Lee L.N., Lefkowitz E.J., Lu J., Matsushima P., McAbren S.M., McHenney M., McLeaster K., Mundy C.W., Nicas T.I., Morris F.H., O'Gara M., Peery R.B., Robertson G.T., Rockey P., Sun P.-M., Winkler M.E., Yang Y., Young-Bellido M., Zhao G., 20ok C.A., Baltz R.H., Jaskunas S.R., Rosteck P.R. Jr., Skatrud I
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NCBI_TaxID=171101;
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"Genome of the bacterium Streptococcus
J. Bacteriol. 183:5709-5717(2001).
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                                                                                 VSNPGTTNTNTSNNSNTNSQASQSNDIDSLLKQLYKLPLSQRHVESDGLVFDPAQITSRT
                                                                                                                                                                                   GDAYIVPHGDHYHYIPKNELSASELAAAEAFLSGRGNLSNSRTYRRQNSDNTSRTNWVPS
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micutes; Lactobacillales; Streptococcaceae;
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Pred. No. 7.4e-176;
9; Mismatches 99;
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Tettelin H., Nelson K.E., Paulsen I.T., Eisen J.A., Read T.D.,
Peterson S., Heidelberg J., DeBoy R.T., Haft D.H., Dodson R.J.,
Durkin A.S., Gwinn M., Kolonay J.F., Nelson W.C., Peterson J.D.,
Umayam L.A., White O., Salzberg S.L., Lewis M.R., Radune D.,
Umayam L.A., White O., Salzberg S.L., Lewis M.R., Radune D.,
Holtzapple E., Khouri H., Wolf A.M., Utterback T.R., Hansen C.L.,
McDonald L.A., Feldblyum T.V., Asinioni S., Dickinson T., Hickey I
Holt I.E., Loftus B.J., Yang F., Smith H.O., Venter J.C.,
Dougherty B.A., Morrison D.A., Hollingshead S.K., Fraser C.M.;
"Complete genome sequence of a virulent isolate of Streptococcus.
                                                                                                    "Complete genome pneumoniae.";
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STRAIN=TIGR4;
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EMBL; AE007418; AAK75283.1; -.
TIGR; SP1174; -.
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                        TETLAGLRNNLTLQIMDNNSIMAEAEKLLALLKGS
                                                                                                                                                       DLFATIKYYVEHPDERPHSNDGWGNASEHVLGKKDHSEDPNKNFKADEE------
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KETLTGLKNNLLFGTQDNNTIMAEAEKLLALLKES
                                                                  PREEKPQSEKPESPKPTEEPEESPEESEEPQVETEKVEEKLREAEDLLGKIQDPIIKSNA
                                                                                                                                    DLLATVKYYVEHPNERPHSDNGFGNASDHVQRNKNGQADTNQTEKPSEEKPQTEKPEEET
                                                                                                                                                                                                                                                                                            DEGDAYVTPHMGHSHWIGKDSLSDKEKVAAQAYTKEKGILPPSPDADVKANPTGDSAAAI
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Q9ANY3
Q9ANY3;
01-JUN-2001
01-JUN-2001
01-MAR-2003
Streptococcus.
NCBI_TaxID=1313;
[1]
                                        Bacteria;
                                                  Streptococcus
                                                                                Pneumococcal
                                        Firmicutes;
                                                                               . (TrEMBLrel. 17, C:
(TrEMBLrel. 17, L:
(TrEMBLrel. 23, L:
I histidine triad)
                                                                                                                                                    PRELIMINARY;
                                                     pneumoniae
                                        Lactobacillales;
                                                                             Last sequence update)
Last annotation update)
d protein B precursor (F
                                                                                                                        Created)
                                                                                                                                                    819
                                        Streptococcaceae;
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Query Match
Best Local Similarity
Matches 544; Conserv
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Dormitzer M., Dagan R., Brewah Y.A., Barren P., Lathigra R.,
Langermann S., Koenig S., Johnson S.;
"Identification and characterization of a novel family of pneumococcal
proteins (the Pht family) that are protective against sepsis.";
Infect. Immun. 69:949-958(2001).
EMBL; AF318954; AAR06759.1; -
InterPro; IPR006270; Strep_his_triad.
TIGRPAMs; TIGR01363; strep_his_triad; 2.
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SIGNAL
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                                                                                                                               DLFATIKYYVEHPDERPHSNDGWGNASEHVLGKKDHSEDPNKNFKADEE-----
                                                                                                                                                                                     YNRVKAAKKVPLDRMPYNLQYTVEVKNGSLIIPHYDHYHNIKFEWFDEGLYEAPKGYTLE
                                                                                                                                                                                                      YNRVKGEKRIPLVRLPYMVEHTVEVKNGNLIIPHKDHYHNIKFAMFDDHTYKAPNGYTLE
                                                                                                                                                                                                                                                              DEGDAYVTPHMTHSHWIKKDSLSEAERAAAQAYAXEKGLTPPSTDHQDSGNTEAKGAEAI
                                                                                                                                                                                                                                                                            DEGDAYVTPHMGHSHWIGKDSLSDKEKVAAQAYTKEKGILPPSPDADVKANPTGDSAAAI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SVSNPGTTNTNTSNNSNTNSQASQSNDIDSLLKQLYKLPLSQRHVESDGLVFDPAQITSR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAHADNIRTKEEIKROKOERSHNHNS---RADNAVAAARAOGRYTTDDGYIFNASDIIED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAHADNVRTKEEINRQKQEHSQHREGGTPRNDGAVALARSQGRYTTDDGYIFNASDIIED
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TETLAGLRNNLTLQIMDNNSIMAEAEKLLALLKGS
                                    PREEKPQSEKPESPKPTEEPEESPEESEEPQVETEKVEEKLREAEDLLGKIQDPIIKSNA
                                                                                                              DLLATVKYYVEHPNERPHSDNGFGNASDHVQRNKNGQADTNQTEKPSEEKPQTEKPEEET
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Pred. No. 6.8e
84; Mismatches
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SIGNAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.

MEDLINE=21101045; PubMed=11159990;

Adamou J.E., Heinrichs J.H., Erwin A.L., Walsh W., Gayle T.

Adamou J.E., Heinrichs J.H., Erwin A.L., Walsh W., Gayle T.

Dormitzer M., Dagan R., Brewah Y.A., Barren P., Lathigra F.

Langermann S., Koenig S., Johnson S.;

"Identification and characterization of a novel family of proteins (the Pht family) that are protective against seps Infect. Immun. 69:949-958 (2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-JUN-2001 (TrEMBLrel. 17, 0
01-JUN-2001 (TrEMBLrel. 17, I
01-MAR-2003 (TrEMBLrel. 23, I
Pneumococcal histidine triad
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Q9ANY2;
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TIGRFAMs; TIGR01363; strep_his_triad; 2.
Signal; Hypothetical protein; Complete p
SIGNAL 1 29 POTENTIAL.
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EMBL; AF318955; AAK06760.1;
EMBL; AE007403; AAK75120.1;
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Bacteria; Firmicutes;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          pneumoniae."
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                                                                                                       AAHADNVRTKEEINRQKQEHSQHREGGTPRNDGAVALARSQGRYTTDDGYIFNASDIIED
                                                                                                                                                              TSHGDHYHYYNGKVPYDAIISEELLMKDPNYKLKDEDIVNEVKGGYVIKVDGKYYVYLKD
                                                                                                                                                                                                         SYELGRHQAGQVKKESNRVSYIDGDQAGQKAENLTPDEVSKREGINAEQIVIKITDQGYV
SVSNPGTTNTNTSNNSNTNSQASQSNDIDSLLKQLYKLPLSQRHVESDGLVFDPAQITSR
                                             TGDAYIVPHGDHYHYIPKNELSASELAAAEAFLSGRGNLSNSRTYRRQNSDNTSRTNWVP
                                                                                                                                               TSHGDHYHYYNGKVPYDAIISEELLMKDPNYQLKDSDIVNEIKGGYVIKVDGKYYVYLKD
                                                                                                                                                                                                                                                                                                                        839
839 AA;
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d protein D precursor (H
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Pred. No. 4.7e-150;
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MEDLINB=21429245; PubMed=11544234;
Hoskins J., Alborn W.E. Jr., Arnold J., Blaszczak L.C., Burgett S.

DeHoff B.S., Estrem S.T., Fritz L., Fu D.-J., Fuller W., Geringer
Gilmour R., Glass J.S., Khoja H., Kraft A.R., Lagace R.E.,

Gilmour R., Glass J.S., Khoja H., Kraft A.R., Lagace R.E.,

LeBlanc D.J., Lee L.N., Lefkowitz E.J., Lu J., Matsushima P.,

McAhren S.M., McHenney M., McLeaster K., Mundy C.M., Nicas T.I.,

Norris F.H., O'Gara M., Peery R.B., Robertson G.T., Rockey P.,

Sun P.-M., Winkler M.E., Yang Y., Young-Bellido M., Zhao G.,

Zook C.A., Baltz R.H., Jaskunas S.R., Rosteck P.R. Jr., Skatrud P.
                                                                                                                                                                                                                            Streptococcus pneumoniae (strain ATCC BAA-255 / R6).
Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
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                                                                                                                                                                                                                    Streptococcus.
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01-MAR-2003 (TYEMBLrel. 23, Last sequence update)
01-MAR-2003 (TYEMBLrel. 23, Last annotation update)
Pneumococcal histidine triad protein D.
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                                                  me of the bacterium Streptococcus cteriol. 183:5709-5717(2001). AE008464; AAK99711.1; -.
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Signal; Hypothetical protein; Complete p:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE
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EMBL; AF318956; AAK06761.1;
EMBL; AE007403; AAK75121.1;
TIGR; SP1004;
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Adamou J.E., Heinrichs J.H., Erwin A.L., Walsh
Dormitzer M., Dagdan R., Brewah Y.A., Barren P.
Langermann S., Koenig S., Johnson S.;
"Identification and Characterization of a nove
proteins (the Pht family) that are protective
infect. Immun. 69:949-958(2001).
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NCBI_TaxID=1313;
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                                                                                                                                                                                           ARGVAVPHGDHYHFIPYSOMSELEERIARIIPLRYRSNHWVPDSRPEQPSPOPTPEPSPG
                                                                                                                                                                                                                                                                                                                                                                                                                     AHADNVRTKDEINRQKQEHVKDNE----KVNSNVAVARSQGRYTTNDGYVFNPADIIEDT
                                                                                                                                                                                                                                                                                                                                                                                                                                           AHADNVRTKEEINRQKQEHSQHREGGTFRNDGAVALARSQGRYTTDDGYIFNASDIIEDT
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                                       VSHTLTAKKENVAPRDQEFYDKAYNLLTEAHKALFXNKGRNSDFQALDKLLERLNDESTN
                                                                                                                                                                                                                                                                            VSNPGTTNTNTSNNSNTNSQASQSNDIDSLLKQLYKLPLSQRHVESDGLVFDPAQITSRT
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LTTSKELSSASDGYIFNPK-DIVEETATAYIVRHG--DHFHYIPK-----
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Best Local Similarity
Matches 298; Conserv
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Q1-MAR-2003
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SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                           Hoskins J., Alborn W.E. Jr., Arnold J., Blaszczak L.C., Burgett DeHoff B.S., Estrem S.T., Fritz L., Fu D.-J., Fuller W., Geringe Gilmour R., Glass J.S., Khoja H., Kraft A.R., Lagace R.E., LeBlanc D.J., Lee L.N., Lefkowitz E.J., Lu J., Matsushima P., McAhren S.M., McHenney M., McLeaster K., Mundy C.W., Nicas T.I., Norris F.H., O'Gara M., Peery R.B., Robertson G.T., Rockey P., Sun P.-M., Winkler M.E., Yang Y., Young-Bellido M., Zhao G., Zook C.A., Baltz R.H., Jaskunas S.R., Rosteck P.R. Jr., Skatrud
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Streptococcus.
NCBI_TaxID=171101;
                                                                                                                                                                                                                                                                                                                                       EMBL; AE008464; AAK99712.1;
                                                                                                                                                                                                                                                                                                                                                     "Genome of the bacterium Streptococcus J. Bacteriol. 183:5709-5717(2001).
                                                                                                                                                                                                                                                                                                                                                                                   Glass J.I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Streptococcus pneumoniae (strain ATCC BAA-255 Bacteria; Firmicutes; Lactobacillales; Strepto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PHTE OR SPR0908.
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VSNPGTTNTNTSNNSNTNSQASQSNDIDSLLKQLYKLPLSQRHVESDGLVFDPAQITSRT
                           GNAYIVPHGGHYHYIPKSDLSASELAAAKAHLAGKNMQPSQLSYSSTASDN------
                                                                                 AHADNVRTKDEINROKQEHVKDNE----KVNSNVAVARSOGRYTTNDGYVFNPADIIEDT
                                                                                                                                       SHGDHYHYYNGKVPYDALFSEELLMKDPNYQLKDADIVNEVKGGYIIKVDGKYYVYLKDA
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Pred. No. 1.3e-62;
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                                                                                                                                   Query Match
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Matches 277
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STRAIN=SE370 / ATCC 700294 / Serotype M1;

STRAIN=SE370 / ATCC 700294 / Serotype M1;

KMEDLINE=Z1192684; PubMed=11296296;

KMEDLINE=Z1192684; PubMed=11296296;

Ferretti J.J., McShan W.M., Ajdic D.J., Savic D.J., Savic G.,

Primeaux C., Sezate S., Suvorov A.N., Kenton S., Lai H.S., Lin

Primeaux C., Sezate S., Suvorov A.N., Canton S., Lai H.S., Lin

Primeaux C., Sezate S., Suvorov A.N., Canton S., Lai H.S., Lin

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                                                                                                                                   Score 949; DB
Pred. No. 5.9e
00; Mismatches
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nes 214;
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Q8NZ82 PRELIMINARY; PRT; 823
Q8NZ82;
Q1-CCT-2002 (TrEMBLrel. 22, Created)
01-CCT-2002 (TrEMBLrel. 22, Last sequence
01-MAR-2003 (TrEMBLrel. 23, Last annotati
Hypothetical protein spyM18_2072.
SpYM18_2072.
Streptococcus pyogenes (serotype M18).
Bacteria; Firmicutes; Lactobacillales; Streptococcus.
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MEDLINE=21927593; PubMed=11917108;
Smoot J.C., Barbian K.D., Van Gompel J.J., Smoot L.M., Chaussee M Sylva G.L., Sturdevant D.E., Ricklefs S.M., Porcella S.F., Parkins L.D., Beres S.B., Campbell D.S., Smith T.M., Zhang Q., Kapur V., Daly J.A., Veasy L.G., Musser J.M.;
"Genome sequence and comparative microarray analysis of serotype group A Streptococcus strains associated with acute rheumatic fevers."
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EMBL; AE010110; AAL98543.1; -
InterPro; IPR006270; Sepp_his_triad.
TIGRRAMS; TIGR01363; strep_his_triad; 4.
Eypothetical protein; Complete proteome.
SEQUENCE 823 AA; 92585 MW; C79E1EB30CEEDF0C (
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                                                          SFVIPHIDHIHVVPYSWL---
                                                                                          NLIIPHKDHYHNIKFAWFDDHTYKAPNGYTLEDLFATIKYYVEHPDERPHSNDGW-----
                                                                                                                                  TQIAFAEQELMLKDKKHYRYDIVDTG-----IEPRLAVDVSSLPMHAGNATYDTGS
                                                                                                                                                                         AAQAYTKEKGILPPSPDADVKANPTGDSAAAIYNRVKGEKRIPLVRLPYMVEHTVEVKNG
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Pred. No. 8.8e-46;
3; Mismatches 272;
                                                        -TRDQIATIKYVMQHPEVRP---DVWSKPGH
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SEQUENCE FROM N.A.
STRAIN=NEM316 / Serotype III;
MEDLINE=22242508; PubMed=12354221;
Glaser P., Rusniok C., Buchrieser C.
Glaser P., Zouine M., Couve E., Lali
Msadek T., Zouine M., Couve E., Lali
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SEQUENCE 822 AA; 92393 MW; 2929A97C8AFCD78F CRC64;
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EMBL; AL766850; CAD46965.1; -.
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KGIS-RYVFAKDLPSETVKNLESKLSKQESVSHTLTAKKENVAPRDQEFYDKAYNLLTEA
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                                       AGQTEDN----DSGSEHSKPSDK----
                                                                                                                                               TPAPGRRKAP-IPDVTPNPGQGHQPDNGGYHPAPPRPNDASQNKHQRDEFKGKTFKELLD
                                                                                                                                                                                                                                        QNSDNTSRTNWVPSVS-NPGTTNTNTSN-----NSNTNSQASQSND-----IDSLLK
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                                                                          PLRYRSNHWVPDSRPEQPSPQPTPEPSPGPQPAPNLKIDSNSSLVSQLVRKVGEGYVFEE
                                                                                                                    QLHRLDLKYRHVEEDGLIFEPTQVIKSNAFGYVVPHGDHYHIIPRSQLSPLEMELADRYL
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Pred. No. 1e-45;
Mismatches 265;
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C., Trieu-Cuot
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Q93GT5;
01-DEC-2001
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"Characterization of a novel histidine triad p
streptococci.";
Submitted (NOV-2001) to the EMBL/GenBank/DDBJ
EMBL; AB073859; BAB71774.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR006270; Strep_his_triad.
TIGRFAMs; TIGR01363; strep_his_triad; 4.
SEQUENCE 825 AA; 92623 MW; DE4ECC199181DFFB
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          I FNASDI I EDTGDAY I VPHGDHYHY I PKNELSASELAAAEAFLS - - - GRGNLSNSRTYRR
                                                       KPGSKRKNIRTKQQIAEQVAKGTKEAKEKGLAQVAHLSKEEVAAVNEAKRQGRYTTDDGY
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                                                                                                                                                     YVTSHGDHYHFYNGKVPYDAIISEELLMTDPNYRFKQSDVINEILDGYVIKVNGNYYVYL
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Q8K5Q1;
01-OCT-2002
01-OCT-2002
01-MAR-2003
STRAIN=MGAS315 / Serotype M3;
MEDLINE=22133808; PubMede=12122206;
Beres S.B., Sylva G.L., Barbian K.D., Li
Mammarella N.D., Liu M.-Y., Smoot J.C.,
Campbell D.S., Smith T.M., McCormick J.
Schlievert P.M., Musser J.M.;
                                                                                                                                                                                           Streptococcus.
NCBI_TaxID=198466;
                                                                                                                                                                                                                                                Streptococcus pyogenes
Bacteria; Firmicutes; I
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Lactobacillales;
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J.K., Leung D.:
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EMBL; AE014169; AAM80331.1; -.
InterPro; IPR006270; Strep_his_triad.
TIGRFAMS; TIGR01363; strep_his_triad;
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                                                                                                   EESGSVIPNVTPLDKRAGMPNWQIIHSAEEVQKALAEGRFATPDGYIFDPRDVLAKETFV
                                                                                                                                                     SFVIPHIDHIHVVPYSWL--
                                                                                                                                                                           NLIIPHKDHYHNIKFAWFDDHTYKAPNGYTLEDLFATIKYYVEHPDERPHSNDGW-----
                                                                                                                                                                                                    TQIAFAEQELMLKDKNHYRYDIVDTG-----IEPRLAVDVSSLPMHAGNATYDTGS
                                                                                                                                                                                                                              AAQAYTKEKGILPPSPDADVKANPTGDSAAAIYNRVKGEKRIPLVRLPYMVEHTVEVKNG
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                                                                                                                                                                                                                                                                                                                      KALFXN----KGRNSDFQALDKLLERLNDESTNKEKLVDDLLAFLAPITHPERLGKPNSQ
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                      LQIMDNNSIMAEAEKLLALLKGSNPSSVSKEK 794
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                                                                          ----VPQVE-----TEKVEAQLKEAEVLLAKVTDSSLKANATETLAGLRNNLT
                                                                                                                         -GNASEHVLGKKDHSEDPNKNFKADEEPVEETPAE----PE----
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DKPKEKQQADK---SNENQQPSEASKEE
                                                                                                                                                                                                                                                       ---TKKVSRKVTKDGKV------GYIMPKDGKDYFYARDQLD----L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              22.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 940; DB 16; Length 8 Pred. No. 1.9e-45; 2; Mismatches 272; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    99:10078-10083 (2002)
                                                                                                                                                                                                                                                                                                                                                                                                           TEDNDSGSDHSKSSDKEVTHTFLGHRIKAYGKGLDGKPY
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                                                                                                                                                  ----TRDQIATIKYVMQHPEVRP---DVWSKPGH
                                                                                                                                                                                                                                                                                                                                                          KSGVTAKHGDHFHYIGFGELEQYE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 823;
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Matches
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SETRAIN=2603 V/R / Serotype V;

MEDLINE=22222988; PubMed=12200547;

MEDLINE=22222988; PubMed=12200547;

Tettelin H., Masignani V., Cieslewicz M.J., Eisen J.A., Peterson S.

Wessels M.R., Paulsen I.T., Nelson K.E., Margarit I., Read T.D.,

Madoff L.C., Wolf A.M., Beanan M.J., Brinkac L.M., Daugherty S.C.,

Medby R.T., Durkin A.S., Kolonay J.F., Madupu R., Lewis M.R.,

DeBoy R.T., Durkin A.S., Kolonay J.F., Madupu R., Lewis M.R.,

Radune D., Fedorova N.B., Scanlan D., Khouri H., Mulligan S.,

Carty H.A., Cline R.T., Van Aken S.E., Gill J., Scarselli M., Mora

lacobini E.T., Brettoni C., Galli G., Mariani M., Vegni F., Maione

Rinaudo D., Rappuoli R., Telford J.L., Kasper D.L., Grandi G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q8DZ81 PRELIMINARY; PRT; 822 AA. Q8DZ81; Q1-MAR-2003 (TrEMBLrel. 23, Created) 01-MAR-2003 (TrEMBLrel. 23, Last sequence update) 01-MAR-2003 (TrEMBLrel. 23, Last annotation update streptococcal histidine triad family protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Complete genome sequence and comparative genomic analysis of an emerging human pathogen, serotype V Streptococcus agalactiae."; Proc. Natl. Acad. Sci. U.S.A. 99:12391-12396(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Streptococcus agalactiae (serotype V).
Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; AE014248; AAN00111.1; -. TIGR; SAG1233; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Complete proteome. SEQUENCE 822 AA;
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ALFXNKGRNSDFQALDKLLERLNDESTNKEKLVDDLLAFLAPITHPERLGKPNSQIEYTE
                                                                      GISRYVFAKDLPSETVKNLESKLSKQESVSHTLTAKKENVAPRDQEFYDKAYNLLTEAHK 452
                                                                                                                                               LRYRSNHWVPDSRPEQPSPQPTPEPSPGPQPAPNLKIDSNSSLVSQLVRKVGEGYVFEEK 392
                                                                                                                                                                                 QLHRLDLKYRHVEEDGLIFEPTQVIKSNAFGYVVPHGDHYHIIPRSQLSPLEMELAD---
                                                                                                                                                                                                      QLYKLPLSQRHVESDGLVFDPAQITSRTARGVAVPHGDHYHFIPYSQMSELEERIARIIP 332
                                                                                                                                                                                                                                                                                                                           KPGSKRKNIRTKQQIAEQVAKGTKEAKEKGLAQVAHLSKEEVAAVNEAKRQGRYTTDDGY
                                                                                                                                                                                                                                                                                                                                                                                                                                        KDAAHADNVRTKEEINROKOEHSOH-REGG-----TPRNDGAVALARSOGRYTTDDGY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                YVTSHGDHYHFYNGKVFYDAIISEELLMTDFNYHFKQSDVINEILDGYVIKVNGNYYVYL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     YVTSHGDHYHYYNGKVPYDAIISEELLMKDPNYKLKDEDIVNEVKGGYVIKVDGKYYVYL 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SYELGLYQARTVKENNRVSYID----GKQATQKTENLTPDEVSKREGINAEQIVIKITDQG
                                                                                                                                                                                                                                                            TPAPGRRKAP - I PDVTPNPGQGHQPDNGGYHPAPPRPNDASQNKHQRDEFKGKTFKELLD
                                                                                                                                                                                                                                                                                          QNSDNTSRTNWVPSVS-NPGTTNTNTSN-----NSNTNSQASQSND-----IDSLLK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 937; DB 16;
Pred. No. 2.9e-45;
                                    SKPSDKE-VTHTFLGHR-----IKAY-----
                                                                                                           -QTDDNDS
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RESULT
OPERATOR

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                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
Matches 271; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Q9ZHG7
Q9ZHG7;
Q1-MAY-1999
01-MAY-1999
01-MAR-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                              Spellerberg B., Rozdzinski E., Martin S., Weber-Heynemann Schnitzler N., Luetticken R., Podbielski A., "Lubetticken R., Podbielski A., "Lubetticken R., Podbielski A.," "Lubb, a protein with similarities to the Lrai adhesin fami attachment of Streptococcus agalactiae to human laminin."; Infect. Immun. 67.871-878(1999).

EMBL: AF066253; AAD13797.; -

InterPro; IPR006270; Strep_his_triad.

TIGRPAMS; TIGR01363; strep_his_triad; 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Streptococcus agalactiae.
Bacteria; Firmicutes; Lactobacillales;
                                                                                                                                                                                                                                                                                                                                                                                                           Hypothetical protein. seQUENCE 822 AA; 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hypothetical 92.4 kDa protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=99115568; PubMed=9916102;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
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  KDAAHADNVRTKEEINRQKQEHSQH-REGG-----TPRNDGAVALARSQGRYTTDDGY
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                                                                                                                         YVTSHGDHYHYYNGKVPYDAIISEELLMKDPNYKLKDEDIVNEVKGGYVIKVDGKYYVYL
                                                                                                                                                                                         SYQLGKHHMGLATKDNQIAYIDDSKGKVKAPKT-NKTMDQISAEEGISAEQIVVKITDQG
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                                                                                  YVTSHGDHYHFYNGKVPYDAIISEELLMTDPNYHFKQSDVINEILDGYVIKVNGNYYVYL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (TrEMBLrel. 10, Created)
(TrEMBLrel. 10, Last sequence update)
(TrEMBLrel. 23, Last annotation update)
                                                                                                                                                                                                                                                                                               22.4%;
llarity 29.4%;
Conservative 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -GKGLD
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                                                                                                                                                                                                                                                                                                                                                                                                        92386 MW; 80E4EDF313481F98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -TEKVEAQLKEAEVLLAKVTDSSLKANATETLAGLRNNLTLQIMDNNSI
                                                                                                                                                                                                                                                                                               99;
                                                                                                                                                                                                                                                                                               Score 934; DB 2;
Pred. No. 4.2e-45;
9; Mismatches 235
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Q8E338;
01-MAR-2003 (TrEMBLrel. 2
01-MAR-2003 (TrEMBLrel. 2
01-MAR-2003 (TrEMBLrel. 2
SEQUENCE FROM N.A.
STRAIN-MEM316 / Serotype III;
MEDLINE=22242508; PubMed=12354221;
Glaser P., Rusniok C., Buchrieser
                                                                                                                                                                                      Streptococcus agalactiae (serotype III Bacteria; Firmicutes; Lactobacillales;
                                                                                                                                                                                                                                          Hypothetical GBS1925.
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Q9AE21;
Q1-JUN-2001 (TrEMBLrel. 17, Created)
Q1-JUN-2001 (TrEMBLrel. 17, Last sequence update)
Q1-MAR-2003 (TrEMBLrel. 23, Last annotation updat
Hypothetical 32.0 kDa protein (Fragment).
Streptococcus agalactiae.
                                                                                                                             MEDLINE=21172873; PubMed=11274116;
Granlund M., Michel F., Norgren M.;
"Mutually exclusive distribution of IS1548
II intron identified in human isolates of g
J. Bacteriol. 183:2560-2569(2001).
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Hypothetical prote:
SEQUENCE 481 AA;
Hypothetical protein.
NON TER 289 28
SEQUENCE 289 AA; 3
                                                           EMBL; AJ290952; CAC35985.1; -.
InterPro; IPR006270; Strep_his_triad.
TIGRFAMs; TIGR01363; strep_his_triad;
                                                                                                                                                                                                                                             SEQUENCE FRO
                                                                                                                                                                                                                                                                                                                                                         Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
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Mol. Microbiol. 45:1499-1513(2002)
EMBL; AL766854; CAD47584.1; -.
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481 AA; 53326 MW;
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73; Mismatches
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Q8E5R2;
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STRAIN=NEM316 / Serotype III;
MEDLINE=22242508; PubMed=12354221;
Glaser P., Rusniok C., Buchrieser C.,
                                                                                                                                                                                                                         Hypothetical SEQUENCE 87
                                                                                                                                                                                                                                                         "Genome sequence of Streptococcus invasive neonatal disease."; Mol. Microbiol. 45:1499-1513 (2002) EMBL; AL766848; CAD46577.1; -
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                                                                                                                                  QEHKNSHHİKTKQVAKKKANKKKVSVKESHKKRKGVAGVDFPTDDGFLLTKDSKILSHPD
                                                                                                                                                        KENNRVSYIDGKQATQKTENLTPDEV----SKREGI----
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Last sequence update)
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Pred. No. 3.9e-09;
5; Mismatches 272;
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ui L., Poyart
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SEQUENCE FROM N.A.

STRAIN=2603 V/R / Serotype V;

MEDLINE=2222988; PubMed=12200547;

MEDLINE=2222988; PubMed=12200547;

Tettelin H., Masignani V., Cieslewicz M.J., Eisen J.A., Peterson S.

Wessels M.R., Paulsen I.T., Nelson K.E., Margarit I., Read T.D.,

Madoff L.C., Wolf A.M., Beanan M.J., Brinkac L.M., Daugherty S.C.,

DeBoy R.T., Durkin A.S., Kolonay J.F., Madupu R., Lewis M.R.,

Radune D., Fedorova N.B., Scanlan D., Khouri H., Mulligan S.,

Radune D., Fedorova N.B., Scanlan D., Khouri H., Mulligan S.,
                                                                                                                                                                                                     Q8E029; PRELIMINARY; PRT; 877 AA.
Q8E029; Ol-MAR-2003 (TrEMBLrel. 23, Created)
Ol-MAR-2003 (TrEMBLrel. 23, Last sequence update)
Ol-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Ol-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Protein of unknown function/lipoprotein, putative.
SAG0907.
                                                                                                                                            Streptococcus.
NCBI_TaxID=216
                                                                                                                                                                          Bacteria; Firmicutes;
                                                                                                                                                                                       Streptococcus agalactiae
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Lactobacillales;
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Matches 200
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Rinaudo D., Rappuoli R., Telford J.L.,
Fraser C.M.;
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                                                                                                   FLDKMPLLEGLDISQNG--IKDLSFLTKYKQLSLIAAANNGITSLKPLAELPNLQFLVLS
                                                                                                                                                          TKINIGQRTNPFQRFGLSLMPNIEVL-GIGFTPINDMTPVLQFKKLKQLWMTNTGITDYS
                                                                                                                                                                                    YNRVKGEKRIPLVRLPYMVEHTVEVKNGNLIIPHKD-----HYHNIKFAW-----FDDHT
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877 AA; 97563 MW;
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 -PEVPQV-
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Pred. No. 5.
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Q1-JUN-2001 (TrEMBLrel. 17, Created)
Q1-JUN-2001 (TrEMBLrel. 17, Last sequence up
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                                                                                Streptococcus
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Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
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01-MAR-2003 (TrEMBLrel. 23, I
FREUMOCOCCAL histidine tria, I
FHELTERUNCATION OR SPR0910.
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d protein E, truncation.
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Pred. No. 1.5e-06;
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                                                          Streptococcaceae;
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D.-J., Fuller W., Geringe
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Geringer C.,
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MEDLINE=21192684; PubMed=11296296;
Perretti J.J., McShan w.M., Ajdic D.J., Savic G., Lyon K.,
Primeaux C., Sezate S., Suvorov A.N., Kenton S., Lai H.S., Lin S.P.,
Qian Y., Jia H.G., Najar F.Z., Ren Q., Zhu H., Song L., White J.,
Yuan X., Clifton S.W., Roe B.A., McLaughin R.;
"Complete genome sequence of an M1 strain of Streptococcus pyogenes.";
Proc. Natl. Acad. Sci. U.S.A. 98:4658-4663(2001).
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InterPro; IPR001611; LRR.
InterPro; IPR007092; LRR SDS22.
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PROSITE; PS50504; LRR_SDS22; 1.
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STRAIN=SF370 / ATC
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                                                                                                     I EASSVIVRVEAEGNQIKSLVLKDKQGSLTFLDVTGNQLTSLEGVNNFTALDILSVSKNQ
                                                                                                                                                                                                                                                                             PLGQ-----LPNL-----KFLVLSNNKISDLSPLASLHQLQELHIDNNQITDLSPVSHKE
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                                                                                                                                           SQIEYTEDEVRIAQLADK----
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19.5%;
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                                                                                                                                                                                                                                  -DLLAFLAP-----ITHPERL-GKPN
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                                                          -SHWIGKDSLSD---KEKVAAQAYTKEKGILPPSPDADVKANP
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Pred. No. 0.00016;
l6; Mismatches 279;
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MEDLINB=22133808; PubMed=12122206;
Beres S.B., Sylva G.L., Barbian K.D., Lei B., Hoff J.S.,
Mammarella N.D., Liu M.-Y., Smoot J.C., Porcella S.F., Parkins
Campbell D.S., Smith T.M., McCormick J.K., Leung D.Y.M.,
Schlievert P.M., Musser J.M.;
"Genome sequence of a serotype M3 strain of group A Streptococc
"Genome sequence of the high-virulence phenotype, and clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; AE014157; AAM79642.1; -.
InterPro; IRR007092; LRR SDS22.
PROSITE; PS50504; LRR SDS22; 1.
Complete proteome; Hypothetical protein.
SEQUENCE 792 AA; 87476 MW; 1D501C439CAE224B
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INLA OR SPYM3_1035.
Streptococcus pyogenes (serotype M3).
Bacteria; Firmicutes; Lactobacillales;
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01-OCT-2002 (TrEMBLrel.
01-MAR-2003 (TrEMBLrel.
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01-OCT-2002
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Proc. Natl. Acad. Sci. U.S.A. 99:10078-10083(2002).
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STRAIN=MGAS315 / S
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120; Conservative
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  PSPGPQP---APNLKIDSNS--
                                          --IGKDIP----DPHAIEHARELEKHKFGMDTLRALGFDEEVILDIVRTHDAPTPFPSNE
                                                                                       ERIARIIPLRYRSNHWVPDSRP-
                                                                                                                                                                                                                                                                                                    STATANGIPGLHFPTSDGFQFNGQGIVGVTKDNILVDHDGHLHPISFADL-----
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Last sequence update)
Last annotation updat
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Pred. No. 0.0006;
1; Mismatches 211;
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    -SLVSQLVRKVGEGY--
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    LSGQTQAQAKQVATRLPQTSSPV

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01-DEC-2001
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Eukaryota; Alveolata;
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Theisen M., Thomas A.W., Jepsen S.;
"Cloning, nucleotide sequencing and analysis of the
glutamate-rich protein (GLURP) from plasmodium reich
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GLURP
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382 KVGEGYVFEEKGISRYVFAKDLPSETVKNLESKLSKQESVSHTLTAKKENVAPRDQEFYD
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                                          VSE-RSASE---PSEHVESVSEQSNNEPSEKKDGPVPSKPFEEIEKVDVQPKIVDLQIIE
                                                                                  IIPLRYRSNHWVPDSRPEQPSPQPTPEPS---PGPQPAPNL----KIDSNSSLVS-QLVR
                                                                                                                                                                  LKQLYKLPLSQRHVESDGLVFDPAQ-ITSRTARGVAVPHGDHYHFIPYSQMSELEERIAR
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J. Biol. Chem. 0:0-0(1998).
EMBL; AB009080; BAA33143.1; -.
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TRFA.
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STRAIN-MCASB323 / Serotype M18;
STRAIN-MCASB323 / Serotype M18;
Smoot J.C., Barbian K.D., Van Gompel J.J., Smoot L.M., Chaussee M.S.,
Sylva G.L., Sturdevant D.E., Ricklefs S.M., Porcella S.F.,
Sylva G.L., Sturdevant D.E., Ricklefs S.M., Porcella S.F.,
Parkins L.D., Beres S.B., Campbell D.S., Smith T.M., Zhang Q.,
Kapur V., Daly J.A., Veasy L.G., Musser J.M.,
"Genome sequence and comparative microarray analysis of serotype M18
"Genome sequence and comparative microarray analysis of serotype M18
                                                                                                                                                            group A Streptococcus strains associated with aci outbreaks.";
Proc. Natl. Acad. Sci. U.S.A. 99:4668-4673(2002)
EMBL; AE010057; AAL97968.1; -.
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Complete proteome; Hypothetical
SEQUENCE 792 AA; 87440 MW; 5
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                                                                                                               InterPro; IPR001611; LRR.
InterPro; IPR007092; LRR_SDS22.
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      5C4DDEBE1BA991A7 CRC64;
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                                                                                                                                                                                                                                      GDSAAAIYNRVKGEKRIPLVRLPYMVEHTVEVKNGNLIIPHKDHYHNIKFAWFDDHTYKA
                                                                                                                                                                                                                                                                                                                                                                                                  SLTVVDLSRNADVDLATLQAPKLETLMVNDTKVSHLDFLKNNPNLSSLSINRAQLQSLEG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SLLKQLYKLPLSQRHVESDGLVFDPAQI----TSRTARGVAVPHGDHYHFIPYSQMSELE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   YVTSHGDHYHY-----YNGKVPYDAIISEELL------MKDP--NYKLKD
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                                                                                                                                                                          PNGYTLEDLFATIKYYVEHPDE
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18.8%; Pred. No. 0.0096;
rative 118; Mismatches 284;
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Matches 150;
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Cherevach I., Davis P., Goodhead I., Stevens K., Mungall K., Cherravach I., Davis P., Goodhead I., Stevens K., Mungall K., Berriman M., Pain A., Hall N., Atkin R., Chillingworth C., D Ormond D., Sanders M., Hayes R., Hall S., Quail M., Barrell Submitted (SEP-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; A1844505; CAD50351.1;
Hypothetical protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=36329;
[1]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Plasmodium falciparum (isolate 3D7).
Eukaryota; Alveolata; Apicomplexa; Haemosporida;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hypothetical protein. MAL6P1.80.
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FDDHTYKAPNGYTLEDLFATIKYYVEHPDERPHSND-----GWGNASEHVLGKKD----
                                                                                                                                                                                                                                                                                                                                                                    ----NFNTFNPSLNLIMNNPKKNNDQNSIFKKEQYSSYEPVKNNDINIFYSNKYDNNSN-
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                                                                                                           NHFLHNNNNDSYNYDIYNHFHTYNNCNLYNDDKNELS-----KKG
                                                                                                                                                                          HINNINKKONLMDE---
                                                                                                                                                                                                                                      YIPYNNMKDKDNIMSPQNNIIYDEQINNINNFTLNNHN---MNNGHNIGDEYSDESYEIR
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                                                ----AVLNRYNEQEQNIPIEHEYNNISYPSLIKNN---KNNS----EKKYLDNLSINL
                                                                            TGDSAAAIYNRV-KGEKRIPL-----VRLPYMVEHTVEVKNGNLIIPHKDHYHNIKFAW
                                                                                                                                           EHDIISDEGDAYVTPHMGHSHWIGKDSL--SDKEKVAAQAYTKEKGILPPSPDADVKANP
                                                                                                                                                                                                        NDESTN-KEKLVDDLLAFLAPITHPERLGKPNSQIEYTEDEVRIAQLADKYTTSDGYIFD
                                                                                                                                                                                                                                                                    -----KKENV-APRDQEFYDKAYNLLT----EAHKALFXNKGRNSDFQALDKLLERL
                                                                                                                                                                                                                                                                                                                                    VSQLVRKVGEGYVFEEKGISRYVFAKDLPSETVKN---LESKLSKQESVSHTLTA----
                                                                                                                                                                                                                                                                                                                                                                                                   PLRYRSNHWVPD----SRPEQPSPQPT---PEPSPGPQPAPN-----LKIDSNSSL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                KEKNEYNNYKISSYNNNDG------DNYGDNNNNLINNSIYYYDSSKNRSIKYGDEYE
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NCBI_TaxID=36329;
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EMBL; AE014834; AAN35541
SEQUENCE 1233 AA; 141
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SEQUENCE
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Submitted (SEP-2002) to the EMBL/GenBank/DDBJ databases
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                                                                 FYYNREQLIMFRHSLCNLLNKLDYSKEDFSNVATSIIRCLSVLTSAPVMGYPIKTKNNKL
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                       FMIKLNKLNEKKNTKIKKIKRNKRRKNVSYVTFLNPSYVRFRSDSSNNDSECSDIP----
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01-NOV-1996 (TrEMBLrel.
01-NOV-1996 (TrEMBLrel.
01-OCT-2002 (TrEMBLrel.
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Borre M.B., Dziegiel M., Hogh B., Petersen E., Rieneck K., Riley E. Meis J.F., Aikawa M., Nakamura K., Harada M., Wind A., Jakobsen P.H. Cowland J., Jepsen S., Axelsen N.H., Vunst J.;
"Primary structure and localization of a conserved immunogenic plasmodium falciparum glutamate rich protein (GLURP) expressed in k the preerythrocytic and erythrocytic stages of the vertebrate life
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Plasmodium falciparum.
Eukaryota; Alveolata;
NCBI_TaxID=5833;
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EMBL; M59706; AAA50613.1; -.
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19.1%; Pred. No. 0.14;
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01-MAR-2001 (TrEMBLrel. 1:
01-MAR-2001 (TrEMBLrel. 1:
01-MAR-2003 (TrEMBLrel. 2:
01-MAR-2003 (TrEMBLrel. 2:
Glutamate-rich protein.
SEQUENCE FROM N.A.
STRAIN=FCCI/HN;
Shan Z.X., Yu X.B., Li X.R., Ma C.L., Fang J.M.;
Shan Z.X., Yu X.B., Li X.R., Ma C.L., Fang J.M.;
"Molecular cloning and structure of the glutamate rich p
gene of Plasmodium falciparum isolate FCC1/HN.";
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                    Eukaryota; Alveo
NCBI_TaxID=5833;
                                                                                                                                        Plasmodium falciparum.
Eukaryota; Alveolata;
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InterPro; IPRO05479; CP8ASE L D2
PROSITE; PS00867; CP8ASE 2; 1.
SEQUENCE 1236.AA; 141482 MW;
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                                                                                    KPSEGESTKPDIVQIKIVQEN
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NCE 5507 AA;
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 DIISDEGDAYVTPHMGHSHWIGKDSLSDKEKVAAQAYTKEKGILPPSPDAD--VKANPTG
                                                                                                                                     LLTEAHKALFXNK---GRNSDFQALDKLLERLND---------
                                                                                                                                                                       -IIEEVGSITEEMVEQDVSDNEEIVEERSVIEEAEENVWIEKEVEEEGLDNEEVIDEEDS
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3; Mismatches
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Pred. No. 1.3;
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Cherevach I., Davis P., Goodhead I., Stevens K., Mungall K.,
Cherevach I., Davis P., Goodhead I., Stevens K., Mungall K.,
Berriman M., Pain A., Hall N., Atkin R., Chillingworth C., Doggett
Ormond D., Sanders M., Hayes R., Hall S., Quail M., Barrell B.;
Submitted (SEP-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; AL844505; CAD50334.1; -. Hypothetical protein. SEQUENCE 1063 AA; 123332 MW
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NCBI_TaxID=36329;
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Q9U459; Q9GPG4;
Q1-MAY-2000 (TrEMBLrel. 13, Created)
Q1-WAY-2000 (TrEMBLrel. 17, Last sequence update)
Q1-WAR-2003 (TrEMBLrel. 23, Last annotation update)
Erythrocyte membrane-associated giant protein antiguella plant protein antiguella plant protein antiguella plant protein antiguella plant plant protein antiguella plant protein antiguella plant plant plant plant plant plant plant plant plant plant plant plant plant plant plant plant plant plant plant plant plant plant plant plant plant plant plant plant plant plant plant plant plant plant plant plant plant plant plant plant plant plant plant plant plant plant plant plant plant plant plant plant plant plant plant plant plant plant plant plant plant plant plant plant plant plant plant plant plant plant plant plant plant plant plant plant plant plant plant plant plant plant plant plant plant plant plant plant plant plant plant plant plant plant plant plant plant plant plant plant plant plant plant plant plant plant plant plant plant plant plant plant plant plant plant plant plant plant plant plant plant plant plant plant plant plant plant plant plant plant plant plant plant plant plant plant plant plant plant plant plant plant plant plant plant plant plant plant plant plant plant plant plant plant plant plant plant plant plant plant plant plant plant plant plant plant plant plant plant plant plant plant plant plant plant plant plant plant plant plant plant plant plant plant plant plant plant plant plant plant plant plant plant plant plant plant plant plant plant plant plant plant plant plant plant plant plant plant plant plant plant plant plant plant plant plant plant plant plant plant plant plant plant plant plant plant plant plant plant plant plant plant plant plant plant plant plant plant plant plant plant plant plant plant plant plant plant plant plant plant plant plant plant plant plant plant plant plant plant plant plant plant plant plant plant plant plant plant plant plant plant plant plant plant plant plant plant plant p
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EMBL; AF202180; AAF15293.3; -.
                                                                                                                                                     Interpro; IPR006763; Ag332.
Interpro; IPR001313; Pumilio/Puf.
Pfam; PF04671; Ag332; 138.
SEQUENCE 5458 AA; 615269 MW;
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                                                                                              4.1%;
18.9%;
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                                                                         Score 172.5; D
Pred. No. 1.9;
62; Mismatches
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Q9LCJ9;
01-OCT-2000
                                                         EMTB OR TRUNCATED FMTB OR MW2087.
Staphylococcus aureus, and
Staphylococcus aureus (strain MW2)
Bacteria; Firmicutes; Bacillales;
                                                                                                                                                         01-OCT-2000 (TrEMBLrel. 15, 01-OCT-2000 (TrEMBLrel. 15, 01-MAR-2003 (TrEMBLrel. 23,
  SEQUENCE FROM N.A.
                                  NCBI_TaxID=1280,
                                                                                                                                       Truncated FmtB.
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--APATEEIDEIESVTEEVVE--EEGPVDEEIVQEEGSVTEEIIQGESKVEEVVEEQGSE
ESITHEIIQEES---HVEKVVQ--QGSVAEEVVENPVSVTEE
                                                              NNLTLQIMDNNSIMAEAEKLLALLKGS-----NPSSVSKE
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                                                                                                                            NEEIFVEEVSASQEIVQNESGTEEILEKVSASQEIVQDGSVTEQIIEEQKPVTEEVVNEE
                                                                                                                                                                                   EEP--VEETPAEPEVPQVE--TEKVEAQLKEAEVLL--AKVTDSSLKAN--ATETLAGLR
                                                                                                                                                                                                                                                                                                            YKAPNGYTLEDLFATIKYYVEHPDERPHSND---GWGNASEHVLGKKDHSEDPNKNFKAD
                                                                                                                                                                                                                                                                                                                                                                                                                                     D--SAAAIYNRVKGEKRIPLVRLPYMVEHTVEVKNGNLI--IPHKDHYHNIKFAWFDDHT
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EMBL; AP004829; BAB95952.1; -.
InterPro; IPR000890; Acetate kin.
InterPro; IPR005877; Gpos YSIRK.
Pfam; PF04450; YSIRK signal; 1.
TIGRPAMS; TIGR01168; YSIRK signal; 1.
PROSITE; PS01075; ACETATE KINASE 1; 1.
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Baba T., Takeuchi F., Kuroda M., Yuzawa
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Yamamoto K., Hiramatsu K.;
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                               D-VAKDELATKANEQKALIAQTADATT-----EEKEQANQQVDAQLT--QGNQNIENA
                                                                 ERLGKPNSQIEYTEDEVRIAQLADKYTTSDGYIFDEHDIISDEGDAYVTPHMGHSHWIGK
                                                                                                GATTEE-----KNAAKDLVLKAKEKAYQDILNAQTTNDVTQIKDQAVADIQGITADTTIK
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DSLSDKEKVAAQAYTKEKGILPPSPDADVKANPTGDSAAAIYNRVKGEKRIPLVRLPYMV
                                                                                                                                                                                                 FEEKGISRYVFAKDLPSETVKNLES----KLSKQESVSHTLTAKKENVAPRDQEFYDKAY
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Chemother. 45:421-431(2000)
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Kuroda H., Cui L.,
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InterPro; IPR005877; Gpos_YSIRK.
InterPro; IPR005897; Gram_pos_anchor.
Pfam; PF04650; YSIRK_signal; I.
TIGREAMS; TIGR01167; LPXTG_anchor; 1.
TIGREAMS; TIGR01168; YSIRK_signal; 1.
SEQUENCE 2478 AA; 262995 MW; 1C118EBE0DB03B34 CRC64;
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Q9LCH2,
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1186
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  VT--
                                               RTYRRQNSDNTSRTNWVPSVSNPGTTNTNTSN--NSNTNSQASQSNDIDSLLKQLYKLPL
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                                                                                                     -NAKEAIATKANERKTA----IAQTQDITAEEIAAANA-----DVDNA
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19.4%; Pred. No. 0.66;
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PMTB (MRP) OR FMTB OR SAV2160 OR SA1964
Staphylococcus aureus (strain Mu50 / Al
Staphylococcus aureus (strain N315).

Sacteria; Firmicutes; Bacillales; Staph
                                                                                                           SPĒCIES=S.aureus (strain Mu50), and S.aureus (strain N315);
MEDLINB=21311952; pubMed=114.18146;
Kuroda M., Ohta T., Uchlyama I., Baba T., Yuzawa H., Kobayashi I.,
Cui L.; Oguchi A., Aoki K.-I., Nagai Y., Lian J.-Q., Ito T.,
Kanamori M., Matsumaru H., Maruyama A., Murakami H., Hosoyama A.,
Mizutani-Ui Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C.,
Sekimizu K., Hirakawa H., Kuhara S., Goto S., Yabuzaki J.,
Kanehisa M., Yamashita A., Oshima K., Furuya K., Yoshino C., Shib,
Hattori M., Ogasawara N., Hayashi H., Hiramatsu K.;
"Whole genome sequencing of meticillin-resistant Staphylococcus
aureus.",
Lancet 357:1225-1240(2001).
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Q99QR6;
01-JUN-2001 (TrEMBLrel. 17,
01-JUN-2001 (TrEMBLrel. 17,
01-MAR-2003 (TrEMBLrel. 23,
EMBL; AP003364; BAB58322.1; -. EMBL; AP003136; BAB43253.1; -. EMBL; AP003136; BAB43253.1; -. InterPro; IPR005877; Gpos_ysīrk.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
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ADNSNASTSSETAEAKQKLAELKQTADQNVNQ
                                                                                                                                                                                                     PYMVEHTVEVKNGNLIIP----HKDHYHNIKFAMF--DDHTYKAPNGYTLEDLFATIKYY
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                                                                                         KVEAQLKEA-----
                                                                                                                           --NPVKKP--
                                                                                                                                                      VEHPDERPHSNDGWGNASEHVLGKKDHSEDPNKNFKADEE-PVEETP--AEPEVPQVETE
                                                                                                                                                                                     LINNIETTNEEK-GNDIGPVRAAYEEGLINIINAATTTGDVTTAKDTAVQKVQQLHA----
                                                                                                                                                                                                                                                                              WIGKDSLSDKEKVAAQAYTKEKGILPPSPDADVKANPTGDSAAAIYNRVKGEKRIPLVRL
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                              -----NNSIMAEAEKLLALLKGSNPSSVSK
                                                           - VDTELNQAKTNVDQSSTNEYVDNAVKEGKAKINAVKTFSEYKKDALAKIEDAYNAKVNE
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                                                                                         -EVLLAKVTDSSLKANATETLAGLRNNLTLQIMD------
                                                                                                                         -AGKKELDQ----AAADKKTQIEQTPNASQQEINDAKQE
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Best Local Similarity
Matches 173; Conserv
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EMBL; AL844509; CAD52358.1; -.
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01-MAR-2003
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Eukaryota; Alveolata;
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                                                    I-SIDDALEKGKLDKSNLSDNEEKL--DV
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NVPSDENTINDKTKEGSTTLKTAMGYITKFKDFIKNKSENYMTT---
                           --LADKYTTSD-
                                                                                                                                                              EHENLSAENVPSDENTINDKTKEGSTTL----
                                                                                                                                                                                         PSPQPTPEPSPGPQPAPNLKIDSNSSLVSQLVRKVGEGYV-----FEEKGISRYVFAKDL
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                                                                            FQALDKLLER----LNDESTNKEKLVDDLLAFLAPITHPERLGKPNSQIEYTEDEVRIAQ
                                                                                                      ----KNSEDKISDDKSSDDIKLDEKQNAGDQN-DLYDN----
                                                                                                                                 PSETVKNLESKLSKQESVSHTLTAKKENVAPRDQEFYDKAYNLLTEAHKALFXNKGRNSD
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17.78;
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                        -----GYIFDEHDIISDEGDAYVTPHMGHSHWIGKDSLSD-
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Last annotation updat
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Pred. No. 1.1;
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Query Match
Best Local Sir
Matches 169;
                                                "Mrp-a new auxiliary gene essential for optimal expression methicillin resistance in Staphylococcus aureus."; Microb. Drug Resist. 5:9-18(1999).

EMBL; Y09927; CAB55329.1; EMBL; Y09927; CAB55329.1; InterPro; IPR001897; Gpos YSIRK.
InterPro; IPR001899; Gram pos anchor.
Pfam; PF04650; YSIRK_signal; 1.
TIGRPAMs; TIGR01167; LPXTG anchor; 1.
TIGRPAMs; TIGR01168; YSIRK_signal; 1.
SEQUENCE 2478 AA; 263031 MW; 6B9859A02D023C74 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=97302526; PubMed=9158773;
Wu S., de Lencastre H., Sali A., Tomasz A.;
"A phosphoglucomutase-like gene essential for the optimal expression of methicillin resistance in Staphylococcus aureus: molecular cloning
                                                                                                                                                                                                                                                                      Jolly L., Wu S.W., Van Heijenoort J., de Lencast Mengin-Lecreulx D., Tomasz A.; "The femRJ15 gene from Stabbylococcus aureus, th which results in reduced methicillin resistance,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Staphylococcus
Bacteria; Firm:
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01-MAR-2003
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01-MAY-2000
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                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
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Drug Resist.
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Last annotation update)
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             Score 170;
Pred. No. 0
Mismatches
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RESULT
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ALZ946240 protein.
Arabidopsis thaliana (Mouse-ear cress).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MVEHTVEVKNGNLIIP----HKDHYHNIKFAWF--DDHTYKAPNGYTLEDLFATIKYYVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAQSIDDVNTAKDNAI---QAIDPIQASTDVKTNARAELLTEMQNKI-----TEILN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IKD-VAKDELATKANEQKALIAQTADATT-----EEKEQANQQVDAQLT--QGNQNIE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AATDDNGVDQ---AKDAGKNSIQSTQPATAVKSNAKNDVDQAVTTQNQAI-----DN
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                                                                                                                                                                                                                                                                                                                                                               ----NNSIMAEAEKLLALLKGSNPSSVSK
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Pfam; PF00612; IQ; 1.
SMART; SM00264; BAG; 1.
SMART; SM00015; IQ; 1.
PROSITE; PS50096; IQ; 1.
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SEQUENCE
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Lin X., Kaul S., Rounsley S.D., Shea T.P., Benito M.-I., Town C.D.,
Fujii C.Y., Mason T.M., Bowman C.L., Barnstead M.E., Feldblyum T.V.,
Buell C.R., Ketchum K.A., Lee J.J., Ronning C.M., Koo H., Moffat K.S.
Cronin L.A., Shen M., VanAken S.E., Umayam L., Tallon L.J., Gill J.E.
Adams M.D., Carrera A.J., Creasy T.H., Goodman H.M., Somerville C.R.,
Copenhaver G.P., Preuss D., Nierman W.C., White O., Eisen J.A.,
Salzberg S.L., Fraser C.M., Venter J.C.;
"Sequence and analysis of chromosome 2 of the plant Arabidopsis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (MAR-2000) to the EMB: AC005397; AAC62882.1; -. InterPro; IPR003103; BAG. InterPro; IPR000048; IQ_region.
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NCBI_TaxID=3702;
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                                                                                                                   417
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                              473
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                                                                                                                                                               STDOHIEEKEIVVNGELVMNLLLKLD---AVEGLHPSIREFRKALATE-LSSIQDKLDSL
                                                                                                                                                                                                                                                    ---AKKSFTEEEAARIIQSMYRGYDVRRWEPIKKLKEIA---TVREQMGDVKKRIEALEA
                                                                                                                                                                                                                                                                                  IPYSQMSELEERIARIIPLRYRS---NHWVPDSRPEQPSPQPTPEPSPG
                                                                                                                                                                                                                                                                                                                                            GSLNALRTEKGSVES-----NSNLQEESNGEIIKPCEAKENREQP--
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                                                                         KNSCASAEKEAVKEQVEIKSQP-SDSPVNLEHSQLTEENKMV---
                                                                                                                   KQESVSHTLTAKKENVAPRDQEFYDKAYNL----LTEAHKALFXNKGRNSDFQALDKLLE
                                                                                                                                                                                                      --PQPAPNLKIDSNSSLVSQLVRKVGEGYVFEEKGISRYVFAKDLPSETVKNLESKLS--
                                                                                                                                                                                                                                                                                                                                                                                                                                    PKERNGGSKSVSHPKRMEKSKETKIAAPLSSKKAESRT--VPEACNVKCEDANAEMKMAE
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Pred. No. 0.31;
8; Mismatches 327;
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A Mungall K., Bowman S., Atkin R., Baker S., Barron A., Brooks K.,
A Mungall K., Bowman S., Atkin R., Baker S., Barron A., Brooks K.,
A Mungall K., Bowman S., Atkin R., Baker S., Barron A., Brooks K.,
A Mungall K., Bowman S., Atkin R., Baker S., Clark L., Clark R.,
A Cronin A., Davies R., Davis P., Dear P., Dearden F., Doggett J.,
A Cronin A., Davies R., Davis P., Dear P., Dearden F., Doggett J.,
A Cronin A., Baser H., Hornsby T., Holroyd S., Horrocks P.,
A Harper D., Hauser H., Hornsby T., Holroyd S., Horrocks P.,
A Harper D., Hauser H., Hornsby T., Johnson D., Kerhornou A.,
A Knights A., Konfortov B., Kyes S., Larke N., Lawson D., Lennard N.,
A Knights A., Konfortov B., Kyes S., Larke N., Lawson D., Lennard N.,
A Knights A., Konfortov B., Kyes S., Larke N., Lawson D., Lennard N.,
A Knights A., Konfortov B., Kyes S., Larke N., Lawson D., Lennard N.,
A Knights A., Konfortov B., Kyes S., Larke N., Cawson D., Lennard N.,
A Knights A., Konfortov B., Kyes S., Larke N., Lawson D., Lennard N.,
A Knights A., Konfortov B., Kyes S., Larke N., Lawson D., Lennard N.,
A Knights A., Konfortov B., Kyes S., Larke N., Lawson D., Lennard N.,
A Knights A., Konfortov B., Kyes S., Larke N., Lawson D., Lennard N.,
A Knights A., Konfortov B., Kyes S., Larke N., Lawson D., Lennard N.,
A Knights A., Konfortov B., Kyes S., Larke N., Lawson D., Lennard N.,
A Knights A., Konfortov B., Kyes S., Larke N., Lawson D., Lennard N.,
A Knights A., Konfortov B., Kyes S., Larke N., Lawson D., Lennard N.,
A Knights A., Konfortov B., Kyes S., Larke N., Lawson D., Lennard N.,
A Knights A., Konfortov B., Kyes S., Larke N., Lawson D., Lennard N.,
A Knights A., Konfortov B., Kyes S., Lawson D., Kerhornou A.,
A Knights A., Konfortov B., Kyes S., Lawson D., Kerhornou A.,
A Knights A., Konfortov B., Kyes S., Lawson D., Kerhornou A.,
A Knights A., Konfortov B., Kyes S., Lawson D., Kerhornou A.,
A Knights A., Konfortov B., Kyes S., Lawson D., Kerhornou A.,
A Knights A., Konfortov B., Kyes S., 
                                                       Query Match
Best Local S
Matches 177
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01-MAR-2003
01-MAR-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Plasmodium falciparum Eukaryota; Alveolata; NCBI_TaxID=36329;
                                                                                                                                                 Sulaton J.E., Craig A., Newbold C., Barrell B.G; "Sequence of Plasmodium falciparum chromosomes 1, Nature 419:527-531 (2002).
EMBL; AL929352; CAD51456 1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.

Devlin K., Baker S., Davies P., Mungal K., Berriman M.,
Hall N., Bowman S., Churcher C., Quail M., Barrell B.;
Submitted (SEP-2002) to the EMBL/GenBank/DDBJ databases.
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01-MAR-2003 (TrEMBLrel.
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                                                         177;
                     24
                                                                             Similarity
KQATQKTENLTPDEVSKREGINAEQIVIKITDQGYVTSHGD--HYHYYNGKVPYDAIISE
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                                                                                                                                     1708 AA;
                                                         Conservative 142;
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                                                                             4.0%;
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                                                                           Score 168.5;
Pred. No. 0.0
                                                       ed. No. 0.62;
Mismatches
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                                                         Indels
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RESULT 45
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ID Q8IEB
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EMBL; AL844509; CAD52344.1; -.
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A Mungall K., Bowman S., Atkin R., Baker S., Barron A., Brooks K.,
A Mungall K., Bowman S., Atkin R., Baker S., Barron A., Brooks K.,
A Mungall K., Bowman S., Atkin R., Baker S., Barron A., Brooks K.,
A Chillingworth T., Christodoulou Z., Clark L., Clark R., Corton C.,
A Chillingworth T., Christodoulou Z., Clark L., Clark R., Corton C.,
A Cronin A., Davies R., Davis P., Dearden F., Doggett J.,
A Cronin A., Davies R., Davis P., Dearden F., Doggett J.,
A Cronin A., Davies R., Davis P., Dearden F., Doggett J.,
A Harper D., Hauser H., Hornsby T., Holroyd S., Harnen D., Kerhornou A.,
A Humphray S., Jagels K., James K.D., Johnson D., Kerhornou A.,
A Knights A., Konfortov B., Kyes S., Larke N., Lawson D., Lennard N.,
A Knights A., Maddison M., Mclean J., Mooney P., Moule S., Murphy L.,
A Cliver K., Ormond D., Price C., Quail M.A., Rabbinowitsch E.,
A Oliver K., Ormond D., Frice C., Quail M.A., Rabbinowitsch E.,
A Cliver K., Sharp S., Smith R., Squares R., Squares S., Stevens K.,
A Taylor K., Tivey A., Unwin L., Whitehead S., Woodward J.,
A Sulston J.E., Craig A., Newbold C., Barrell B.G;

"Sequence of Plasmodium falciparum chromosomes 1, 3-9 and 13.";
                                                                                                            Matches
                                                                                                                                   Query Match
Best Local
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Q81223;
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EMBL; Z98547; CAD49084.1;
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Eukaryota; Alveolata;
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18.6%;
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Apicomplexa;
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11; Mismatches
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exa; Haemosporida;
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| ID 097255 PRELIMINARY; PRT; 1826 AA.  AC 097255 PRELIMINARY; PRT; 1826 AA.  DT 01-MAY-1999 (TrEMBLrel. 10, Created)  DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)  DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)  DE Hypothetical 216.3 kDa protein.  GN PFC0325C, MAL3P3.1.  OS Plasmodium falciparum (isolate 3D7).  CC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.  OK NCBI_TaxID=36329; | SUL'   | 795 YGYNHHIVGGTNTTTYLKULPKKSYKRREESGEINNESMNLESGEEYRMMQ-KKKNTTF 85 527SDGYIFDEHDIISDEGDAYVTPHMGHSHWIGKDSLSD | Qy 273 QLYKLPLSQRHVESDGLVFDPAQITSRTARGVAVPHGDHYHFIPY 317  | Qy  64 DHYHYYNGKVPYDAIISEELLMKDPNYKLKDEDIVNEVKGG 104  |
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| 795 YGYNHHIVGGTNTTTYLKNLPKKSYKRREESGEINNESMNLESGEEEVRMMQ-KKKNTTF 527SDGYIFDEHDIISDEGDAYVTPHMGHSHWIGKDSLSD 854 KHIDENNMYYKHNELLNEYNTIDDFDNLNNNINRNRIYMHKNRISNEQNNKFNLNNNEL 564KEKVAAQAYTKEKGILPPSPDADVKANPTGDSAAAIYNRVKGEKRIP  | Db 667DDEENVHKSKYMNKNYYNDYKDYNKGNAVNNYYEKDKLKRY 708  Qy 373 SSLVSQLVRKVGEGYVFEEKGISRYVFAKDLPSETVKNLESKLSKQESVSHTLTAKKE 430  Qy | 189 GDHYHYIPKNELSASELAAAEAFLSGRGN   | Matches 170; Conservative 11; Mismatches 312; Indels 320; Gaps 42;  Qy 12 VKENNRVSYIDGKQATQKTENLTPDEVSKREGINAEQIVIKITDQGYVTSHG 63 | SEQUI<br>STRA<br>MEDL<br>Bowm<br>Chur<br>Chur<br>Gent<br>Horr<br>Mung<br>Rutti<br>Horr<br>Whit<br>"The<br>"The<br>"The<br>pall<br>Whit<br>"The<br>"The<br>SEQUI |

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Best Local S
Matches 189
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Pfam; PF00047; ig; 50.
Pfam; PF00018; SH3; 1.
SMART; SM00408; IGC2; 15.
SMART; SM00326; SH3; 1.
PROSITE; PS500835; IG LIKE; 50.
PROSITE; PS50082; SH3; 1.
Immunoglobulin domain; SH3 domain.
SEQUENCE 16215 AA; 1841509 MW; 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FlyBase; FBgn0003432; sls.
InterPro; IPR003961; FN III.
InterPro; IPR007110; Ig-like.
InterPro; IPR003598; Ig_c2.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR0031452; SH3.
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C9NFS3;
01-OCT-2000
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"Characterization of Drosophila D-Titin Submitted (FEB-2000) to the EMBL/GenBan)-i- SIMILARITY: CONTAINS 1 SH3 DOMAIN.
EMBL; AJ271740; CAB93524.1; -. HSSP; P56276; 1TLK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Drosophila melanogaster (Fruit fly).
Bukaryota; Metazoa; Arthropoda; Hexapoda;
Neoptera; Endopterygota; Diptera; Brachyce
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   D-titin.
SLS OR D-TITIN OR CG1915 OR CG18242 OR CG18245 OR CG18857.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=7227;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                   4902
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                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
    VPHGDHYHYIPKNELSASELAAAE----AFLSGRGNLSNSRTYRRQNSDN----TSRTNW
                                             RQQLKSVQRVTKQIDKFKIEEVELRHLQAQQAITEEYQTGTAEETVVMIDESSKGSISKV
                                                                                                                                     VEQVQRTKEIQRLKSMESVEIMEMTDQIDKLITQQQ------NAKDLIPWKEM
                                                                                                                                                                                                                            AI--PWITMRE----KLKAVESVQQQLNKFDLDEVYLQPLEG--QIETEGQ----LPQQAQ
                                                                                                                                                                                                                                                                                                                   KSWTEETINLKATPIEKKKPAPKLEAAKVVLKSIKTERDOGIMSLGATLEQIIAGKTEKE
                                                                                                                                                                                                                                                                                                                                                            KQATQKTENLTPDEVSKRE----GINAEQIVIKI----TDQGYVTSHGDHYHYYNGKVPYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         KHNNYDNHNNIDGNDVYYKHP--YGIEEGRAYDKNYYHDNELNDHHLNYNDNYMNTKVNI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LDSYPYEMVEHKNKYTSNMNNQYDNKDSSYLYDDVSSSFNNKKYTKLII--KDNLCNNKY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LVRLPY-MVEH----TVEVKN-----------GNLTTPHKDHYHNIKF
                                                                                                                                                                                ADNVRTKEEINRQKQEHSQHREGGTPRNDGAVALARSQGRYTTDDGYIFNASDIIE----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LGKKDHSEDPNKN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (TrEMBLrel. 15, (TrEMBLrel. 15, (TrEMBLrel. 23,
                                                                                                                                                                                                                                                                                                                                                                                                     4.0%; Score 166; Dilarity 19.1%; Pred. No. 21; Conservative 126; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -HEDHNNN
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EMBL/GenBank/DDBJ
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Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches 362;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               242C8765E00F7603 CRC64;
                                                                                                                                                                                                                                                                       DEDIVNEVKGGYVIKVDGKYYVYLKDAAH
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                                                                                                                                                                                                                                            CG1915 protein.
SLS OR CG1915 OR CG18242 OR
Drosophila melanogaster (Fro
STRAIN=Berkeley;
MEDLINE=20196006; PubMed=10731132;
Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.
Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.
George R.A., Lewis S.E., Richards S., Ashburner M., Henderson
                                                                                                                                                                                                                                                                                                                 Q917U4;
01-MAR-2001 (TrEMBLrel.
01-OCT-2002 (TrEMBLrel.
01-MAR-2003 (TrEMBLrel.
                                                                                                                                                                                Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygo
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                     Ephydroidea; Drc
NCBI_TaxID=7227;
                                                                                                                                                                                                                                                                                                                                                                                                        Q9I7U4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      5781
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PKPTEPQPQPVLWARGQKKPQKPDEQKQELPKSLEIAV-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                QPLTSVEDTVISQTSERQKLVQQQSFIEEAQRQQFVQVEDSQMMSLEEYEHQKIINQRTQ 5237
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EEP-----VEETPAE-----PEVPQVETEKVEAQLKEAEVLLAK-VTDSSLKANATE 752
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                --RPKSTKEVT-EELFE-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DSAAAIYNRVKGEKRIPLVR-----LPYMVEHTVE--VKNGNLIIPHKDHYHNIKFAWFD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TEETVEEEETAE--DQQLVVEESKKVKKVKK 5809
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TLAGLRNNLTLQIMDNNSIMAEAEKLLALLK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           KKPKLTQQVTEEETPHEEIIKESEEVVQEQEEIVEEKKKVKKVKKPKTVAEKQLKEEEIP 5780
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DHTYKAPNGYTLEDLFATIKYYVEHPDERPHSNDGWGNASEHVLGKKDHSEDPNKNFKAD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      E--KGISRYVFAKDLPSETVKNLESKLSKQESVSHTLTAKKENVAP
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                                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
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22,
23,
                                                                                                                                                                                                                                                   (Fruit fly)
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                                                                                                                                                                                                                                                                                                                 Created)
Last sequence update)
Last annotation updat
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                                                                                                                                                                                                                                Pterygota;
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      S.N.,
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RA Ballew R.M., Basu A., MIR. H.J., MIGNEWS-FLAMINOCH C., Baldwin D.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew II., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,
RA Fosler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Melson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Spier E., Spradling A.C., Stapleton M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Skupski M.P., Smith T.,
RA Spier E., Zhong W., Stong R., Weissenbach J.,
RA Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
RA Zheng X.H., Zhong F. N., Zhong W., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F. N., Zhong W., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong W., Zhon M., Zhang S., Yao Q.A.,
RA Zheng X.H., Zhong F. N., Zhong W., Zhong S., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong W., Zhong W., Zhou S., Zhu X., Smith H.O.,
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RA Zheng X.H., Zhong W., Zhong W., Zhong S., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong W., Zhong W., Zhou S., Zhu X., Smith H.O.,
RA Shang R., Shang R., Wang S., Zhong W., Zhou S
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RA Evans C.A., Gocayne J.D., Amanatides P.G., Brandon R.C., Rogers Y.,
RA Banzon J., An H., Baldwin D., Banzon J., Besson K.Y., Busam D.A.,
RA Carlson J.W., Center A., Champe M., Davenport L.B., Dietz S.M.,
Dodson K., Dorsett V., Doup L.E., Doyle C., Dresnek D., Farfan D.,
RA Ferriera S., Frise E., Galle R.F., Garg N.S., George R.A.,
RA Gonzalez M., Houck J., Hoskins R.A., Hostin D., Howland T.J.,
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RA Gonzalez M., Saragas V., Park S., Patel S., Pfeifer B.,
RA Facleb J., Paragas V., Park S., Patel S., Pfeifer B.,
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InterPro; IPR003991; FN_III.

InterPro; IPR003599; Ig_-Like.

InterPro; IPR007110; Ig_-Like.

InterPro; IPR007110; Ig_-Like.

InterPro; IPR003508; Ig_-C2.

InterPro; IPR00306; Ig_-MCC.

InterPro; IPR001422; SH3

Pfam; PF00041; fn3; 5.

Pfam; PF00041; fn3; 5.

Pfam; PF00018; SH3; 1.

SMART; SM00409; IG; 53.

SMART; SM00408; IGC2; 46.

SMART; SM00408; IGC2; 46.

SMART; SM00326; SH3; 1.

PROSITE; PS50035; IG_LIKE; 50.

PROSITE; PS50035; SH3; 1.
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GDAYVTPHMGHSHWIGK------DSLSDKEKVA-AQAYTKEKGILPPSPDADVKANPTG
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                                                   PKPTEPQPQPVLWARGQKKPQKPDEQKQELPKSLEIAV-
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                                                                                                                     QKAYEEATDELTEEPIPQPQPVMWERGKKKP----QKPQEEVTEIPKTLEIAVDTLEEEV
                                                                                                                                                 QEFYDKAYNLLTE----AHKALFXNKGRNSDFQALDKLLERLNDESTNKEKLVDDLLAFL
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| GKKON 9           | STANDER   STAN | B 4      |
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| TRON 21           | 64 TTDDGVIENASDIIEDFGDAVIVDHGDHVHVIDKNELSASELL   | ર        |
| DEQA 85           | 92 DESIKSTNPVLNFTPYELPLNNKLSSDNYNISSNNIPIYEKNYNY   | B        |
| RSQGRY 163        | 123 ADNVRTKEEINRQKQEHSQHREGGTPRNDGAVALARS  | Ş        |
| :  <br>RKNEQH 791 | 734 DLILNNPILMNNVFSLRNTKKKIVIDETLSFLNPYIEEHLRSGGKSYISKDLRKNE   | 망        |
| ҮГКДААН 122       | SEELLMKDPNYKLKDEDIVNEVKGGYVIKVDGKYYV   | Ş        |
| RCYEY             | 5 PDRVKSCLITAIFKLCSRNNIRDHVVAKKIIDKYKNSKITDLC  | 문 4      |
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|                   | L; AL929355; CAD51726.1; UENCE 1373 AA; 159691 MW; C   | SOR      |
|                   | ace of Plasmodium falciparum chromos<br>419:527-531 (2002)   | RRT      |
|                   | aylor K., Tivey A., Unwin L., Whitehead S., Woodward J<br>ulston J.E., Craig A., Newbold C., Barrell B.G:  | Ŗ Ŗ      |
| K.,               | K., Sharp S., Smith R., Squares R., Squar  | R A      |
|                   | ine A., Maddison M., Mclean J., Mooney P., Moule S., Mur<br>liver K., Ormond D., Price C., Quail M.A., Rabbinowitsch   | RA R     |
| N.,               | nights A., Konfortov B., Kyes S., Larke N., Lawson D., Lenna   |          |
| C                 | Hauser H., Hornsby T., Holroyd S., Horrocks P.,  |          |
| , ;               | n A., Davies R., Davis P., Dear P., Dearden F., Doggett  | R.       |
|                   | e C.O., Burrows C., Cherevach I., Chillingworth C.,  | R R A    |
| •                 | Pain A., Berriman M., Churcher   | R R      |
|                   | SEQUENCE FROM N.A. MEDLINE=22255708: PubMed=12368867:  | R R<br>X |
|                   | ID≈36329;  | R OX     |
|                   | Plasmodium falciparum (isolate 3D7).<br>Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.   | ဂ္ဂဂ္ဂ   |
|                   | riozooc.   | S E      |
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|                   | -MAR-2003 (TrEMBLrel. 23, Created)   | 333      |
|                   | 88   |          |
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|                   | 5781 TEETVEEEETAEDQQLVVEESKKVKKVKK 5809  | В        |
|                   | IAEA<br>   | γQ       |
| KEEEIP 5780       | 5721 KKPKLTQQVTEBETPHEEIIKESBEVVQEQEEIVEEKKKVKKVKKPKTVAEKQLKE  | ф        |
| LKANATE 752       | PVEETPAEPEVPQVETEKVEAQLKEAEVLLAK-VTDSS   | δ        |
| RRLKKT 5720       | 5672RPKSTKEVT-EELFEEQPEEEISPEEEVPQKEVIEEIEEIVEEKRRL  | ф        |
| KNFKAD 706        | 647 DHTYKAPNGYTLEDLFATIKYYVEHPDERPHSNDGWGNASEHVLGKKDHSEDPNKNF  | δÕ       |
| K 5671            | 5623VLWQRGKKKIPKSEPTEEVHPDEVDAQIETVVKEDEMIVEEKRRIKKTK-   | ğ        |
| KFAWFD 646        | 594 DSAAAIYNRVKGEKRIPLVRLPYMVEHTVEVKNGNLIIPHKDHYHNIKF  | Ş        |
| KPEP 5622         | 5565 LIKPVQPEPQPVLWERKKKKPQPQDVIEEKLDVAPTKTYEKAVDVLPDEPKVEEKPE   | Д        |

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|          | KLIFLVKSN 1370   | 1362 | 밁  |
|          | KLLALLKGS 785  | 777  | Ş  |
| DN 3     | TTTKKKAVFINSTNLNILQTLKKIENNINTNVIEVSKMDSLISCFYNNTKVLIKIKII       | 1302 | 밁  |
| AE .     | VTDSSLKANATETLAGLRNNLTLQIMDNNSIMAEAE 776                         | 741  | Ş  |
| ĎK J     | VDINVDNSDHLNEITKNKKNKGDQFDMIDLNELPKKIDPTKSSDINIEEEKKLWDK 130     | 1246 | 멍  |
| -X       | EHV-LGKKDHSEDPNKNFKADEEPVEETPAEPEVPQVETEKVEAQLKEAEVLLAK 740      | 687  | Ş  |
| Ę        | ILSNKNYFTSKKYDNNNDMGGIRKKSLHNEQVENRDVT-KMKVNEKGNNNNNNDGCTNKL 124 | 1187 | Дb |
| AS 686   | IIPHKDHYHNIKFAWFDDHTYKAPNGYTLEDLFATIKYYVEHPDERPHSNDGWGNAS        | 630  | Ş  |
| MS 118   | ALFNGLISNNSPLKDPIKSSYVSTISMKKNMS                                 | 1155 | В  |
| JNI.     | QAYTKEKGILPPSPDADVKANPTGDSAAAIYNRVKGEKRIPLVRLPYMVEHTVEVKNGNL 629 | 570  | 5  |
| MAA 115  | KEFNRFPSDNYHNKINNKTNVYNWKIKGNINTVANNKKELTEKEKWAA                 | 1107 | 망  |
| /AA 569  | EDEVRIAQLADKYTTSDGYIFDEHDIISDEGDAYVTPHMGHSHWIGKDSLSDKEKVAA       | 512  | 8  |
| YS 110   | RNNVFINEENENEKRTDNVNVDDYNEQNYERF-DDNKDIHYS                       | 1066 | 망  |
| YT 511   | XNKGRNSDFQALDKLLERLNDESTNKEKLVDDLLAFLAPITHPERLGKPNSQIEYT         | 456  | 8  |
| 106      | DDDDEEDEEYEDDEEENEEYVDESDDDEDENHDDDDYHEEEQYN                     | 1016 | 及  |
| LF       | VFAKDLPSETVKNLESKLSKQESVSHTLTAKKENVAPRDQEFYDKAYNLLTEAHKALF 455   | 398  | 8  |
| Yac      | LHNIVNTQKDRNYYDEEDDEDEY 101                                      | 986  | g  |
| - XRY    | NHWVPDSRPEQPSPQPTPEPSPGPQPAPNLKIDSNSSLVSQLVRKVGEGYVFEEKGISRY 397 | 338  | Ş  |
| ×        | KKKKKSVQREEAADENKGIKNDINQTEEDIK 985                              | 955  | ф  |
| /RS      | PLSQRHVESDGLVFDPAQITSRTARGVAVPHGDHYHFIPYSQMSELEERIARIIPLRYRS 337 | 278  | Ş  |
| <u> </u> | NKNKKNEKNQNDNNNNNNNNNNNNNNNNNHIDGNQNNSEVINKDKVKK 954             | 908  | 8  |
| - Ř      | LSNSRTYRRQNSDNTSRTNWVPSVSNPGTTNTNTSNNSNTNSQASQSNDIDSLLKQLYKL 277 | 218  | Ş  |
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US-09-107-132A-5095
US-09-117-197-49
US-09-124-867-2
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; Sequence 56, Application US/08961083
; Patent No. 6159469
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GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEPHONE: (301) 309-851
TELEFAX: (301) 309-8512
INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US
                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: linear MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REGISTRATION NUMBER: 36,373
REFERENCE/DOCKET NUMBER: PB
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 309-8504
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PRIOR APPLICATION DATA:
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MEDIUM TYPE: Diskett
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TITLE OF INVENTION:
NUMBER OF SEQUENCES:
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STREET: 9410 Key West Avenue
CITY: Rockville
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OPERATING SYSTEM:
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                                                                                                                                            AHADNVRTKEEINRQKQEHSQHREGGTPRNDGAVALARSQGRYTTDDGYIFNASDIIEDT
                                                                                                                                                             AHADNVRTKEEINRQKQEHSQHREGGTPRNDGAVALARSQGRYTTDDGYIFNASDIIEDT
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ARGVAVPHGDHYHFIPYSQMSELEERIARIIPLRYRSNHWVPDSRPEQPSPQPTPEPSPG
                                            VSNPGTTNTNTSNNSNTNSQASQSNDIDSLLKQLYKLPLSQRHVESDGLVFDPAQITSRT 300
                                                                                                                                                                                                    SHGDHYHYYNGKVPYDAIISEELLMKDPNYKLKDEDIVNEVKGGYVIKVDGKYYVYLKDA
                                                                                     GDAYIVPHGDHYHYIPKNELSASELAAAEAFLSGRGNLSNSRTYRRQNSDNTSRTNWVPS
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                          VSNPGTTNTNTSNNSNTNSQASQSNDIDSLLKQLYKLPLSQRHVESDGLVFDPAQITSRT
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ZIP: 20850
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Sequence 56, Application US/09536784
Patent No. 6573082
GENERAL INFORMATION:
             TELEFAX: (301) 309-8
INFORMATION FOR SEQ ID NO: 56:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette, 3.50 inch, 1.4N

COMPUTER: HP Vectra 486/33

OPERATING SYSTEM: MSDOS version 6.2

SOFTWARE: ASCII Text

CURRENT APPLICATION NUMBER: US/09/536,784

FILING DATE: 30-Oct-1997

CLASSIFICATION: <Unknown>
                                                                                                                                                                                           PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/961,083
FILING DATE: OCT-30-1997
ATTORNEY/AGENT INFORMATION:
NAME: Michelle S. Marks
                                                                                           REGISTRATION NUMBER: 41,971
REFERENCE/DOCKET NUMBER: PB
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 309-8504
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Choi et. al. TITLE OF INVENTION: Streptococcus pneumoniae Antigens and Vaccines NUMBER OF SEQUENCES: 452
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STREET: 9410 Key West
CITY: Rockville
STATE: Maryland
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West Avenue
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486/33
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RESULT 3
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; Sequence 8, Application U
; Patent No. 6582706
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STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ
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APPLICANT: Johnson, Leslie S.
APPLICANT: Adamou, John E.
TITLE OF INVENTION: Vaccine Compositions
TITLE OF INVENTION: Pneumoniae Group A.
TITLE OF INVENTION: Motifs
FILE REFERENCE: 469201-44
CURRENT APPLICATION MUMBER: US/9/468,65
CURRENT FILING DATE: 1999-12-02
PRIOR APPLICATION NUMBER: 60/113,048
PRIOR APPLICATION NUMBER: 60/113,048
PRIOR PILING DATE: 1998-12-21
NUMBER OF SEG ID NOS: 14
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 8
LENGTH: 819
TYPE: PRT
ORGANISM: Streptococcus pneumoniae
ORGANISM: Streptococcus pneumoniae
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Similarity 99.9%;
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Pred. No. 1.4e-314;
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APPLICANT: Adamou, John B.
TITLE OF INVENTION: Vaccine Compositions Comprising Streptococcus
TITLE OF INVENTION: Pneumoniae Group A and B Having Selected Structu
TITLE OF INVENTION: Motifs
FILE REFERENCE: 469201-444
CURRENT APPLICATION NUMBER: US/09/468,656A
CURRENT FILING DATE: 1999-12-02
PRIOR APPLICATION NUMBER: 60/113,048
PRIOR FILING DATE: 1998-12-21
NUMBER OF SEQ ID NOS: 14
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 10
LENGTH: 819
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ORGANISM: Streptococcus pneumoniae
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                                                                          NKEKLVDDLLAFLAPITHÞERLGKÞNSQIEYTEDEVRIAQLADKYTTSDGYIFDEHDIIS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Johnson, APPLICANT: Adamou,
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TITLE OF INVENTION: Vaccine Compositions Comprising Streptococcus
TITLE OF INVENTION: Pneumoniae Group A and B Having Selected Stru
TITLE OF INVENTION: Motifs
FILE REFERENCE: 469201-444
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TYPE: PRT
ORGANISM: Streptococcus pneumoniae
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91; Mismatches 144;
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JS-08-961
; Sequence 66, App.
; Patent No. 6159469
; PATENT INFORMATION:
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US-08-961-083-66
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                 Query Match
Best Local Similarity
                                                                                                                                                                                  TELEFAX: (301) 309-8512 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                               NAME: Brookes, A. Anders
REGISTATION NUMBER: 36,373
REFERENCE/DOCKET NUMBER: PB
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 309-8504
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NUMBER OF SEQUENCES:
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                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA: APPLICATION NUMBER:
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OPERATING SYSTEM: MSI
OPERATE: ASCII Text
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TOPOLOGY: lin
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US-09-536-784-66
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; Sequence 66, Application
; Patent No. 6573082
; Patent INFORMATION:
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COUNTY, 20850
ZIP: 20850
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 7
                                                                                                                                                                                 APPLICANT: Choi et. al.
TITLE OF INVENTION: Streptococcus
NUMBER OF SEQUENCES: 452
                                                                                                                             CORRESPONDENCE ADDRESS:
ADDRESSEE: Human Genome
STREET: 9410 Key West Av
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                                                                                                   STATE: Maryland
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                                                                                                                   CITY: Rockville
                                                                                                                                                                                                                                                                 Application
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                    486/33
                                                                                                                                    Avenue
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                                    1.4Mb
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US-09-536-784-66
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FILING DATE: CCT-30-1997
ATTORNEY/AGENT INFORMATION:
NAME: Michelle S. Marks
REGISTRATION NUMBER: 41,971
REFERENCE/DOCKET NUMBER: PB340P3
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 309-8504
TELEPHONE: (301) 309-8504
TELEFAX: (301) 309-8512
INFORMATION FOR SEQ ID NO: 66:
SEQUENCE CHARACTERISTICS:
LENGTH: 763 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 63.6%; Score 2649.5; DB 4; Best Local Similarity 66.8%; Pred. No. 4e-197; Matches 519; Conservative 77; Mismatches 132;
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MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 66:
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APPLICATION NUMBER: US/09/536,784
FILING DATE: 30-Occ-1997
CLASSIFICATION: <Unknown>
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                                                                                                                                                OPERATING SOFTWARE:
                                                                       SYELGLYQARTV-KENNRVSYIDGKQATQKTENLTPDEVSKREGINAEQIVIKITDQGYV
                     AAAIYNRVKGEKRIPLVRLPYMVEHTVEVKNGNLIIPHKDHYHNIKFAWFDDHTYKAPNG
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AEAIYNRVKAAKKVPLDRMPYNLQYTVEVKNGSLIIPHYDHYHNIKFEWFDEGLYEAPKG
                                                                                                                                                                                                                                                                                                         SPOPAPNPOPAPSNPIDEKLVKEAVRKVGDGYVFEENGVSRYIPAKDLSAETAAGIDSKL
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STRANDEDNESS: single
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|--|--|--|--|--|--|--|---|---|--|--|--------------|--|
| 481 KEKLVDDLLAFLAPITHPERLGKPNSQIEYTEDEVRIAQLADKYTTSDGYIFDEHDIISD 540 | 421 VSHTLTAKKENVAPRDQEFYDKAYNLLTEAHKALFXNKGRNSDFQALDKLLERLNDESTN 480<br> | 361 PQPAPNLKIDSNSSLVSQLVRKVGEGYVFEEKGISRYVFAKDLPSETVKNLESKLSKQES 420 | 301 ARGVAVPHGDHYHFIPYSQMSELEERIARIIDLRYRSNHWVPDSRPEQPSPQPTPEPSPG 360<br>   - | 241 VSNPGTTNTNTSNNSNTNSQASQSNDIDSLLKQLYKLPLSQRHVESDGLVFDPAQITSRT 300 | 181 GDAYIVPHGDHYHYIPKNELSASELAAAEAFLSGRGNLSNSRTYRRQNSDNTSRTIMVPS 240 | 121 AHADNVRTKEEINRQKQEHSQHREGGTPRNDGAVALARSQGRYTTDDGYIFNASDIIEDT 180 | 61 SHGDHYHYYNGKVPYDAIISEELLMKDDNYKLKDEDIVNEVKGGYVIKVDGKYYVYLKDA 120<br> | 1 SYELGLYQARTVKENNRVSYIDGKQATQKTENLTPDEVSKREGINAEQIVIKITDQGYVT 60 | 28.9%; Score 1203.5; DB 4; Length 484;<br>Local Similarity 45.8%; Pred. No. 3.6e-85;<br>hes 259; Conservative 77; Mismatches 120; Indels 109; Gaps 10; | 8-656A-6 NO. 6582706 L INFORMATION. CANT: JOHNSON, Leslie S. CANT: Adamou, John E. OF INVENTION: Vaccine Compositio OF INVENTION: Motifs REFERENCE: 469201-44 NT APPLICATION NUMBER: US/09/468, NT APPLICATION NUMBER: 60/113,048 FILING DATE: 1998-12-21 R OF SEQ ID NOS: 14 RE: PatentIN Ver. 2.1 NO 6 1 PAT NISM: Streptococcus pneumoniae 8-656A-6   | 710 VEET 743 | 656 YTLEDLFATIKYYVEHPDERPHSNDGWGNASEHVLGKKDHSEDPNKNFKADEEP 709<br> |

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                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; MOLECULE TYPE: protein US-08-961-083-182
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                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 182, Application US/08961083 Patent No. 6159469
                                                                                                                                                                                                                                                                                                                                                                                         Matches
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INFORMATION FOR SEQ ID NO:
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MEDIUM TYPE: Diskette, 3.50
COMPUTER: HP Vector 486/33
OPERATING SYSTEM: MSDOS Vers
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
LENGTH: 447 amino acid
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REFERENCE/DOCKET NUMBER: 98
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 309-8504
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APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: amino acid
STRANDEDNESS: sir
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CLASSIFICATION: 435
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STATE: Maryland
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                                                                                                                                                                    DVRTKDEINRQKQEHVKDNE----KVNGNVAVARSQGRYTTNDGYVFNPADIIEDTGNA
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VAVPHGDHYHFIPYSQMSELEERIARIIPLRYRSNHWVPDSRPEQPSPQPTPEPSPGPQP 363
                                ----NTQSVAKGSTSKPANKSENLQSLLKELYDSPSAQRYSESDGLVFDPAKIISRTPNG
                                                                 PGTTNTNTSNNSNTNSQASQSNDIDSLLKQLYKLPLSQRHVESDGLVFDPAQITSRTARG 303
                                                                                                    YIVPHGGHYHYIPKSDLSASELAAAKAHLAGKNMQPSQLSYSSTASDN------
                                                                                                                                                                                                                                              DHYHYYNGKVPYDALFSEELLMKDPNYQLKDADIVNEVKGGYIIKVDGKYYVYLKDAAHA
                                                                                                                                                                                                                                                                         DHYHYYNGKVPYDAIISEELLMKDPNYKLKDEDIVNEVKGGYVIKVDGKYYVYLKDAAHA 123
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9410 Key West Avenue
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                                                                                                                                                                                                                                                                                                                                                                                     28.5%; Score 1187.5;
46.3%; Pred. No. 5.5e
ative 72; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Streptococcus pneumoniae Antigens and Vaccines: 452
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MSDOS version 6.2
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                                                                                                                                                                                                                                                                                                                                                                                                        .5e-84;
                                                                                                                                                                                                                                                                                                                                                                                                                        DB 3; Length 447;
                                                                                                                                                                                                                                                                                                                                                                                         117;
                                                                                                                                                                                                                                                                                                                                                                                       Indels 109;
                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                        176
                                                                                                                                     243
                                                                                                                                                                                                                                              120
                                                                                                                                                                                                                                                                                                                   60
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                                                                                                      224
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TOPOLOGY: linear;

MOLECULE TYPE: protein;

SEQUENCE DESCRIPTION: SEQ ID NO: 182: US-09-536-784-182
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US-09-536-784-182
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GENERAL INFORMATION:
                                                                                                              Matches
                                                                                                                           Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                 TELEPHONE: (301) 30 TELEFAX: (301) 30 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/961,083
FILING DATE: OCT-30-1997
ATTORNEY/AGENT INFORMATION:
NAME: Michelle S. Marks
REGISTRATION NUMBER: 41,971
REFERENCE/DOCKET NUMBER: PB340P3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: ASCII Text CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM: MEDIUM TYPE: Diskette,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION: Streptococcus pneumoniae NUMBER OF SEQUENCES: 452
                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                           TELECOMMUNICATION INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Choi et.
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                                                                                                              257;
 64
DHYHYYNGKVPYDAIISEELLMKDPNYKLKDEDIVNEVKGGYVIKVDGKYYVYLKDAAHA 123
                                                           LGLYQARTVKENNRVSYIDGKQATQKTENLTPDEVSKREGINAEQIVIKITDQGYVTSHG
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VAIPHGDHYHFIPYSKLSALEEKIARMVP-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US/09/536,784 FILING DATE: 30-Oct-1997 CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDIUM TYPE: Diskette, 3.50 inch, 1
COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GFVMSHGDHNHYFFK 446
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TLTAKKENVAPRDQEFYDKAYNLLTEAHKALFXNKGRNSDFQALDKLLERLNDESTNKEK 483
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APNIKIDSNSSIVSQIVRKVGEGYVFEEKGISRYVFAKDIPSETVKNIESKISKQESVSH 423
                                  LNOHRSQENKDNNRVSYVDGSQSSQKSENLTPDQVSQKEGIQAEQIVIKITDQGYVTSHG
                                                                                                                                                                                                                                                         STRANDEDNESS: single
                                                                                                                                                                                                                                                                              TYPE: amino acid
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STATE: Maryland
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                                                                                                                                                                                                                                                                                                LENGTH: 447 amino acids
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                                                                                                              Conservative
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                                                                                                                           28.5%;
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                                                                                                                                                                                                                                                                                                                                       182:
                                                                                                          72;
                                                                                                        Score 1187.5; DB 4;
Pred. No. 5.5e-84;
72; Mismatches 117;
                                                                                                                                                                                                                                                                                                                                                                                                              PB340P3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1.4Mb
                                                                                                                                           DB 4;
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                                                                                                          Indels 109;
                                                                                                                                         Length
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US-09-134-001C-5080
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SEQ ID NO 5080
LENGTH: 3696
TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 5080, Application US/09134001C Patent No. 6380370
                                                                                                                                                                                                                  Matches
                                                                                                                                                                                                                                   Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Lynn Doucette-Stamm et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: GTC-007
CURRENT APPLICATION NUMBER: US/09/134,001C
CURRENT FILING DATE: 1998-08-13
PRIOR APPLICATION NUMBER: US 60/064,964
PRIOR APPLICATION NUMBER: US 60/064,964
PRIOR APPLICATION NUMBER: US 60/055,779
PRIOR APPLICATION NUMBER: US 60/055,779
PRIOR APPLICATION NUMBER: US 60/055,779
                                                                                                                                                                                                                                                                                        ORGANISM: Staphylococcus epidermidis -09-134-001C-5080
     1409
                                                                                                                                              1299
                                                                       1354 EANRKIE----EAKIEAKDNIQRNSTRDQVNEAKTNGINKIENITPATTVKSEARQAVQ
                                      111
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                                                                                                                                                                            15 NNRVSYI---PGKQATQKTENLTPDEVSKREGINAEQIVIKITD-----QGYVTSHGDHYH
                                                                                                                                                                                                                                    Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PGTTNTNTSNNSNTNSQASQSNDIDSLLKQLYKLPLSQRHVESDGLVFDPAQITSRTARG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VAVPHGDHYHFIPYSQMSELEERIARIIPLRYRSNHWVPDSRPEQPSPQPTPEPSPGPQP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NKANEQINHIQNTPDATNEEKQEAINRVSAELARVQAQINAEHTTQGVKTIKDDAITSLS 1468
                                    ---GKYYVYLKDAAHADNVRTKEEINR-----QKQEHSQHREGG--TPRNDGAVALA
                                                                                                          YYNGKVPYDAIISEELLMKDPNYKLKDEDIVNEVKGGYVIKVD---
                                                                                                                                             NNQIDGIVSDGRQSINA---ITPDTSIKRNAKN--DIDIKAADKKIKIQRINDATDEEIQ
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                                                                                                                                                                                                                3.9%;
llarity 18.5%;
Conservative 141
                                                                                                                                                                                                                  141;
                                                                                                                                                                                                              Score 163; DB 4; Length 3696;
Pred. No. 0.0054;
1; Mismatches 348; Indels 31
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                                                                                                                                                                                                                  316;
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                                                                                                                                                                                                                Gaps
                                      157
                                                                         1408
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APPLICANT: Lynn Doucette-Stamm et al TITLE OF INVENTION: NUCLEIC ACID AND AMINO AC TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOST FILE REFERENCE: GTC-007
CURRENT APPLICATION NUMBER: US/09/134,001C CURRENT FILING DATE: 1998-08-13
PRIOR APPLICATION NUMBER: US 60/064,964
PRIOR APPLICATION NUMBER: US 60/055,779
PRIOR FILING DATE: 1997-08-14
                                                                                                                                                                                                                                 RESULT 12
US-09-134-001C-3159
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                                                                                                                                                                                              Sequence 3159, Application US/09134001C Patent No. 6380370
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LENGTH: 10182
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                                                         6171 NNAQKDAEKNLVNSASTLEQVQQNLQTAQQLDNAMGELRQSI-AKKDQVKADSKYLNEDP
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700 NKNFKADE----EPVEETPAEPEVPQVETEKVEAQLKEAEVLL--AKVTDSSLKANATE
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)%; Pred. No. 0.055;
126; Mismatches 368; Indels 320
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US-09-513-783A-6
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SEQ ID NO 6
LENGTH: 812
TYPE: PRT
ORGANISM: Artificial Sequence
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GENERAL INFORMATION:
APPLICANT: Giuliano, Kenneth A.
APPLICANT: Kapur, Ravi
TITLE OF INVENTION: A System for Ce
FILE REFERENCE: 97-022-L1
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CURRENT FILING DATE: 2000-02-25
NUMBER OF SEQ ID NOS: 180
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                                                         PERLGKPNSQIEYTEDEVRIAQLADKYTTSDGYIFDEHDIISDEGDAY----
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; APPLICANT: DZIEGIEL, MORTEN;BORRE, MARTIN;JEPSEN, SOREN;
; VUUST, JENS;RIENECK, KLAUS;WIND, ANNETTE;JAKOBSEN, PALLE H.
; TITLE OF INVENTION: MALARIA ANTIGEN
; NUMBER OF SEQUENCES: 19
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/409,658
; FILING DATE: 18-SEP-1989
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AAAIYNRVKGEKRIPLVRLPYMVEH-TVEVKNGNLIIPHKDHYHNIKFAWFDDHTYKAPN
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20.2%; Pred. No. 0.0097;
tive 106; Mismatches 278;
                                                      DDKNEKVEHEIVEVEEILP--EDKNEKGQHEIVE
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APPLICANT: Sakowicz, Roman
APPLICANT: Beraud, Christophe
TITLE OF INVENTION: Antifungal Assay
FILE REFERENCE: 1015
CURRENT APPLICATION NUMBER: US/09/541,782
CURRENT FILING DATE: 2000-04-03
NUMBER OF SEQ ID NOS: 10
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 6
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US-09-541-782-6
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Patent No. 6284480
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 LTAKKENVAPRDQEFYDKAYNLL------
                                                                                                                              NKDLLCQEQARKLEVLDLNVKS-----SREQLQYVSKSNQEHKKEVEALQLQLVNSSTE
                                                                                                                                                                    MSEL----EERIARIIPLRYRSNHWVPDSRPEQPSPQPTPEPSPGPQPAPNLKI-----
                                                                                                                                                                                                                                                                                                            -----YR-----RQNSDNTSRTNWVPSVSNPGTTNTNTSNNSNTNSQASQS
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                                                          LESVKSENEKLKNELVLBIEKRKKYETNEAKITTVATDLSQYYRESKEYIASLYEKLDRT
                                                                                                                                                                                                                                          NDIDSLLKQLYKLPLSQRHVESDGLVFDPAQI----TSRTARGVAVPHGDHYHFIPYSQ
                                                                                                                                                                                                                                                                                                                                                                                         GDAYIVPHGDHYHYIPKNELSASELAAAEAFLSGRGNLSNSRT-------
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18.6%;
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| Query Match  Best Local Similarity 18.6%; Pred. No. 0.017;  Matches 182; Conservative 136; Mismatches 357; Indels 301; Gaps 41;  Qy 23 GKQATQKTENLTPDEVSKREGINAEQIVIKITDQGYVTSHGDHYHYYN 70  | RESULT 16 US-09-723-820-6 ; Sequence 6, Application US/09723820 ; Patent No. 6468760 ; GENERAL INFORMATION:    APPLICANT: Nislow, Corey ; APPLICANT: Sakowicz, Roman ; APPLICANT: Sakowicz, Roman ; APPLICANT: Beraud, Christophe ; TITLE OF INVENTION: Antifungal Assay FILE REFERENCE: 1015 ; CURRENT APPLICATION NUMBER: US/09/723,820 ; CURRENT FILING DATE: 2000-11-28 ; PRIOR APPLICATION NUMBER: 09/541,782 ; PRIOR APPLICATION NUMBER: 09/541,782 ; PRIOR FILING DATE: 2000-04-03 ; NUMBER OF SEQ ID NOS: 10 ; SOFTWARE: FastSEQ for Windows Version 4.0 ; SEQ ID NO 6 ; LENGTH: 1073 ; Type: PRT ; ORGANISM: S.pombe US-09-723-820-6 | Db 861 NGQLLDSKSKAIHSNGRSMYDHCLALAESQKQGVNLEVQTLDRLLQKVK | Db 578 ERNNKENENNFWNLKFNLLTMLRSFHGSFTDETNGYFTLLNDFNASMEELLNTHSN 633  Qy 452 KALFXNKGRNSDFQALDKLLERLNDESTNKEKLVDDLLAFLAPIT 496 |
|---|---|--|---|
| RESULT 17  US-08-961-083-118  Sequence 118, Application US/08961083  Patent NO. 6152469  GENERAL INFORMATION: APPLICANT: Choi et. al. TITLE OF INVENTION: Streptococcus pneumoniae Antigens and Vaccines NUMBER OF SEQUENCES: 452  CORRESPONDENCE ADDRESS: ADDRESSE: Human Genome Sciences, Inc. STREET: 9410 Key West Avenue CITY: Rockville STATE: Maryland COUNTRY: USA ZIP: 20850 COMPUTER READABLE FORM: | Qy 579 LPPSPDADVKANPTGDSAAAIYNRVKGEKRIPLVRLPYMVEHTVEVK 625 Db 809ADILHSHLNDTNSNIRKANEIMNNRSEEPLRNAASQAEIVGANKERIQKTVE 860 Qy 626 NGNLIIPHKDH-YHNIKFAWFDDHTYKAPNGYTLEDLFATIKYYVEHPDERP 676   ::: ::: ::::::::::::::::::::::::::  |  | Qy 181 GDAYIVPHGDHYHYIPKNELSASELAAAEAFLSGRGNLSNSRT  |

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; TOPOLOGY: linear; MOLECULE TYPE: protein US-08-961-083-118
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Best Local
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TELEPAX: (301) 309-8512
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REGISTRATION NUMBER: 36,373
REFERENCE/DOCKET NUMBER: PB
TELECOMMUNICATION INFORMATION
TELEPHONE: (301) 309-8504
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION: 435
FRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US
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Local Similarity 19.2%; Pred. No. 0.022;
1es 154; Conservative 111; Mismatches 284; Indels 25
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STRANDEDNESS: sir
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-VEVKNGNLIIPHKDHYHNIKFAWFDDHTY-----KAPNGYT-LEDLFATIK-----Y 667
                                                            TDTAKYFVKVK---
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                                                                                                                                     E--ENTETSTQDFQL--EYKKIEIKDIDSVELYGKENDRY-----RRYL---SLSEAP
                                                                                                                                                                          SQIEYTEDEVRIAQLADKYTTSDGYIFDEHDIISDEGDAYVTPHMGHSHWIGKDSLSDKE
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TOPOLOGY: linear;
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MOLECULE TYPE: protein
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SEQUENCE DESCRIPTION: SEQ ID NO:
US-09-536-784-118
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US-09-536-784-118
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Patent No. 6573082
GENERAL INFORMATION:
APPLICANT: Choi et. al.
TITLE OF INVENTION: Streptococcus pneumoniae Antigens and Vaccines
NUMBER OF SEQUENCES: 452
                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
Matches 154; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INFORMATION FOR SEQ ID NO: 118: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: ASCII Text
CURRENT APPLICATION UNDATA:
APPLICATION NUMBER: US/09/536,784
FILING DATE: 30-Oct-1997
CLASSIFICATION: <UNKnown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/961,083
FILING DATE: OCT-30-1997
ATTORNEY/AGENT INFORMATION:
NAME: Michelle S. Marks
REGISTRATION NUMBER: 41,971
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION
TELEPHONE: (301) 309-850
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
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                           213
                                                                                                                       153 AVALARSOGRYTTDDGYIFNASDIIEDTGDAYIVPHGDHYHYIPKNELSASELAAAEAFL 212
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SGRGNLSNSRTYRRQNSDNTSRTNWVPSVSNPGTTNTNTSNNSNTNSQASQSNDIDSLLK 272
                                                                                                                                                                    LKIEGYQYIGYIK-TKKQDNTELSRTVDGKYSAQRDSQPNSTKTSDVVHSADLEWNQGQG 134
                                                                         KVSL---QGEASGDDG-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb
COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.2
                                                                                                                                                                                                                  IKVDGKYYV-YLKDAAHADNVRTKEEINRQKQEHSQHREGGTPRND-------G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: Human Genome Sciences,
STREET: 9410 Key West Avenue
CITY: Rockville
STATE: Maryland
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 1040 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX: (301) 309-8512
                                                                                                                                                                                                                                                                  3.5%; Score 144; DB 4; Length 1040; ilarity 19.2%; Pred. No. 0.022; Conservative 111; Mismatches 284; Indels 25
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SEQ ID NO 2
                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                             Sequence
                                                                                                                                                                                                                                                                                                                                                                               Patent No.
                                                                                                                                                                                                      TITLE OF INVENTION: Use of Protein Tyrosine Phosphatase Zeta as a TITLE OF INVENTION: Treatment and Visualization of Brain Tumors FILE REFERENCE: 262/235 AGY
CURRENT APPLICATION NUMBER: US/09/816,703A
CURRENT FILING DATE: 2001-03-23
NUMBER OF SEQ ID NOS: 2
                                                                                                                                                                                                                                                                                                          APPLICANT: Melcher, Thorsten APPLICANT: Mueller, Sabine APPLICANT: Chin, Daniel
LOCATION: (1)..(2314)
OTHER INFORMATION: Krueger, N.X. and Saito, H.: A human transmembrane protein-tyrosi
OTHER INFORMATION: ne-phosphatase, PTP zeta, is expressed in brain and has an N-term
OTHER INFORMATION: inal receptor domain homologous to carbonic anhydrases; Proc. Nat
OTHER INFORMATION: 1. Acad. Sci. USA 89 (16), 7417-7421 (1992
                                                                                                                                          TYPE: PI
                                                                                    FEATURE:
NAME/KEY: Reference
                                                                                                                     ORGANISM: Homo sapiens
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                                                                                                                                                                                                                                                                                                         Mueller, Sak
Chin, Daniel
                                                                                                                                                                                        version 3.0
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Proc. Nat
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LOCATION: (1)..(2314
OTHER INFORMATION: L
OTHER INFORMATION: D
OTHER INFORMATION: C
                   OTHER INFO
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LOCATION: (324)...(324)
OTHER INFORMATION: Glycosylation; N-linked
NAME/KEY: SITE
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LOCATION: (312)..(406)
OTHER INFORMATION: Fibronectin Type-III
NAME/KEY: SITE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY: SITE
LOCATION: (105)...(105)
OTHER INFORMATION: Glycosylation; N-linked
                                                                              LOCATION: (997)..(9
                                                                                                                                                                           LOCATION: (677)...(OTHER INFORMATION: NAME/KEY: VARSPLIC
                                                                                                                                                                                                                                                      OTHER INFORMATION: Chondroitin sulfate (potential)
                                                                                                                                                                                                                                                                                                         LOCATION: (629)..(629)
OTHER INFORMATION: Glycosylation; N-linked (GLCNAC...)
                                                                                                                                                                                                                                                                                                                                                                      LOCATION: (602)..(602)
OTHER INFORMATION: Glycosylation; N-linked (GLCNAC...)
                                                                                                                                                                                                                                                                                                                                                                                                              LOCATION: (587)..(587)
OTHER INFORMATION: Chondroitin sulfate (potential)
NAME/KEY: SITE
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OTHER INFORMATION: Glycosylation; N-linked
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OTHER INFORMATION: Glycosylation;
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OTHER INFORMATION: Glycosylation;
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OTHER INFORMATION: Glycosylation;
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LOCATION: (134)..(134)
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LOCATION: (25)..(2314)
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OTHER INFORMATION: Extracellular (potential)
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OTHER INFORMATION:
                                                                                                                                   LOCATION: (755)..(1614)
OTHER INFORMATION: Splicing
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INFORMATION: Glycosylation;
KEY: SITE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BINDING
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                                                                                                                       BINDING
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                                          (1017)..(1017)
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                                                                              sulfate
                      N-linked (GLCNAC...)
                                                                                                                                                                                                N-linked (GLCNAC...)
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                      (potential)
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OTHER INFORMATION: Glycosylation; N-linked (GLCNAC...)

1308

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US-09-816-703A-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY: misc_feature
LOCATION: (2222)..(2222)
OTHER INFORMATION: Ancestral active
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LOCATION: (1998)..(2314)
OTHER INFORMATION: Protein-tyrosine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LÓCATION: (1932)..(1932)
OTHER INFORMATION: Active site;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OTHER INFORMATION: Protein-tyrosine phosphatase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OTHER INFORMATION: Cytoplasmic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LOCATION: (1636)..(1661)
OTHER INFORMATION: Transmembrane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LOCATION: (1617)..(1617)
OTHER INFORMATION: Glycosylation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LOCATION: (1561)..(1561)
OTHER INFORMATION: Glycosylation; N-linked
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OTHER INFORMATION: Glycosylation; N-linked
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OTHER INFORMATION:
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OTHER INFORMATION: Missing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY: SITE
LOCATION: (161)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OTHER INFORMATION: Chondroitin sulfate (potential)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OTHER INFORMATION: Chondroitin sulfate (potential)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IAME/KEY: DOMAIN
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                                                                                                                                                             1091 SISSTKGMFPGSLAHTTTKVFDHEISQVPENNFSVQPTHTVSQASGDTSLKPVLSANSEP
                    1205
                                                                                                                                                                                                                                                                                                                                                                                                                                                     169;
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                                                                                                                                                                                                210
                                                                                                                                                                                                                                                                                                          994 GEW----SGASSDS
                                                                                                                                                                                                                                                                                                                                            111 GKYYVYLKDAAHADNVRTKEEINRQKQEHSQHREGGTPRNDGAVAL-----ARSQGRYT 164
                                                                                                                                                                                                                                                                                                                                                                               954 VGVTYQGSLFSGPSHI-----PIPKSSLITPTASLLQPTHALSG-------D
                                                                                                                                                                                                                                                                                                                                                                                                                S1 IKITDQGYVTSHGDHYHYYNGKVPYDAIISEELLMKDPNYKLKDEDIVNEVKGGYVIKVD
                  DPILVETPKVDKISSTMLHLIVSNSASSENMLHSTSVPVFDVSPTSHMHSASLQGLTISY
                                                     DGLVFDPAQ----
                                                                                         ASSDPASSEMLSPSTQLLFYETSASFSTEVLLQPSFQASDVDTLLKTV--LPA----VPS
                                                                                                                          SVSNPGTT------NTNTSNNSNTNSQAS-QSNDIDSLLKQLYKLPLSQRHVES
                                                                                                                                                                                                    AFLSGRG--
                                                                                                                                                                                                                                    TSVFGDDNKALSKSETIYGNETELQIPSFNEMVYPSESTVMPNMYDNVNKLNASLQETSV 1090
                                                                                                                                                                                                                                                                       T----DDGYIFNASDIIEDTGDAYIVPHGDHYHY-----IPK----NELSASELAAAE 209
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Pred. No. 0.12;
                                                     --ITSRTARGVAVPHGDHYHFIPYSQMSELEERIARIIPLRY 335
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TELEX: 248345
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                   ZIP: 22040-0747
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                       ATTORNEY/AGENT INFORMATION:
NAME: MULTPHY JT., Gerald M.
REGISTRATION NUMBER: 28,977
REFERENCE/DOCKET NUMBER: 82
                                                                                                                                                                                                                              COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
CURRENT APPLICATION DATA:
                                                                      TELECOMMUNICATION INFORMATION: TELEPHONE: 703-241-1300
                                                                                                                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION: DNA Expressi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                       STREET: P.O. Box 747
CITY: Falls Church
STATE: Vircini
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES:
                                                                                                                                                                                               APPLICATION NUMBER: FILING DATE: 13-AUC
                                                   TELEFAX:
                                                                                                                                                                                  CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                          COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1717
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                                                                                                                                                                                                                                                                                                                                             22040-0747
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DAYVTPHMGHSHWIGK---DSLSDKEKVA--AQAYTKEK---GIL-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ----RNSDFQALDKLLERLNDESTNKEKLVDDLLAFLAPITHPERLGKPNSQIEY----
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                                                                                                                                                                                                                                                                                                                                                            USA
                                                     703-241-2848
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Garoff, Henrik
Liljestrom, Peter
                                                                                                                                                                                               13-AUG-1992
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                                                                                                                                                                                                                     US/07/920,281C
                                                                                                                          28,977
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                                                                                                           828-103P
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                                                                                                                                                                                                                                                        Version
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Matches

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RESULT 21
US-08-466-277-2
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                                                                                                                                                                                                  Sequence 2, Application US/08466277
Patent No. 6190666
GENERAL INFORMATION:
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Best Local
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TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity
                                                                                                                            APPLICANT: Garoff, Henrik
Liljestrom, Peter
TITLE OF INVENTION: DNA Expression Systems
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1971
                  CORRESPONDENCE ADDRESS:
ADDRESSEE: Birch, Stewart,
STREET: P.O. Box 747
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1862
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                                                                                           NUMBER OF SEQUENCES:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                56 QGYVTSHGDHYHYYNG-KVPYDAIISEELLMKDPNYKLKDEDIVNEVKGGYVIKVDGKYY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EKLLLLKMOMHPSEANKSRYOS-RKVENMKATVVDRLTSGARLYTGADVGRIPTYAVRYP 1920
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HKALF-----XNKGRNSDFQALDKLLERLNDESTNKEKLVDDLLAFLAP---ITHP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LGRAGAYIFSSDTGS---GHLQQKSVRQ----HNLQCAQLDAVQEEKMYPPK---LDTER 1861
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AYLASRAAERPVPAPR-KPTPAPRTAFRNKLPLTFGDFDEHEVDALASGITFGDFDDVLR 1811
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    Falls Church
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                                                                                                              Alphaviruses
                                            Kolasch
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Best Local
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INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 2431 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                          1713
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: 07/920,281
FILING DATE: «Unknown»
ATTORNEY/AGENT INFORMATION:
NAME: Murphy Jr., Gerald M.
REGISTRATION NUMBER: 28,977
REFERENCE/DOCKET NUMBER: 828-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, V
CURRENT APPLICATION DATA:
APPLICATION UMBER: US/08/466,277
FILING DATE: 06-Jun-1995
CLASSIFICATION: <Unknown>
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TELEPHONE: 703-241-1300
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                            1812
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                                                                                                                                   1862
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554
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               56 QGYVTSHGDHYHYYNG-KVPYDAIISEELLMKDPNYKLKDEDIVNEVKGGYVIKVDGKYY 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
HWIGKDSLSDKE---KVAAQAYTKEKGI-----LPPSP-----
                                          RPVYSPTVIERFSSPDVAIAACNEYLSRNYPTVASYQITDEYDAYLDMVD--
                                                                                                                                                                                                                          LGRAGAYIFSSDTGS---GHLQQKSVRQ----HNLQCAQLDAVQEEKMYPPK---LDTER 186
                                                                                                                                                                                                                                                                                                              AYLASRAAERPVPAPR-KPTPAPRTAFRNKLPLTFGDFDEHEVDALASGITFGDFDDVLR 1811
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                                                                                                                                                                             HKALF-----XNKGRNSDFQALDKLLERLNDESTNKEKLVDDLLAFLAP---ITHP
                                                                                                                                                                                                                                                                    ISR----YVFAKDLPSETVKNLESKLSKQESVSHTLTAKKENVAPRDQEFYDKAYNLLTEA
                                                                                                                                                                                                                                                                                                                                                           HWVPDSRPEQPSPQPTPEPSPGPQPAPNLKI-----DSNSSLVSQLVRKVGEGYVFEEKG 393
                                                                                                                                                                                                                                                                                                                                                                                                                                                 -SQRHVESDGLVFDPAQITSRTARGVAVPHGDHYHFIPYSQMSELBERIARIIPLRYRSN 338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ASTTDHSDRSLRGFDLDW-----TTDSSSTASDTMSLPSLQSCDIDSIYEPMAPIVV 1712
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                                                                                    ERLGKPNSQIEYTEDEVRIA----QLADKYTTSDGY-IFDEHDIISDEGDAYVTPHMGHS
                                                                                                                                   EKLLLLKMQMHPSEANKSRYQS-RKVENMKATVVDRLTSGARLYTGADVGRIPTYAVRYP
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Pred. No. 0.14;
3; Mismatches 253;
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--DADVKAN----
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RESULT 22
US-08-714-741-32
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Best Local Similarity
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GENERAL INFORMATION:
                                                                                                                                                                          Matches 110;
                                                                                                                                                                                                                                                                                                                                            TELEFAX: (212) 840-071
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 8991 amino aci
                                                                                                                                                                                                                                                                     STRANDEDNESS:
TOPOLOGY: lin
MOLECULE TYPE:
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TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                       TELECOMMUNICATION INFORMATION: TELEPHONE: (212) 840-3333
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES: 4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Frommer Esq., William S.
REGISTRATION NUMBER: 25,506
REFERENCE/DOCKET NUMBER: 45431
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: FILING DATE: 16-SEP CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CITY: New York
STATE: New York
                                                                                                                                                                                                                                                                                                                              TYPE: amino acid
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                     GGLEKALTDEKVGLNNTPKALDTAPKALDTALNELGPDGDE-
                                                                                                                                  PSVSNPGTTNTNTSNNSNTNSQASQSNDIDS----LLKQLYKLPLSQRHVESDGL----
                                                                                               PGGETPDGLDKEASEDSNIGALPNQVSDLENQVSELDREVTRLPSDLKDTEGNNVGDYVK
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McDaniel, Larr,
Swiatlo, Edwin
Swiatlo, Janet
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VENTION: PNEUMOCOCCAL GENES, PORTIONS THEREOF,
VENTION: EXPRESSION PRODUCTS THEREFROM, AND USES OF SUCH GENES,
VENTION: PORTIONS AND PRODUCTS
EQUENCES: 47
                                                                                                                                                                                                                                                                                                                                                                                                      (212) 840-0712
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Crain, Marilyn J.
Hollingshead, Susan
Tart, Rebecca
                                                                                                                                                                          Conservative
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                                                         --VFDPAQITSRTARGVAVPHGDHYHFIPYSQMSELEERIARI 330
                                                                                                                                                                                                                                                                                                                                                                                                                                                               454312-2460
                                                                                                                                                                                          Score 141; DB Pred. No. 1.1;
                                                                                                                                                                        Mismatches 230;
                                                                                                                                                                                                             DB 4; Length 8991;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 14, Application US/08976255
Patent No. 6136581
TELEX: 67-3510
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
                                                                                                                                                                                                                             SOFTWARE: FastSEQ for Windows 2.0 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/976,255 FILING DATE: NO. 6136581ember 21, CLASSIFICATION 435 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                  ZIP: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
MEDIUM TYPE: STORAGE
                                                                                             REFERENCE/DOCKET NUMBER: 22
TELECOMMUNICATION INFORMATION:
                                                                                                                              ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Plowman, Gregory
TITLE OF INVENTION: KINASE GENES AND USES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STATE: Cal:
                                                                                                                                                                                                                                                                                                                                          OPERATING SYSTEM:
                                                                                                                                                                                            APPLICATION NUMBER: 60/031,675 FILING DATE: No. 6136581ember
                                                         TELEFAX:
                                                                           TELEPHONE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Suite 4700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          633 West Fifth Street
                                                         (213) 955-0440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Jono,
                                                                                                                                                                                                                                                                                                                                                              IBM Compatible
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                                                                             (213) 489-1600
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736 -VLLAKVTDSSLKANAT
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                                                                                                                                             VISDAGDGHRGTEVTP-
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                                                             EKR-----SEEVPG-----TSPSALVLVQEQPLPEPVLPEQSPAAQDSCLEARKSQPDE 116;
                                                                                                 HSNDGWGNASEHVLGKKDHSEDPNKNFKADEEPVEETPAEPEVPQVETEKVEAQLKEAE-
                                                                                                                                                                                                                                                               KEKVAAQAYTKE-----KGILPPSPDADVKANP--TGDSAAAIYNRVKGEKRIPLVRLPY 616
                                                                                                                                                                                                                                                                                                                                           PNSQIEYTEDEVRIAQLADKYTTSDGYIFDEHDIISDEGDAYVTPHMGHSHWIGKDSLSD
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                       751
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                                                                                                                                           -ETFTAGSQGSYRD-
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OTHER INFORMATION: Description of Artificial Sequence:
OTHER INFORMATION: EYFP-DEVD-MAP4-EBFP construct
US-09-513-783A-22
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US-09-513-783A-22
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SEQ ID NO 22
LENGTH: 1610
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PATENT NO. 6416959
GENERAL INFORMATION:
APPLICANT: Giuliano, Kenneth A.
APPLICANT: Kapur, Ravi
TITLE OF INVENTION: A System for Cel
FILE REFERENCE: 97-022-L1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches 174;
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CURRENT APPLICATION NUMBER: US/09/513,783A
CURRENT FILING DATE: 2000-02-25
NUMBER OF SEQ ID NOS: 180
SOFTWARE: PatentIn Ver. 2.0
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TYPE: PRT
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                     DVAPPMEEEIVPGNDTTSPKETETTLPIKMDLAPPEDVLLTKETELAP---
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                                                                                                                                       GKPNSQIEYTEDEYRIAQLADKYTTSDGYIFDEHDIISDEGDAY-----
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                                                                                                   EITKPDVILANVTQPSTESDMFLAQDMELLTGTEAAHANNIILPTEPDESSTK
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19.8%; Pred. No. 0.14;
                                                                                                                                                                                 ----ALETMAEQTTDVVHSPSTDTTPGPDTEAALAKDIE-----
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                                      ; MOLECULE TYPE: US-08-447-031A-2
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Patent No. 5851794
GENERAL INFORMATION:
 Query Match
                                                                                                                            TELEFAX: (703) 836-202
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                   TELECOMMUNICATION INFORMATION: TELEPHONE: (703) 836-6620
                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: WO PFILING DATE: 22-OCT-1991
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/861,804
FILING DATE: 21-AUG-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: PatentIn Release #1.0, Version CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/447,031A FILLING DATE: 22-MAY-1995
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APPLICANT: SWITALSKI, Lech
TITLE OF INVENTION: A COLLAGEN BINDING PROTEIN AS
TITLE OF INVENTION: ITS PREPARATION
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                                                                      TYPE: ami
                                                                                                                                                                                                                        NAME: McGowan, Malcolm K.
REGISTRATION NUMBER: 39,3
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: SE 9003374-7 FILING DATE: 22-OCT-1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE: 22 CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
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HOOK, Magnus
JONSSON, Hans
LINDBERG, Martin
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P.O. Box 1404
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 Score 136.5;
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Length 1183;
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                                                                                           IMAEAEKLLALLKGSNPSSVSKE 793
                                                                                                                                KYDEGKKIEYTVTEDH----
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                                                                                                                                - VKDYTTDINGTTITNKYTPGETSATVTKNWD--
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CURRENT FILING DATE: 2000-02-25
NUMBER OF SEQ ID NOS: 180
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 4
LENGTH: 812
TYPE: PRT
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GENERAL INFORMATION:
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Best Local (
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APPLICANT: Kapur, Ravi
TITLE OF INVENTION: A System for Cell Based
FILE REFERENCE: 97-022-L1
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VSLSEIEEALAKNDVRSAE-IPVAQ-ETVVSETEVVLATEVVLP--
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                               ANPTGDSAAAIYNRVKGEKRIPLVRLPYMVEHTVEVKNGNLIIPHKDHYHNIKFAWFDDH
                                                                  SSTKDVAPPMEEEIVPGNDTTSPKETETTLPIKMDLAPPEDVLLTKETELAP
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Pred. No. 0.061;
2; Mismatches 3
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US-09-513-783A-32
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CURRENT FILING DATE: 2000-02-25
NUMBER OF SEQ ID NOS: 180
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 32
LENGTH: 1056
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APPLICANT: Giuliano, Kenneth A.
APPLICANT: Giuliano, Kenneth A.
APPLICANT: Kapur, Ravi
TITLE OF INVENTION: A System for Cell Based Screening
FILE REFERENCE: 97-022-L1
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
                                                                                                                                                                                      327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  771
442 KAYNLLTEAHKALFXNKGRNSDFQALDKLLERLND----ESTNKEKLVDDLLAFLAPITH
                                                                                                                                                                                                                                                                                                                299 PLLDGDEKTGNSESKKKPCLD-TSQVEGIPS-SKP-TLLANGDHGMEGNNTAGSPTD---
                                                                                                                                                                                                                                                                                                                                                       211 -FLSGRGNLSNSRTYRRONSDNTSRTNWVPSVSNPGTTNTNTSNNSNTNSQASQSNDIDS
                                                                                                                                                                                                                                                                                                                                                                                                                                            187 HYQQNTPIGDGPVLL-----PDNHYLSYQSALSKDPNEKRDHMVLLEFVTAAGITLG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          142 HREGGTPRNDGAVALARSQGRYTTDDGYIFNASDIIEDTGD-----AYIVPHG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      127 NRIELKGIDFKEDGNILGHKLEYNYNSHNVYIMADKQKNGIKVNFKIRHNIEDGSVQLAD 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           705 ADEEPVEETPAE-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              53 ITDQGY-----VTSHGDHYHYYNGKVPYDAIISEELLMKDP-NYKLKDE-----DIV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           99 NEVK-GGYVIKVDG-------KYYVYLKDAAHADNVRTKEEINRQKQEHS----Q 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      67 VTTFGYGLQCFARYPDHMKQHDFFKSAMPEGYVQERTIFFKDDGNYKTRAEVKFEGDTLV 126
                                                               SPCSESCVS-----PEVTIETLQPATELSKAAEVESVKEQLPAK
                                                                                                                                                                                                                                                                       LLKQLYKLP---LSQRHVESDGLVFDPAQITSRTARGVAVPHGDHYHFIPYSQMSELEER
                                                                                                                                                                                                                                                                                                                                                                                                 MDELYKKGDEVDGADLSLVDALTEPPPEIEGEIKRDFMAALEAEPYDDIVGETVEKTEFI
                                                                                                                                                                                      IARIIPLRYRSNHWVPDSRPEQPSPQPTPEPSPGPQPAPNLKIDSNSSLVSQLVRKVGEG
                                                                                                                                                                                                                                FLEERVDYPDYQSSQNWPEDASFCFQPQQVLDTDQ---AEPFNEH---
                                                                                                    YVFEEKGISRYVFAKDLPSETVKNLE-----SKLSKQESVSHTLTAKKENVAPRDQEFYD
                                                                                                                                             LADLLFVSSGPTNASAFTERDNPS----EDSYGMLPCDSF---ASTAVVSQEWSVGAPN
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19.7%;
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Pred. No. 0.093;
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| Query Match 3.2%; Score 134; DB 1; Length 2308;  Best Local Similarity 19.2%; Pred. No. 0.46;  Matches 169; Conservative 123; Mismatches 276; Indels 310; Gaps 44;  Qy 51 IKITDQGYVTSHGDHYHYYNGKVPYDAIISEELLMKDPNYKLKDEDIVNEVKGGYVIKVD 110 | TELEX: 66 INFORMATION FO SEQUENCE CHA LENGTH: 2 TYPE: ami TOPOLOGY: MOLECULE TYP | ; REFERENCE/DOCKET NUMBER: 7683-021 ; REFERENCE/DOCKET NUMBER: 7683-021 ; TELECOMMUNICATION INFORMATION: ; TELEPHONE: (212)790-9090 ; TELEFAX: (212)869-8864/8741 | CLASSIFICATION: 435  ATTORNEY/AGENT INFORMATION:  NAME: Misrock, S. Leslie  PECISTATION UNDER. 10 072 | SOFTWARE: PATENTIN COLORS #1.0, Version #1.25  SOFTWARE: PATENTIN Release #1.0, Version #1.25  CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/015,973  PILING NATE: 10.5002 | ~ # 5  | : New York<br>E: New York<br>TRY: U.S.A.  | R OF SE<br>SPONDEN<br>RESSEE:                                 | GENERAL INFORMATION:  GENERAL INFORMATION:  APPLICANT: Schlessinger, Joseph  TITLE OF INVENTION: BYOSEPHATASE, PETA  TITLE OF INVENTION: BYOSEPHATASE, PETA | RESULT 28 US-08+015-973-1 ; Sequence 1, Application US/08015973 . Datent No \$604094 | QY 757 ERNETEGIMDINISHABARKITALIKGSNESSVSKEK 794                        | 705 ADEKEVBETPAB   | 649 TYKARNGYTLEDLERYLKYYEHE - DEKENSUGWGN ASEN VIGKKU-NSEUPKNEK | 630 VSLSEIEEALAKNDVRSAE-IPVAQ-ETVVSETEVVLATEVVLP | 576VIERNAMSHA KANDADAKAWA                                | 525EITKPDVILANVTQPSTESDMFLAQDMELLTGTEAAHANNILLPTEPDE                            | Db 490 524 OV 498 PERLGKDNSOIEVTEDEVRIAGIADKYTTSDGYIEDEHDIISDEGDAY 545 |
|--|--|---|---|--|--|---|---|---|--|---|--|---|--|--|---|--|
| TITLE OF INVENTION: A MOVEL REFLOR-LIFE ENGEROLINGSINE TITLE OF INVENTION: PHOSPHATASE-BETA NUMBER OF SEQUENCES: 9 CORRESPONDENCE ADDRESS: ADDRESSE: PENNIE & EDMONDS STREET: 1155 Avenue of the Americas CITY: New York                   | 4-1<br>, Application US/08448164<br>5925236<br>NFORMATION: NOVEL BECEPTOR TYPE   | Oy 675 RPHSNDGWGNASEHVLGKKDHSEDPNKN 702   | Qy 627 GNLIIPHKDHYHNIKFAWFDDHTYKAPNGYTLEDLFA-TIKYYVEHPDE 674  | OY 583 PDADVKANPTGDSAAAIVNRVKGEKRIPLVRLPYMVEHTVEVKN 626  | OY 542 GDAYVTPHMGHSHWIGKDSLSDKEKVAAQAYTKEKGILPPS 582 | Qy 511TEDEVRIAQLADKYTTSDGYIFDEHDIISDE 541 | OY 460RNSDFQALDKLLERLNDESTNKEKLVDDLLAFLAPITHPERLGKPNSQIEY 510 | Qy 445 NL-LTEAH   | OY 396 RYVFAKDLPSETVKNLESKLSKQESVSHTLTAKKENVAPRDQBFYDKAY 444                         | QY 336 RSNHWVPDSRPEQPSPQPTPEPSPGPQPAPNLKIDSNSSLVSQLVRKVGEGYVFEEKGIS 395 | Qy 287 DGLVFDPAQITSRTARGVAVPHGDHYHFIPYSQMSELEERIARIIPLRY 335 | QY 240 SVSNPGTTNTNTSNNSNTNSQAS-QSNDIDSLLKQLYKLPLSQRHVES 286<br> | Qy 210 AFLSGRGNLSNSRTYR-RQNSDNTSRTNWVP 239 :     | QY 165 TDDGYIFNASDIIEDTGDAYIVPHGDHYHYIPKNELSASBLAAAE 209 | OY 111 GKYYVYLKDAAHADNVRTKEEINRQKQEHSQHREGGTPRNDGAVALARSQGRYT 164   : :   :   : |  |

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Best Local S
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SEQUENCE CHARACTERISTICS:
LENGTH: 2308 amino aci
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
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REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 7683-021
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US 08/015,973
FILING DATE: 10-FEB-1993
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                                                                                                                                                                                                            1265 ASEKYEPVLLKSESSHQVVP-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                51 IKITDQGYVTSHGDHYHYYNGKVPYDAIISEELLMKDPNYKLKDEDIVNEVKGGYVIKVD 110
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-----RNSDFQALDKLLERLNDESTNKEKLVDDLLAFLAPITHPERLGKPNSQIEY----
                                                       SVPIGNGHVAITAVSPHRDGSVTSTKLLFPSKATSELSHSAKSDAGLVGGGEDGDTDDDG 1425
                                                                                                                                RHVFATPVLSIDEPLNTLINKLIHSDEI----LTSTKSSVTGKVFAGIPTVASDTFVSTDH
                                                                                                                                                                    RYVFAKDLPS--ETVKNLESKLSKQESVSHTLTAKKENVAPR------DQEFYDKAY
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                    Query Match
Best Local (
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 Matches 169;
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                                                                                                                                                                             INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS
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APPLICANT:
APPLICANT:
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OPERATING SYSTEM: PC-D
SOFTWARE: PATENTIN DATA:
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Margolis, Richard U.
TITLE OF INVENTION: A NEW CLASS OF RPTPASES: THEIL
TITLE OF INVENTION: STRUCTURAL DOMAINS AND LIGANDS
                                                                                        MOLECULE TYPE:
                                                                                                                                                                                                                                                    TELECOMMUNICATION INFORMATION: TELEPHONE: 212 790-9090
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CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                    NAME: Coruzzi, Laura A. REGISTRATION NUMBER: 30742 REFERENCE/DOCKET NUMBER: 7
                                                                                                                                                                                                                                                                                                                                                             FILING DATE: 2
CLASSIFICATION:
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                                                                                                           TOPOLOGY:
                                                                                                                          STRANDEDNESS:
                                                                                                                                              TYPE:
                                                                                                                                                                                                                  TELEX: 66141 PENNIE
                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US/08/081,929
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      675 RPHSNDGWGNASEHV-----LG----KKDHSEDPNKN 702
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5. 6160090
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Barnea, Gilad
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SYSTEM: PC-DOS/MS-DOS
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                    3.2%; Score 134;
19.2%; Pred. No. 0
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                                   Length 2308;
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Gaps
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51 IKITDQGYVTSHGDHYHYYNGKVPYDAIISEELLMKDPNYKLKDEDIVNEVKGGYVIKVD 110

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US-09-599-652-2
                                                                                                         Sequence 2, Application US/09599652
Patent No. RE37741
GENERAL INFORMATION:
APPLICANT: HOSTETTER, MARGARET
APPLICANT: GALE, CHERYL A.
                   TITLE OF INVENTION:
                                                        APPLICANT:
                                                                        APPLICANT:
 NUMBER OF SEQUENCES:
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KENDRICK, KATHLEEN
IVENTION: CANDIDA ALBICANS GENE,
IVENTION: PROTEIN, ANTIBODIES, A)
SEQUENCES: 12
                                                                                          BENDEL, CATHERINE M
                                                                        TAO, NIAN-JUN
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; MOLECULE TYPE:
US-09-599-652-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches 159;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX: 612-305-1228
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE: 03-MAY-1996
ATTORNEY/AGENT INFORMATION:
NAME: MUETING, DAIM M.
REGISTRATION UNMBER: 33,977
REFERENCE/DOCKET NUMBER: 110.
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
ADDRESSEB: MUETING, RAASCH, GEBHARDT & SCHWAPPACH,
STREET: 119 NORTH FOURTH STREET, SUITE 203
CITY: MINNEAPOLIS
STATE: MINNEAPOLIS
STATE: MINNESOTA
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: PatentIn Release #1.0, Version CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: amino acid
STRANDEDNESS: sir
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM PC
OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US/09/599,652 FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEPHONE: 612-305-1217
TELEFAX: 612-305-1228
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                   443
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AYNLITEAHKALFXNKGRNSDFQALDKLLER-LNDESTNKEKLVDDLLAFLAPITHPERL 501
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                                                                                                                               LNSASQSQISLNALEKQRQTQEQEQTQAAEPEEETSFSDNIKVKQEPKSNLEFVKVTIKK
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                                                                                        VGEGYVFEEKGISRYVFAKDLPSETVKNLESKLSKQESVSHTLTAKKENVAPRDQEFYDK 442
                                                                                                                                                                  IPLRYRS----NHWVPDSRPEQPSPQPTPEPSPGPQPAPNLKI----DSNSSLVSQLVRK 382
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IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
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Pred. No. 0.3;
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   Query Match
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APPLICANT: HOSTET
                                                                                                                                                INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT:
APPLICANT:
APPLICANT:
                                                                                                                                                                                                   TELEPHONE: 612-305-1217
                                                                                                                                                                                                                                                      CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: MUETING, ANN M.
REGISTRATION NUMBER: 33,
                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION DATA: APPLICATION NUMBER: US
                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
ADDRESSEE: MUETING, RAASCH, GEBHARDT & SCHWAPPACH,
STREET: 119 NORTH FOURTH STREET, SUITE 203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION: CANDIDA ALBICANS GENE, TITLE OF INVENTION: PROTEIN, ANTIBODIES, F. NUMBER OF SEQUENCES: 12
                                                     MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PatentIn Release #1.0,
                                                                                         STRANDEDNESS:
                                                                           TOPOLOGY:
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                 GENERAL INFOR APPLICANT:
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                                                                                                                                                                                                                                                                           KVKIPNAIQFKKFKEVNVMSRRVVSPDMDDLNVSQFLPELSEDSGFKDLNFANYSNNTNR
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HOSTETTER, MARGARET K. GALE, CHERYL A. BENDEL, CATHERINE M. TAO, NIAN-JUN
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8; Mismatches
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Best Local Similarity
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INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
SEQUENCE 1664 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: amino acid
STRANDEDNESS: sin
TOPOLOGY: linear
MOLECULE TYPE: prot
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: MUETING, ANN M.
REGISTRACION NUMBER: 33,977
REFERENCE/DOCKET NUMBER: 11
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US 0 FILING DATE: 03-MAY-1996 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION:
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
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VGEGYVFEEKGISRYVFAKDLPSETVKNLESKLSKQESVSHTLTAKKENVAPRDQEFYDK
                                                         LNSASQSQISLNALEKQRQTQEQEQTQAAEPEEETSFSDNIKVKQEPKSNLEFVKVTIKK
                                                                                                                                 SRDKLETTKEHDAPEHNNENFIDAKSTNTNKGQLLVSSDDHLDSFDRS-YNHTEQSILNL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VNENHAPTYINTSPNKSIMKKATPKA---SPKKVA-----FTVTNPE 178
                                                                                            IPLRYRS----NHWVPDSRPEQPSPQPTPEPSPGPQPAPNLKI----DSNSSLVSQLVRK
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Pred. No. 0.3;
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; APPLICANT: Meyer, Thomas F.;
TITLE OF INVENTION: PROCESS;
NEGATIVE HOST CELLS
; NUMBER OF SEQUENCES: 6
; CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07
; FILING DATE: 01-JUL-1987
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                     IQGQGNSRVSLNQHSKWHLTGDSQVHNLSLADSHIHLNNASDAQSANKYHTIKINHLSGN 863
                                                                                                                                                                     DAHFSKNNEVVFEDDWINRTFKAAEIAVNOSASFSSGRNVDDITANITATDNAKVNLGYK
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                                                         ---QSNDIDSLLK-----QLYKLPLSQRHV-----
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                                                                                              -- NGDEVCVRSDYTGYVTCNTGNLSDKALNSFDXATKINGNVNLNQNAALVLGKAALWGK
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Patent No. 6326483
                                                                                                                                                                                                                                           APPLICANT: Kwiatkowski, David J.
APPLICANT: Sampson, Julian R.
APPLICANT: Povey, Sue
APPLICANT: van Slegtenhorst, Marjon
APPLICANT: van Slegtenhorst, Marjon
APPLICANT: Halley, Dicky
TITLE OF INVENTION: Compositions and N
TITLE OF INVENTION: Sclerosis-1 (TSC-1
NUMBER OF SEQUENCES: 28
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version
CURRENT APPLICATION DATA:
APPLICATION UMBER: US/09/457,708
FILING DATE:
                                                                                                                                                                                        STREET: 1455 Peni
CITY: Washington
                                                                                                                                                           COUNTRY:
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INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: not relevant MOLECULE TYPE: protein HYPOTHETICAL: NO
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REGISTRATION NUMBER: 36,912
REFERENCE/DOCKET NUMBER: BR
TELECOMMUNICATION INFORMATION:
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STRANDEDNESS: no
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                                                    WKV----SLQKEQARYNQLQEQRDTMVTKLHSQIRQLQHDREEFYNQSQELQTKLEDC--
                                                                                                                        LLYERFKRQQHALRNRRLLRKVIKAAALEEHNAAMKD-----
                                                                                                                                                           -IYNRVKGEKRI------PLVRLPYMVEHTVEVKNGNLIIPHKDHYHNIKFAWFDDHT
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Pred. No. 0.
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US-09-950-046A-2
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GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEPHONE: (202) 639-6585
TELEFAX: (202) 639-6604
INFORMATION FOR SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                     Local
                                                                                                                                                                                                                                                                                                                                                                                                                STRANDEDNESS: not relevant TOPOLOGY: not relevant MOLECULE TYPE: protein HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Sanzo, Michael A.
REGISTRATION NUMBER: 36,912
REFERENCE/DOCKET NUMBER: BR
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US/09/950,046A
FILING DATE: 12-Sep-2001
CLASSIFICATION: «UNKNOWN»
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
ADDRESSEE: Vinson & Elkins
STREET: 1455 Pennsylvania Avenue,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE DESCRIPTION: SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                  ANTI-SENSE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES:
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155; Conserv
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                                                                                             HYIPKNELSAS-ELAAAEAFLSGRGNLSNSRTYRRQNSDNTSRTNWVPSVSNPG-TTNTN
                                                                                                                                  EHVRIHPELVTGSKDHELD-PRRWKRLETHDVVIECAKISLDPTEASYEDGYSVSH----
                                                                                                                                                                       EHSQ-HREGGTPRNDGAVALARSQGRYTTDDGYIFNASDIIEDT----GDAYIVPHGDHY 192
                                                                                                                                                                                                           KPGHVAEV---YLVHLHASVYALFHRLYGMYPCNFVSFLRSHYSMKENLETFEEVVKPMM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 1164 amino acids
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ilarity 18.8%;
Conservative 122
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ley, Dicky
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                                                                                                                                                                                                                                                                                 Score 132; DB Pred. No. 0.22; Pred. No. 0.22; Mismatches
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                                                                                                                                                                       COMPUTER: Hr ... MSUCOPERATING SYSTEM: MSUCOPERATING SYSTEM: MSUCOPERATION DATA
                                                                                                                              CURRENT APPLICATION DATA:
APPLICATION NUMBER: US,
FILING DATE:
                       ATTORNEY/AGENT INFORMATION: NAME: A. Anders Brookes
                                                                                                                                                                                                                                              COMPUTER READABLE FORM: MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: NUMBER OF SEQUENCES:
                                                                           PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT:
                                                                                                                                                                                                                                                                                                                        STREET: 9410 Ker
CITY: Rockville
STATE: Maryland
                                                                                                                                                                                                                                                                                     COUNTRY: U
                                                            FILING DATE
                                                                                                                CLASSIFICATION:
     REGISTRATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ----TLAGLRNNLTLQIMDNNSIMAEAEKLLALLKGSNPSSVSKEK
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                                                                                                                                                                                                                                                                                                                                                           E: Human Genome Sciences,
9410 Key West Avenue
                                                                                                                                                                                                                                                                                                           USA
                                                                                                                                                                                                                             E: Diskette, 3.50 inch, 1.4Mb storage HP Vectra 486/33
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELECOMMUNICATION INFORMATION: TELEPHONE: (301) 309-8504
TELEPAX: (301) 309-8512
INFORMATION FOR SEQ ID NO: 458:
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MOLECULE TYPE:
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LENGTH: 2032 amino aci
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                                                             AMDETTILAGAHFQIWDQAKTQVLREGTVDATGVITFGGLPQGQYILVETKAPEGYTVSD
                                                                                             YMVEHTV-----EVKNGNLIIPHKDHYHNIKFAWFDDHTY-----KAPNGYTLED
                                                                                                                           RSLVTSSAAGSTDTVSNQVSITGNGSEVVHGDDNGDVVVDIDHSGGHATGTKGKIQLKKT
                                                                                                                                                           KGILPPSP--DADVKANP---TGDSAAAIYNRVKGEKRIPL-----
                                                                                                                                                                                                                         KYTTSDGYIFDEHDIISDEGDAYVTPHMGHSHWIGKDSLSDKEKVA-----AQAYTKE
                                                                                                                                                                                                                                                          EYHKDDPDHVYWHVMINGAQSVLDDVVITDTP--SPNQVLDPESLVIYGTN------
                                                                                                                                                                                                                                                                                                                        GSAS-----YD-----NTASYTNQGSSRD--VTGKVSIQHGGESVKKGG
                                                                                                                                                                                                                                                                                                                                                    TLTAKKENVAPRDQEFYDKAYNLLTEAHKALFXNKGRNSDFQALDKLLERLNDESTNK--
                                                                                                                                                                                                                                                                                                                                                                                                                                                     FKPLPAFDLNAQKSGVYNAVTKEITWTIAVNLSNNRLVDAFLTDPILTNQTYLAGSLKVY 844
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TARGVAVPHGDHYHFIPYSQMSELEERIARIIPL-RYR-----SNHWVPDSRP 346
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LTM--VPNSLVVKDTTTGAQLTLGKD-----FMVEITR---NADGETGFKVSFI---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VSNPGTTNTNTSNNSNTNSQASQSNDIDSLLKQLYKLPLSQRHVESDGLV-FDPAQITSR 299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GDAYIVPHGDHYHYIPKNELSASELAAAEAFLSGRGNLSNSRTYRRQNSDNTSRTNWVPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADNVRTKEEINROKQEHSQHREGGTPRNDGAV--ALARSQGRYTTDDGYIFNASDIIEDT 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEEL---LMKDPN----YKLKDEDIVNEVKGG-----YVIKVDGKYYV-YLKDAAH 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LTSD--NNPNGLDAEATVTATYGKMLDKRNIDYDEANQEFTWEINYNYGEQTIPKDQAVI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LTPDEVSKREGINAEQIVI----KITDQ---GYVTSHGD-----HYHYYNGKVPYD-AII
                                                                                                                                                                                         --VTEDGTITPDKSVILEEGKDYTLE-----VTTDNETGQQKIVVKMAHIEAPYYMEY 1041
                                                                                                                                                                                                                                                                                                                                                                                      EGNTKPDGSVEKVKPTQPLTDITMEEPSEKNQNTWRVDFPNDSRTYVIEFKTSVDEKVIE
                                                                                                                                                                                                                                                                                                                                                                                                                     EGYVFEEKGISRYVFAKDL------PSETVKN------LESKLSKQESVSH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EQPSPQ-PTPEPSPGPQPAPNLKID-----SNSSLVSQLVR---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative 127;
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                                                                                                                                                                                                                                                                                        ----EKLVDDLLAFLAPITHPERLGKPNSQIEYTEDEVRIAQLAD
                               ---TI-----KYYVEHPDERPHSNDGWGNASEHVLGKKDHS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 132;
Pred. No. 0.
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                                                                                                                                                                                                                                                                                                              Matches
                                                                                                                                                                                                                                                                                                                              Query Match
Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: (301) 309-85 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: A. Anders Brookes
REGISTATION NUMBER: 36,373
REFERENCE/DOCKET NUMBER: PB
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 309-8504
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION: PRIOR APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM: MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE: protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION:
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                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: amino a
                                                                                                                                                                                                                                                                                                           Local Similarity
mes 185; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STREET:
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VSNPGTTNTNTSNNSNTNSQASQSNDIDSLLKQLYKLPLSQRHVESDGLV-FDPAQITSR 299
                                                                                                                                                                      TDTMGDNLTFEPDSLHLYSVTFDDKGNEVVGAELVEGKDYKVVINGDGSFAIDFLHDVTG 600
                                                                                                                                                                                                        SEEL---LMKDPN----YKLKDEDIVNEVKGG-----YVIKVDGKYYV-YLKDAAH
                                                                                                                                                                                                                                        LTSD---NNPNGLDAEATVTATYGKMLDKRNIDYDEANQEFTWEINYNYGEQTIPKDQAVI
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                                   GAV-----DY-----QNSTIGWTLAV-----
                                                                  GDAYIVPHGDHYHYIPKNELSASELAAAEAFLSGRGNLSNSRTYRRONSDNTSRTNWVPS
                                                                                                      AVKIDYKTKVD---
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                                                                                                                                    ADNVRTKEEINRQKQEHSQHREGGTPRNDGAV--ALARSQGRYTTDDGYIFNASDIIEDT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      USA
                                                                                                                                                                                                                                                                                                           3.2%; Score 132; DB 4; Length 2032; ilarity 19.5%; Pred. No. 0.54; Conservative 127; Mismatches 316; Indels 32
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                                                                                                      -----GIVEGDVAVNNRVDVGTGQHSEDDG-TASQQNIIKNT
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                                  ----NQNNYLMENAVITDTYEPVPG
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RESULT 39
US-09-071-035-466
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Patent No. 6448043
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                                                                           MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb
COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.2
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Gil H. Choi
TITLE OF INVENTION: Enterococcus faecalis Polynucleotides and Polypeptides
                                                                                                                                                                                     COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
PRIOR APPLICATION DATA
                                                                                                                                                                                                                                            ADDRESSEE: Human Genome Sciences,
STREET: 9410 Key West Avenue
CITY: Rockville
STATE: Maryland
                 APPLICATION NUMBER: FILING DATE: CLASSIFICATION:
                                                                                                                                                                                                             ZIP: 20850
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FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: A. Anders Brookes
REGISTRATION NUMBER: 36,373
REFERENCE/DOCKET NUMBER: PB36
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 309-8504
TELEPAX: (301) 309-8512
INFORMATION FOR SEQ ID NO: 466:
SEQUENCE CHARACTERISTICS:
LENGTH: 2032 anino acids
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                                                                                1042 RSLVTSSAAGSTÓTVSNQVSITGNGSEVVHGDDNGDVVVDIDHSGGHATGTKGKIQLKKT 110
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   33 LTPDEVSKREGINAEQIVI----KITDQ---GYVTSHGD-----HYHYYNGKVPYD-AII 79
                                                                                                                                                                                                                                                                                                                                                                              TLTAKKENVAPRDQEFYDKAYNLLTEAHKALFXNKGRNSDFQALDKLLERLNDESTNK--
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AMDETTILAGAHFQIMDQAKTQVLREGTVDATGVITFGGLPQGQYILVETKAPEGYTVSD 116:
                                      YMVEHTV------EVKNGNLIIPHKDHYHNIKFAWFDDHTY-----KAPNGYTLED
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                                                                                                                                                                  --VTEDGTITPDKSVILEEGKDYTLE-----VTTDNETGQQKIVVKMAHIEAPYYMEY 104:
                                                                                                                                                                                                         KYTTSDGYIFDEHDIISDEGDAYVTPHMGHSHWIGKDSLSDKEKVA-----
                                                                                                                                                                                                                                                  EYHKDDPDHVYWHVMINGAQSVLDDVVITDTP--SPNQVLDPESLVIYGTN
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                                                                                                                           KGILPPSP--DADVKANP---TGDSAAAIYNRVKGEKRIPL--
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                                                                                                                                                                                                Query Match-
Best Local S
Matches 141
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                                                                                                                                                                                                                                                                                                                                                                               INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
LENGTH: 1093 amino acids
                                                                                                                                                                                                                                                                                                   TOPOLOGY: unknown MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/0:
FILING DATE: April 2, 199
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Ploppy disk
COMPUTER: IBM PC compatible
COMPATER: PATENT PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
CURRENT APPLICATION DATA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Wu, FOON KIN
TITLE OF INVENTION: PROTEIN CELLULAR FACTOR USEFUL FOR
TITLE OF INVENTION: REGULATING GENE EXPRESSION
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REGISTRATION NUMBER: 29,775
REFERENCE/DOCKET NUMBER: UT:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 713-787-1540
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: FILING DATE: 19930
                                                                                                                                                                                                                                                                                                                                           STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX: 713-749-2679
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Kammerer, Patricia A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY: US
ZIP: 77210
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                                                                             131 EINROKQEHSOHREGGTPRNDGAVALARSQGRYTTDDGYIFNASDIJEDTG--
                                                                                                                                                                                                     141;
                                                                                                                                                             75 YDAIISEELLMKDPNYKLKDEDIVNEVKGGYVIKVDGKYYVYLKDAAHAD----NVRTKE 130
                                                                                                                                                                                                                     Similarity
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                                       IALEPKEQKHEDRQSNTP---SPPVSTFSSGTSTTSDIEVLDHESVISESSASSRQETTD
                                                                                                                   HEETVNKESDMKVPTVSLKVSESVIDVK------TTMESISNTSTQSLTAETKD 224
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Gaynor, Richard B.
                                                                                                                                                                                                     Conservative 129;
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                                                                                                                                                                                                                                                                                                                                             unknown
                                                                                                                                                                                                                     3.1%; Score 131; DB 16.7%; Pred. No. 0.24;
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-DAYIVPHGDHYHYIPKNELSASELAAAEAFLSGRGNLSNSRTYRR 226
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                                                                                                                                                                                                     Mismatches
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                                                                                                                                                                                                                                      DB 5; Length 1093;
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US-09-417-197-49
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                                                                                                                                                                                                                                                       Sequence 49, Application US/09417197

Patent No. 6518021

GENERAL INFORMATION:
APPLICANT: Ole THASTRUP, et al.

TITLE OF INVENTION: A Method For Extracting Quantitative Information Relating Of INVENTION: On A Cellular Response
                                                                                                                 SOFTWARE: PatentIn
SEQ ID NO 49
LENGTH: 968
                  OTHER INFORMATION: EGFP-p85alpha fusion -09-417-197-49
                                                                                                                                                                       FILE REFERENCE: 3759-0110P
CURRENT APPLICATION NUMBER: US/09/417,197
CURRENT FILING DATE: 1999-10-07
NUMBER OF SEQ ID NOS: 143
                                                      TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
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                                                    Sequence 5, Application US/09324867A Patent No. 6251632 GENERAL INFORMATION:
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APPLICANT: Lillicrap, David
APPLICANT: Cameron, Cherie
APPLICANT: No. 6251632ley, Colleen
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17.0%; Pred. No. 0.22;
ative 105; Mismatches 253;
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; SEQ ID NO 5
; LENGTH: 2115
; TYPE: PRT
; ORGANISM: Sus s
US-09-324-867-5
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APPLICANT: Hough, Christine
TITLE OF INVENTION: Canine Factor VIII Gene, Pr
FILE REFERENCE: 1669.0010002/JAG/BJD
CURRENT APPLICATION NUMBER: US/09/324,867A
CURRENT FILING DATE: 1999-06-03
EARLIER APPLICATION NUMBER: 09/035,141
EARLIER APPLICATION NUMBER: 09/035,141
EARLIER APPLICATION NUMBER: 60/039,953
EARLIER FILING DATE: 1998-03-059
EARLIER FILING DATE: 1997-03-06
NUMBER OF SEQ ID NOS: 63
SOFTWARE: Patentin Ver. 2.0
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Matches 141; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                              ASLTKDDVLFKVNIS----LVKTNKARVYLKTNRKIHIDDAALLTENRASATFMDKNTTA 1010
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LVSQLVRKVGEGYVFEEKGISRYVFAKDLPSETVKNLESKLSKQESVSHTLTAKKENVAP
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AVPRRRVKQSLKQIRLPLEEIKPERGVVLNATSTRWSESSPILQGAKRNNLSLPFL 1254
                                      QVETEKVEAQLKEAEVLLAKV-TDSSLKANATET-----LAGL-RNNLTLQIM 766
                                                                                                                                                                                                                                             GQSSGQGRIRVAVEEEELSKGKEMMLPNSELTFLTNSADVQGNDT------HSQGKK
                                                                                                                                                                                                                                                                                      -----KVAAQAYTKEKG---ILPPSP-----DADVKANPTGDSAAAIYNRVKGEK 607
                                                                                                                                                                                                                                                                                                                            SG-------LNHVSNWIKGPLGKNPLSSERGPSPELLTSSGSGKSVK 1050
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                                                                                                                     YYVEHPDERPHSNDGWGNASEHVLGKKDHSEDPNKNFKA--DEEPVEETPAEPEVP----
                                                                                                                                                              SREEMERREKLVQEKVDLPQVYTATGTKNFLRNI----FHQSTEPSVEGFDGGS-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -GFLLSGKNVIEPRSFAQNSRPPSASQKQFQTITSP-EDDVELDPQSGERTQALEELSVP
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                                                                               -HAPVPQDSRSLNDSAERAETHI---
                                                                                                                                                                                                     -RIPLVRLPYMVEHTVEVKNGNLIIPHKDHYHNIKFAWFDDHTYKAPNGYTLEDLFATIK 666
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3.1%; Score 130; DB . 19.7%; Pred. No. 0.82;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               84; Mismatches 233;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ----SPTIPSDT-----LSAETERTHSLGPPHPQVNF
                                                                               -----AHFSAIREEAPL-EAPGNRTGPGPRS 1198
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RESULT 43 US-09-107-532A-5095

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GENERAL INFORMATION:
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Best Local (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY: misc feature LOCATION: (B) LOCATION 1...525 SEQUENCE DESCRIPTION: SEQ ID NO: 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE: protein HYPOTHETICAL: YES ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RMATION FOR SEQ ID NO: 5095: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: 60/051571
FILING DATE: July 2, 1997
ATTORNEY/AGENT INFORMATION:
NAME: Ariniello, Pamela Deneke
REGISTRATION NUMBER: 40,489
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/107,532A
FILING DATE: 30-Jun-1998
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REFERENCE/DOCKET NUMBER: TELECOMMUNICATION INFORMATION: TELEPHONE: (781)893-5007
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ADDRESSEE: GENOME THERAPEUTICS CORPORATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Lynn A Doucette-Stamm TITLE OF INVENTION: NUCLEIC ACID
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                                                                                                            183
                                                                                                                                                                                   126 VRT---KEEINROKQEHSQHREGGTPRNDGAVALARSQGRYTTDDGYIFNASDIIEDTGD 182
                                   243 NPGTTNTNTSNNSNTNSQASQSNDIDSLLKQLYKLPLSQRHVESDGLVFDPAQITSRTAR
                                                                                                                                               209 ATAEDKKADLNROKAE-AEAEQARIREQQRLAEQARQQAAQ-----
                                                                                                                                                                                                                          160 KAVEDKKAENDAKLKE---
                                                                                                                                                                                                                                                                                                     108
 296 QSSATEESTTPESSTEESTA-
                                                                                                                                                                                                                                                              66 YHYYNGKVPYDAIISEELLMKDPNYKLKDEDIVNEVKGGYVIKVDGKYYVYLKDAAHADN 125
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                                                                                                          AYIVPHGDHYHYIPKNELSASELAAAEAFLSGRGNLSNSRTYRRQNSDNTSRTNWVPSVS 242
                                                                                                                                                                                                                                                                                                   QAREAQVSNTSSNYIDAV-----LNADSLADAIGRVQAMTTMVKANNDLMEQQKQDK 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: 60/085,598 FILING DATE: 14 May 1998
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ZIP: 02354
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: amino acid
TOPOLOGY: linear
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21.1%;
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AND AMINO ACID SEQUENCES RELATING
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-----PESSATEES----TTAPESSATEE
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US-08-826-267-2
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                                                                                                                                                                                                                                         Matches
                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/014,21
PILING DATE: 27 MARCH (1996)
ATTORNEY/AGENT INFORMATION:
NAME: Amy E. Mandragouras
REGISTRATION NUMBER: DFN-
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: (6
INFORMATION FOR
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                   Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: FILING DATE: 1997
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                  293
                                                                                                             188
                                                                                                                                           201 SASELAAAEAFLSGRGNL-----
                                                                                                                                                                        140 TPEFDGCLEYNHEEWIEIRVAFED-YISNATHMLSRLEELQD-
                                                                                                                                                                                                      147 TPRNDGAVALARSQG-.--RYTTDDGYIFNASDI---IEDTGDAYIVPHGDHYHYIPKNEL
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                                                                                                                                                                                                                                       al Similarity
136; Conserv
                                                                                                                                                                                                                                                                                                                                                1: 2860 amino acids amino acid
----PAQITSRTARGVAVPHG-----DHYHFIPYSQMSELEERIARIIPLRYR----SNHW : | | | : : | | | : : | | | :
                                              NLLPKVS-----TMLDRLHSTRQHLHQMWHVRKLKLDQCFQLRLFEQDAEK---MFDWI
                                                                            NWVPSVSNPGTTNTNTSNNSNTNSQASQSNDIDSL-LKQLYKLPLSQRHVESDGLVFD--
                                                                                                          -PQDLEGARNMIEEHSQLKKKVIKAPIEDLDLEGQKLLQRIQSSESFPKKNSGSGNADLQ
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(617)227-5941
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Pred. No. 1.6;
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GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence
                                                                                        PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/049,460
FILING DATE: 19 APR 1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/872,643
FILING DATE: 17 APR 1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                     SOFTWARE: PatentIn Release #1.0, Version CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/188,228
                                                                                                                                                                                                                                                                                                                                   ZIP: 60606
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Suzuki, Shintaro
TITLE OF INVENTION: CADHERIN MATERIALS AND
             ELECOMMUNICATION INFORMATION: TELEPHONE: (312) 474-6300
                                                                                                                                                                                                                                                                                    MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                           NAME: No. 5597725and, Greta E. REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 31340
                                                                                                                                                                                                       CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                     COUNTRY: U
                                                                                                                                                                                                                           FILING DATE:
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                                                           RESULT 46
US-08-332-643-42
; Sequence 42, Application U;
; Patent No. 5639634
; GENERAL INFORMATION:
; APPLICANT: Suzuki, Shi
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Best Local Similarity
Matches 132; Conserv
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SEQUENCE CHARACTERISTICS:
SECUENCE: 916 amino acid
                                            APPLICANT: Suzuki, Shintaro TITLE OF INVENTION: CADHERII NUMBER OF SEQUENCES: 56
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall,
ADDRESSEE: Bicknell
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              Marshall,
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                                              CADHERIN MATERIALS
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                O'Toole,
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Pred. No. 0.28;
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                Gerstein, Murray
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                                                                METHODS
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US-08-332-643-42
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: (312) 984-9740
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 4
SEQUENCE CHARACTERISTICS:
LENGTH: 916 amino acids
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APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION DATA: APPLICATION NUMBER: US,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: NO. 5639634and, Greta
REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                LVRLPYMVEHTVEVKNGNLIIPHKDHYHNIKFAWFDDHTYKAPNGYTLEDLFATIKYYVE
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                                                                                                                                                                                                                                                                                                                                                                                       ----PAPNLKIDSNSSLVSQLVRKVGEGYVFEEKGISRYVFAKDLPSE-TVKNLESKLS 416
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19.9%; Pre
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Pred. No. 0.28;
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                                                                                                                                                                                                        Query Match
                                                                                                                                                                           Matches 132;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE: 01-NOV-1994
CCLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/872,643
FILING DATE: 17 APR 1992
APPLICATION NUMBER: US/08/049,460
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL
                                                                                                                                                                                                                                                                                                                                                  INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION:
NAME: NO. 5646250and, Greta
REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 31
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: Patentin Rel
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US
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                                                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS:
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                 TYPE:
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                                                                                                                                                                                         Local Similarity
                                                                                                                                                                                                                                                                                                                                                                      TELEX:
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322 ELEERIARIIPLRYRSNHWVPDSRPEQ-----PSPQPTPEPSPGPQ----
                                                                 264 SNDIDSLLKQLYKLPLSQRHVESDGLVFDPAQITSRTARGVAVPHGDHYHFIPY--SQMS
                                                                                                                                    218 LSNSRTYRRONSDNTSRTNWVPSVSNPGTT------NTNTSNNSNTNSQASQ
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Pred. No. 0.
                                -VGADGTVF-----ATRELQVPSEQVAFTVTAWDSQTA 110
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US-08-296-791-6
US-08-296-791-6
; Sequence 6, Application US/08296791
; Patent No. 6245337
; GENERAL INFORMATION:
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                                                                                                                                                                                           MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version
CURRENT APPLICATION DATA:
REFERENCE/DOCKET NUMBER: 31,801
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 781-1989
TELEFAX: (415) 398-3249
                                                                                ATTORNEY/AGENT INFORMATION:
NAME: Trecartin, Richard F.
REGISTRATION NUMBER: 31,801
                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES: 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: St. Geme III, Joseph W. APPLICANT: Falkow, Stanley TITLE OF INVENTION: Haemophilus AdTITLE OF INVENTION: Protein
                                                                                                                                      APPLICATION NUMBER: FILING DATE: 25-AUG CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                           STATE:
                                                                                                                                                                                                                                                                                                                                                          STREET: 4 Embarcade: CITY: San Francisco
                                                                                                                                                                                                                                                                                                          ZIP:
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SEQUENCE CHARACTERISTICS:
LENGTH: 1848 amino acids
TYPE: amino acid
TOPOLOGY: unknown
-08-296-70
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                                                                                                                                          PDERPHSNDGWGNASEHVLGKKDH-----SEDPNKNFKADEE---PVEETPAEPEVPQV 722
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                                                                                                                    PEEVPTDT----NAEEAQALQQTQPTTVAAAETTSPNSKPAEETQQPSEKTNAEPVTPVV 127
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18.6%; Pred. No. 0.86;
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APPLICANT: Washington University,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches 161;
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REGISTRATION NUMBER: 31,801
REFERENCE/DOCKET NUMBER: FF
TELECOMMUNICATION INFORMATION:
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NAME: Trecartin, Richard F.
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APPLICATION NUMBER: 1
FILING DATE: 25-AUG-
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NUMBER OF SEQUENCES:
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CITY: San Francisco
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TELEFAX: (415) 398-3249
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY: United States ZIP: 94111-4187
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TGEPNHNELTLFDASNATRNNLEVTLANGSVDRGAWKYKLRNVNGRYDLYN--
                                                                                                                                                                                                                                       TPRNDGAVALARSQGRYTTDDGYI-----FNASDI------
                                                                                                                                                                                                                                                                       ENNEVVVEDDWINRNFKATTMNVTGNASLY--SGRNVANITSNITASNNAOVHIGYKTGD
                                                                                                                                                                                                                                                                                                                                                                                                              SNENWLYMGRTSDAAKRNVMNHINNERMNGFNGYFGEEETKATQNGKLNVTFNGKSDQNR
                              HVE---SDGLVFDPAQITSR----TARGVAVPHG----
                                                                                                 DNTSRTNWVPSVSNPGT-----TNTNTSNNSNTNSQASQSNDIDSLLKQLYKLPLSQR 282
                                                                                                                                                                                                                                                                                                                                            FLLTGGTNLNGDLNVEKGTLFLS - - GRPTPHARD - - -
                                                                                                                                                                                                                                                                                                                                                                            -LTPDEVSKREGINAEQIVIKITDQGYVTSHGDHYHYYNGKVPYDAIISEELLMKDPNYK
                                                                   -NTLTVN---SLSGNGSFYYWVDFTN-NKSNKVVVNKSATGN
                                                                                                                                                                                                                                                                                                        ----LKDEDIVNEVKGGYVIKVDGKYYVYLKDAAHADNVRTKEEINRQKQEHSQHREGG
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4 Embarcadero Center, Suite 3400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative 109;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       unknown
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18.6%;
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Pred. No. 0.86;
                                                                                                                                                                                                       -GYVTCHNSNLSEKALNSFNPTNLRGNVNLTENASFTLGK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches 271;
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                               DHYHFIPYSOMSE
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SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 176
LENGTH: 783
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
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US-09-513-783A-176
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
APPLICANT: Giuliano, K
APPLICANT: Kapur, Ravi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 176, Application Patent No. 6416959
                                                                                                                                                                                                                                                                        Matches
                                                                                                                                                                                                                                                                                       Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILE REFERENCE: 97-022-L1
CURRENT APPLICATION NUMBER: US/09/513,783A
CURRENT FILING DATE: 2000-02-25
NUMBER OF SEQ ID NOS: 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                       Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1176
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218 LSNSRTYRRQNSDNTSRTNWVPSVSNPGTTNTNTSNNSNTNSQASQSNDIDSLLKQLYKL
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                                                                                                                          138 LGHKLEYNYNSHNVYIMADKQKNGIKVNFKIRHNIEDGSVQLADHYQQNTPIGDGPVLL-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      323 LEERIARIIPLRYRSNHWVP-DSRPEQPSPQPTPE----PSPGPQPAPNLKIDSNSSLV 376
                                                                                                                                                                                                 78
                                                                                                                                                                                                                                   62 HGDHYHYYNGKVPYDAIISEELLMKDP-NYKLKDE-----DIVNEVK-GGYVIKVDG--
                                                       -----PDNHYLSTQSALSKDPNE-
                                                                                       RSQGRYTTDDGYIFNASDIIEDTGDAYIVPHGDHYHYIPKNELSASELAAAEAFLSGRGN
                                                                                                                                                              ------KYYVYLKDAAHADNVRTKEEINRQKQEHS----QHREGGTPRNDGAVALA 157
                                                                                                                                                                                                 HMKQHDFFKSAMPEGYVQERTIFFKDDGNYKTRAEVKFEGDTLVNRIELKGIDFKEDGNI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A System for Cell Based
                                                                                                                                                                                                                                                                                     3.1%; Score 128; DB 4; 17.3%; Pred. No. 0.24;
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                                                       -KRDHMVLLEFVTAAGITLGMDE
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|       | SVDTLLSPTALIDSILRESEPAPASVTALTDARGHTDT 611                   | 574 | Db  |
|-------|--|-----|-----|
|       | TEKVEAQLKEAEVLLAKVTDSSLKANATET 753                           | 724 | γQ  |
| S 573 | ASPMASPG-GSIDERPLSSSPLVRVKEEPPSPPQSPRVEEASPGRPS              | 528 | Db  |
| - 723 | PDERPHSNDGWGNASEHVLGKKDHSEDPNKNFKADEEPVEETPAEPEVPQVE         | 672 | Ş   |
| - 527 | ISDITELAP  | 519 | Db  |
| н 671 | VRLPYMVEHTVEVKNGNLIIPHKDHYHNIKFAWFDDHTYKAPNGYTLEDLFATIKYYVEH | 612 | δ   |
| - 518 | HVHGSGPYSAPSPAYSSSSLYAPDAVASSGPI                             | 487 | Db  |
| L 611 | HSHWIGKDSLSDKEKVAAQAYTKEKGILPPSPDADVKANPTGDSAAAIYNRVKGEKRIPL | 552 | .Qγ |
| E 486 | SNRILGVKRKIPL  | 453 | ДĎ  |
| G 551 | PERLGKPNSQIEYTEDEVRIAQLADKYTTSDGYIFDEHDIISDEGDAYVTPHMG       | 498 | Ş   |
| Q 452 | TDVQLMKGKQECMDSKLLAMKHENEALWREVASLRQKHAQQQKVVNKLIQFLISLVQ    | 396 | Db  |
| Н 497 | TEAHKALFXNKGRNSDFQALDKLLERLNDESTNKEKLVDDLLAFLAPITH           | 448 | 8   |
| L 395 | PERDDTEFQHPCFLRGQEQLLENIKRKVTSVSTLKSEDIKIRQDSVTKLL           | 346 | DЬ  |
| L 447 |  | 390 | δ   |
| K 345 | NNMASFVRQLNMYGFRKVVHIEQGGLVK                                 | 318 | Db  |
| F 389 | NHWVPDSRPEQPSPQPTPEPSPGPQPAPNLKIDSNSSLVSQLVRKVGEGYVF         | 338 | δδ  |
| Н 317 | LVSDPDTDALICWSPSGNSFHVFDQGQFAKEVLPKYFKH                      | 279 | рь  |
| S 337 | PLSQRHVESDGLVFDPAQITSRTARGVAVPHGDHYHFIPYSQMSELEERIARIIPLRYRS | 278 | Ş   |
| - 278 | LYKSGLRSRAQASNSAVEMDLPVGPGAAGPSNVPAFLTKLWT-                  | 237 | 뮍   |

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: //gn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep:*
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Sequence 56, Appl Sequence 194, Appl Sequence 8, Appli Sequence 66, Appl Sequence 383, App Sequence 380, App Sequence 380, App Sequence 376, App Sequence 376, App Sequence 377, App Sequence 377, App Sequence 38, Appli Sequence 38, Appli Sequence 24, Appli Sequence 24, Appli
                                                                                                                                                                             Description
    US-09-765-272-182
US-09-884-465A-394
US-09-884-465A-371
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Sequence 182, App Sequence 379, App Sequence 379, App Sequence 10, Appl Sequence 15, Appl Sequence 15, Appl Sequence 15, Appl Sequence 371, App Sequence 371, App Sequence 372, App Sequence 372, App Sequence 372, App Sequence 372, App Sequence 373, App Sequence 374, App Sequence 374, App Sequence 375, App Sequence 376, App Sequence 377, App Sequence 378, App Sequence 379, App Sequence 379, App Sequence 370, App Sequence 371, App Sequence 371, App Sequence 372, App Sequence 373, App Sequence 374, App Sequence 375, App Sequence 377, App Sequence 377, App Sequence 377, App Sequence 378, App Sequence 5187, App Sequence 5187, App Sequence 5187, App Sequence 5187, App Sequence 5187, App Sequence 5187, App Sequence 5187, App Sequence 5187, App Sequence 5187, App Sequence 5187, App Sequence 5187, App Sequence 5187, App Sequence 5187, App Sequence 5187, App Sequence 5187, App Sequence 5187, App Sequence 5187, App Sequence 5187, App Sequence 5187, App Sequence 5187, App Sequence 5187, App Sequence 5187, App Sequence 5187, App Sequence 5187, App Sequence 5187, App Sequence 5187, App Sequence 5187, App Sequence 5187, App Sequence 5187, App Sequence 5187, App Sequence 5187, App Sequence 5187, App Sequence 5187, App Sequence 5187, App Sequence 5187, App Sequence 5187, App Sequence 5187, App Sequence 5187, App Sequence 5187, App Sequence 5187, App Sequence 5187, App Sequence 5187, App Sequence 5187, App Sequence 5187, App Sequence 5187, App Sequence 5187, App Sequence 5187, App Sequence 5187, App Sequence 5187, App Sequence 5187, App Sequence 5187, App Sequence 5187, App Sequence 5187, App Sequence 5187, App Sequence 5187, App Sequence 5187, App Sequence 5187, App Sequence 5187, App Sequence 5187, App Sequence 5187, App Sequence 5187, App Sequence 5187, App Sequence 5187, App Sequence 5187, App Sequence 5187, App Sequence 5187, App Sequence 5187, App Sequence 5187, App Sequence 5187, App Sequence 5187, App Sequence 5187, App Sequence 5187, App Sequence 5187, App Sequence 5187, App Sequence 5187, App Sequence 5187, App Sequence
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RESULT 1
US-09-765-272-56
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Patent No. US20020061545A1
GENERAL INFORMATION:
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Best Local (
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                                                                                                                                                                                            TOPOLOGY: linear MOLECULE TYPE: protein SEQUENCE DESCRIPTION: SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.2
SOFTWARE: ASCII Text
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REGISTRATION NUMBER: 36,373
REFERENCE/DOCKET NUMBER: PB340P2
TELECOMMUNICATION INFORMATION:
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FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
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CORRESPONDENCE ADDRESS:
ADDRESSEE: Human Genome Sciences,
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                                                                                                                       796; Conservative
           61
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                                                                                                                                       Similarity
                                                                SHGDHYHYYNGKVPYDAIISEELLMKDPNYKLKDEDIVNEVKGGYVIKVDGKYYVYLKDA
           SHGDHYHYYNGKVPYDAIISEELLMKDPNYKLKDEDIVNEVKGGYVIKVDGKYYVYLKDA
                                                                                                                                                                                                                                    TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US/09/765,272
FILING DATE: 22-Jan-2001
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STATE: Maryland
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STREET: 9410 Key West Avenue CITY: Rockville
                                                                                                                                                                                                                                                                LENGTH: 796 amino acids
                                                                                                                                                                                                                                                                                                           TELEPHONE: (301) 309-8504
TELEFAX: (301) 309-8512
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10 US-09-815-242-12955
12 US-09-815-242-12955
12 US-10-172-502-14
15 US-10-037-182-16
15 US-10-037-182-11
15 US-10-037-182-14
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US-09-815-242-12996
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Pred. No. 1.2e-291
; Mismatches 0;
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Sequence 12996, A
GENERAL INFORMATI
Sequence 4, Appli
Sequence 2, Appli
Sequence 12955, A
Sequence 11, Appl
Sequence 16, Appl
Sequence 11, Appl
Sequence 11, Appl
Sequence 11, Appl
Sequence 11, Appl
Sequence 12, Appl
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APPLICANT: Shire Biochem, Inc.
APPLICANT: Hamel, Josee
APPLICANT: Brodeur, Bernard
APPLICANT: Martin, Denis
APPLICANT: Charland, Nathalie
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US-09-884-465A-7
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                                                   PRIOR APPLICATION NUMBER: 60/212,683
PRIOR FILING DATE: 2000-06-20
NUMBER OF SEQ ID NOS: 384
SOFTWARE: PatentIn version 3.1
SEQ ID NO 7
                                                                                                                                                                                                                                                                             Sequence 7, Application US/09884465A Publication No. US20030077293A1
                                                                                                                        CURRENT APPLICATION NUMBER: US/09/884,465A
CURRENT FILING DATE: 2001-06-20
                                                                                                                                                 APPLICANT: Charland, Nathalie
APPLICANT: Ouellet, Catherine
TITLE OF INVENTION: Streptococcus Antigens
FILE REFERENCE: 055190-0044
       LENGTH: 840
TYPE: PRT
ORGANISM: Streptococcus
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RESULT 3
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(S-09-789-787-194); Sequence 194, Application US/09769787; Publication No. US20030091577A1
(GENERAL INFORMATION:
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Best Local S
Matches 616
APPLICANT: Microbial Technics Limited
APPLICANT: Gilbert, Christophe FG
APPLICANT: Hansbro, Philip M
TITLE OF INVENTION: Proteins
FILE REFERENCE: PWC/P21129WO
CURRENT APPLICATION NUMBER: US/09/769,787
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nilarity 75.2%;
Conservative 65
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Pred. No. 2e-223;
5; Mismatches 104;
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PRIOR APPLICATION NUMBER: GB 98
PRIOR FILING DATE: 1998-03-27
PRIOR APPLICATION NUMBER: US 60
PRIOR FILING DATE: 1999-03-19
NUMBER OF SEQ ID NOS: 388
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 194
LENGTH: 826
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Best Local Similarity
Matches 549; Conserv
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                                       KANATETLAGLRNNLTLQIMDNNSIMAEAEKLLALLKGS
                                                                                                                      YTLEDLLATVKYYVEHPNERPHSDNGFGNASDHVQRNKNGQADTNQTEKPSEEKPQTEKP
                                                                                                                                              YTLEDLFATIKYYVEHPDERPHSNDGWGNASEHVLGKKDHSEDPNKNFKADEE-----P
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                                                                   EEETPREEKPQSEKPESPKPTEEPEESPEESEEPQVETEKVEEKLREAEDLLGKIQDPII
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BER: GB 9816337.1
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APPLICANT: Ouellet, Catherine
TITLE OF INVENTION: Streptococcus Antigens
FILE REFERENCE: 055190-0044
CURRENT APPLICATION NUMBER: US/09/884,465A
CURRENT FILING DATE: 2001-06-20
PRIOR APPLICATION NUMBER: 60/212,683
PRIOR FILING DATE: 2000-06-20
PRIOR FILING DATE: 2000-06-20
PRIOR FILING DATE: 2000-06-20
NUMBER OF SEQ ID NOS: 384
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Best Local Similarity
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APPLICANT: Hamel, Josee
APPLICANT: Brodeur, Bernard
APPLICANT: Martin, Denis
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TYPE: PRT
ORGANISM: Streptococcus
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                      DSAAAIYNRVKGEKRIPLVRLPYMVEHTVEVKNGNLIIPHKDHYHNIKFAWFDDHTYKAP
                                                                        PRDITSDEGDAYVTPHMTHSHWIKKDSLSEAERAAAQAYAKEKGLTPPSTDHQDSGNTEA
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KGAEAIYNRVKAAKKVPLDRMPYNLQYTVEVKNGSLIIPHYDHYHNIKFEWFDEGLYEAP
                                                                                                                EHDIISDEGDAYVTPHMGHSHWIGKDSLSDKEKVAAQAYTKEKGILPPSPDADVKANPTG
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                                                                                                                                                                                                       Matches
                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                              TELEPHONE: (301) 309-8504
TELEFAX: (301) 309-8512
INFORMATION FOR SEQ ID NO: 66:
                                                                                                                                                                                                       Local Similarity
nes 519; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/961,083
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch
COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version
SOFTWARE: ASCII Text
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES: 452
CORRESPONDENCE ADDRESS:
ADDRESSEE: Human Genome Sciences,
                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION DATA:
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TITLE OF INVENTION: Streptococcus pneumoniae
122
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                     AAHADNVRTKEEINRQKQEHSQHREGGTPRNDGAVALARSQGRYTTDDGYIFNASDIIED 179
                                                              TSHGDHYHYYNGKVPYDAIISEELLMKDPNYKLKDEDIVNEVKGGYVIKVDGKYYYYLKD 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HPESDEKENHAGLNPSADNLYKPSTDTEETEEEAEDTTDEAEIPQVENSVINAKIADAEA
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AAHADNIRTKEEIKRQKQERSHNHNS---RADNAVAAARAQGRYTTDDGYIFNASDIIED
                                                                                                                                    SYELGRHQAGQVKKESNRVSYIDGDQAGQKAENLTPDEVSKREGINAEQXVIKITDQGYV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STREET: 9410 Key West Avenue
CITY: Rockville
STATE: Maryland
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Brookes, A. Anders
REGISTRATION NUMBER: 36,373
REFERENCE/DOCKET NUMBER: PB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US/09/765,272 FILING DATE: 22-Jan-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                               TYPE: amino acid
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                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 763 amino acids
                                                                                                                                                                                                       Conservative
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                                                                                                                                                                                                       Score 2649.5; DB 9
Pred. No. 1.8e-182;
7; Mismatches 132;
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APPLICANT: Brodeur, Bernard
APPLICANT: Martin, Denis
APPLICANT: Martin, Denis
APPLICANT: Martin, Denis
APPLICANT: Obellet, Catherine
TITLE OF INVENTION: Streptococcus Antigens
FILE REFERENCE: 055190-0044
CURRENT APPLICATION NUMBER: US/09/884,465A
CURRENT FILING DATE: 2001-06-20
PRIOR APPLICATION NUMBER: 60/212,683
PRIOR FILING DATE: 2000-06-20
NUMBER OF SEQ ID NOS: 384
SOPTWARE: Patentin version 3.1
SEQ ID NO 383
TENET 1126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 6
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TYPE: PRT

ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Unknown Organism
NAME/KEY: MISC_FEATURE
LOCATION: (1). (1)
OTHER INFORMATION: Xaa = Methionine or
NAME/KEY: MISC_FEATURE
LOCATION: (557)...(557)
OTHER INFORMATION: Xaa = Glycine or no
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 383, Application US/09884465A Publication No. US20030077293A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Shire Biochem, Inc.
APPLICANT: Hamel, Josee
APPLICANT: Brodeur, Bernard
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               APPLICANT: Brodeur, Bernard
APPLICANT: Martin, Denis
APPLICANT: Charland, Nathalie
APPLICANT: Ouellet, Catherine
TITLE OF INVENTION: Streptococcus Antigens
FILE REFERENCE: 055190-0044
CCURRENT APPLICATION NUMBER: US/09/884,465A
CURRENT FILING DATE: 2001-06-20
PRIOR APPLICATION NUMBER: 60/212,683
PRIOR APPLICATION NUMBER: 60/212,683
PRIOR APPLICATION NUMBER: 60/212,683
PRIOR APPLICATION STREET
SECONOMISSION 384
SOFTWARE: Patentin version 3.1
SEQ ID NO 382
LENGTH: 1365
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US-09-884-465A-382
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; LOCATION: (550)..(558)
; OTHER INFORMATION: Xaa =
US-09-884-465A-383
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                                                                                                                                                                                                                                                                               Sequence 382, Application US/09884465A
Publication No. US20030077293A1
GENERAL INFORMATION:
APPLICANT: Shire Biochem, Inc.
APPLICANT: Hamel, Josee
APPLICANT: Brodeur, Bernard
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 45.6
Best Local Similarity 64.9
Matches 366; Conservative
   ORGANISM: Artificial Sequence
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Pred. No. 4.7e-128;
3; Mismatches 101;
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APPLICANT: Shire Biochem, Inc.
APPLICANT: Hamel, Josee
APPLICANT: Brodeur, Bernard
APPLICANT: Martin, Denis
APPLICANT: Charland, Nathalie
APPLICANT: Charland, Nathalie
APPLICANT: Ouellet, Catherine
TITLE OF INVENTION: Streptococcus Antigens
FILE REFERENCE: 055190-0044
CURRENT APPLICATION UNMBER: US/99/884,465A
CURRENT FILING DATE: 2001-06-20
                                                                                                                                                                                                      RESULT 8
US-09-884-465A-380
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NAME/KEY: MISC PEATURE
LOCATION: (1) 7(1)
OTHER INFORMATION: Xaa = Met!
NAME/KEY: MISC PEATURE
LOCATION: (557) .. (557)
OTHER INFORMATION: Xaa = Gly:
NAME/KEY: MISC PEATURE
LOCATION: (558) .. (558)
OTHER INFORMATION: Xaa = Pro:
US-09-884-465A-382
                                                                                                                                                       Sequence 380, Application US/09884465A Publication No. US20030077293A1 GENERAL INFORMATION:
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367; Conservative
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Pred. No. 2.2e-127;
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PRIOR FILING DATE: 2000-06-20
NUMBER OF SEQ ID NOS: 384
SOFTWARE: PatentIn version 3.1
SEQ ID NO 380
LENGTH: 1139
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Best Local Similarity
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LGTKDNNTISAEVDSLLALLKESQPAPI
             LQIMDNNSIMAEAEKLLALLKGSNPSSV
                                                                        FKADEEPVEETPAEPEVPQVETEKVEAQLKEAEVILAKVTDSSLKANATETLAGLRNNLT
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                                                TEETEEEAEDTTDEAEIPQVENSVINAKIADAEALLEKVTDPSIRQNAMETLTGLKSSLL
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60.7%; Pre
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Pred. No. 1.4e-120;
Pred. No. 1.7e-120; I
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RESULT 9
US-09-884-465A-378
Sequence 378, Application US/09884465A
Publication No. US20030077293A1
GENERAL INFORMATION:
APPLICANT: Shire Biochem, Inc.
APPLICANT: Hamel, Josee

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Best Local Similarity
Matches 345; Conserv
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OTHER INFORMATION: Xaa = Methionine of
NAME/KEY: MISC FEATURE
LOCATION: (570). (570)
OTHER INFORMATION: Xaa = Glycine or no
NAME/KEY: MISC FEATURE
LOCATION: (571). (571)
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APPLICANT: Ouellet, Catherine
TITLE OF INVENTION: Streptococcus Antigens
FILE REFERENCE: 055190-0044
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                                                                                                                                                                                                                                                                               SLSEAERAAAQAYAKEKGLTPPSTDHQDSGNTEAKGAEAIYNRVKAAKKVPLDRMPYNLQ
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                               LQIMDNNSIMAEAEKLLALLKGSNPSSV 790
                                                                  TEETEEEAEDTTDEAEIPQVENSVINAKIADAEALLEKVTDPSIRQNAMETLTGLKSSLL
                                                                                                   FKADEEPVEETPAEPEVPQVETEKVEAQLKEAEVLLAKVTDSSLKANATETLAGLRNNLT
                                                                                                                                       NGFGNASDHVRKNKADQDSKPDEDKEHDEVSEPTHPESDEKENHAGLNPSADNLYKPSTD
LGTKDNNTISAEVDSLLALLKESQPAPI 568
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Pred. No. 1.9e.
71; Mismatches
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Best Local S
Matches 314
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SEQ ID NO 381
LENGTH: 1238
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APPLICANT: Shire Biochem,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY: MISC FEATURE LOCATION: (430) ... (430) OTHER INFORMATION: Xaa = GNAME/KEY: MISC FEATURE LOCATION: (431) ... (431)
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APPLICANT: Ouellet, Catherine
TITLE OF INVENTION: Streptococcus Antigens
FILE REFERENCE: 055190-0044
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NAME/KEY: MISC_FEATURE
LOCATION: (1)...(1)
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OTHER INFORMATION: Xaa =
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                                   WGNASEHVLGKKDHSEDPNKNFKADEEPVEETPAEPEVPQVETEKVEAQLKE 733
                                                                                                             VEVKNGNLIIPHKDHYHNIKFAWFDDHTYKAPNGYTLEDLFATIKYYVEHPDERPHSNDG
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                                                                                                                                                                                       SDKEKVAAQAYTKEKGILPPSPDADVKANPTGDSAAAIYNRVKGEKRIPLVRLPYMVEHT
FGNASDHVXXNMQPSQLSYSSTASDNNTQSVAKGSTSKPANKSENLQSLLKE
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Martin, Denis
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Pred. No. 4.2e-1
7; Mismatches
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4.2e-111;
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APPLICANT: Charland, Nathalie
APPLICANT: Ouellet, Catherine
TITLE OF INVENTION: Streptococcus Antigens
FILE REFERENCE: 055190-004
CURRENT FILING DATE: 2001-06-20
PRIOR APPLICATION NUMBER: 60/212,683
PRIOR APPLICATION NUMBER: 60/212,683
PRIOR FILING DATE: 2000-06-20
NUMBER OF SEQ ID NOS: 384
SOFTWARE: Patentin version 3.1
SEQ ID NO 376
LENGTH: 999
TYPE: PRT
ORGANISM: Artificial Sequence
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Matches
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LOCATION: (1)..(1)
OTHER INFORMATION: Xaa = Methionine
NAME/KEY: MISC_FEATURE
LOCATION: (430)..(430)
OTHER INFORMATION: Xaa = Glycine ox
NAME/KEY: MISC_FEATURE
LOCATION: (431)..(431)
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APPLICANT: Hamel, Josee
APPLICANT: Brodeur, Bernard
APPLICANT: Martin, Denis
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                                     WGNASEHVLGKKDHSEDPNKNFKADEEPVEETPA------
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 FGNASDHV--XXDLTEE---QIKAAQKHLEEVKTSHNGLDSLSSHEQDYP
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o. US20030077293A1
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FEATURE:
FEATURE:
OTHER INFORMATION: Unknown Organism
NAME/KEY: MISC_FEATURE
LOCATION: (1)...(1)
OTHER INFORMATION: Xaa = Methionine o
NAME/KEY: MISC_FEATURE
LOCATION: (570)...(570)
OTHER INFORMATION: Xaa = Glycine or r
NAME/KEY: MISC_FEATURE
LOCATION: (571)...(571)
OTHER INFORMATION: Xaa = Proine or n
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PRIOR FILING DATE: 2000-06-20
NUMBER OF SEQ ID NOS: 384
SOFTWARE: PatentIn version 3.1
SEQ ID NO 377
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Best Local Similarity
Matches 307; Conserv
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APPLICANT: Hamel, Josee
APPLICANT: Brodeur, Berna
APPLICANT: Martin, Denis
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622 VEVKNGNLIIPHKDHYHNIKFAWFDDHTYKAPNGYTLEDLFATIKYYVEHPDERPHSNDG 681
||||||:|||||||:|| 932 VEVKNGSLIIPHYDHYHNIKFEWFDEGLYEAPKGYTLEDLLATVKYYVEHPNERPHSDNG 991
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                                                                                                                                                                                                                                                                                                                                                                                                     RIARIIPLRYRSNHWVPDSRPEQPSPQPTPEPSPGPQPAPNLK-IDSN---SSLVSQLVR
                                                                                                SDKEKVAAQAYTKEKGILPPSPDADVKANPTGDSAAAIYNRVKGEKRIPLVRLPYMVEHT
                                                                                                                                                                                                                                                  KAYNLLTEAHKALFXNKGRNSDFQALDKLLERLNDESTNKEKLVDDLLAFLAPITHPERL
                                                                                                                                                                                                                                                                                                     KVGDGYVFEENGVSRYIPAKNLSAETAAGIDSKLAKQESLSHKLGAKKTDLPSSDREFYN
                                                                                                                                                    GKPNAQITYTDDEIQVAKLAGKYTTEDGYIFDPRDITSDEGDAYVTPHMTHSHWIKKDSL
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68;

Indels

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871

751

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APPLICANT: Charland, Nathalie
APPLICANT: Ovellet, Catherine
TITLE OF INVENTION: Streptococcus Antigens
FILE REFERENCE: 055190-004
CURRENT APPLICATION NUMBER: US/09/884,465A
CURRENT FILING DATE: 2001-06-20
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DB 11;
Length
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682

WGNASEHV

689

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Sequence 6, Application US/09884465A
Publication No. US20030077293A1
GENERAL INFORMATION:
APPLICANT: Shire Biochem, Inc.
APPLICANT: Hamel, Josee
APPLICANT: Brodeur, Bernard
APPLICANT: Martin, Denis
APPLICANT: Charland, Nathalie
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US-09-884-465A-6
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CURRENT FILING DATE: 2001-06-20
PRIOR APPLICATION NUMBER: 60/212,683
PRIOR FILING DATE: 2000-06-20
NUMBER OF SEQ ID NOS: 384
SOFTWARE: Patentin version 3.1
SEQ ID NO 6
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Best Local Similarity
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APPLICANT: Ouellet, Catherine
TITLE OF INVENTION: Streptococcus
FILE REFERENCE: 055190-0044
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 DESGFVMSHGDHNHYFFKKDLTEEQIKAAQKHLEE--
                                   EGDAYVTPHMGHSHWIGKDSLSDKEKVAAQAYTKEKGILPPSPDADVKANPTG-DSAAAI
                                                                           QPTLPNNSLATPSP-SLPINPGTSHEKHE-
                                                                                                             KEKLVDDLLAFLAPITHPERLGKPNSQIEYTEDEVRIAQLADKYTTSDGYIFDEHDIISD
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41.2%; Pred. No. 4.6e-81;
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Publication No. US20030091577A1
GENERAL INFORMATION:
APPLICANT: Microbial Technics Limited
APPLICANT: Gilbert, Christophe FG
APPLICANT: Hansbro, Philip M
TITLE OF INVENTION: Proteins
FILE REFERENCE: PWC/P21129WO
CURRENT APPLICATION NUMBER: US/09/769,787
CURRENT APPLICATION NUMBER: US/09/769,787
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SOFTWARE: PatentIn Ver. 2.1
SEQ_ID_NO_38
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Best Local Similarity
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PRIOR FILING DATE: 1998-03-27
PRIOR APPLICATION NUMBER: US 60/125164
PRIOR FILING DATE: 1999-03-19
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                                 VSHTLTAKKENVAPRDQEFYDKAYNLLTEAHKALFXNKGRNSDFQALDKLLERLNDESTN
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----LTTSKELSSASDGYIFNPK-DIVEETATAYIVRHG--DHFHYIPK-----SNQIG 410
                                                                                                             POPAPNLKIDSNSSLVSQLVRKVGEGYVFEEKGISRYVFAKDLPSETVKNLESKLSKQES
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45.8%; Pred. No. 2e-78;
ative 77; Mismatches 1
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US-09-769-744A-24
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LENGTH: 484
TYPE: PRT
ORGANISM: Streptococcus pneumoniae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
Matches 259; Conserv
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CURRENT FILING DATE: 2001-01-26
PRIOR APPLICATION NUMBER: PCT/GB99/02452
PRIOR FILING DATE: 1999-07-27
PRIOR APPLICATION NUMBER: GB 9816336.3
PRIOR FILING DATE: 1998-07-27
PRIOR APPLICATION NUMBER: US 60/125329
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Hanniffy, Sean B
APPLICANT: Hansbro, Philip M
TITLE OF INVENTION: Proteins
FILE REFERENCE: PMC/P21122WO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRICE FILING DATE: 1999-0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Le Page, Richard WF APPLICANT: Wells, Jeremy M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: PatentIn Ver.
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 364
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                                                                                                                                                                                                              241 VSNPGTTNTNTSNNSNTNSQASQSNDIDSLLKQLYKLPLSQRHVESDGLVFDPAQITSRT
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                                                                                                                                                                                                                                                                           181 GDAYIVPHGDHYHYIPKNELSASELAAAEAFLSGRGNLSNSRTYRRQNSDNTSRTNWVPS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 SYELGLYQARTVKENNRVSYIDGKQATQKTENLTPDEVSKREGINAEQIVIKITDQGYVT
                             VSHTLTAKKENVAPRDQEFYDKAYNLLTEAHKALFXNKGRNSDFQALDKLLERLNDESTN
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                                                                                                                                                                                                                                                                                                                                       AHADNVRTKEEINRQKQEHSQHREGGTPRNDGAVALARSQGRYTTDDGYIFNASDIIEDT
                                                                                                                                                                                                                                                                                                                                                                                                        SHGDHYHYYNGKVPYDAIISEELLMKDPNYKLKDEDIVNEVKGGYVIKVDGKYYVYLKDA
                                                                                                                                                                                                                                                         GNAYIVPHGGHYHYIPKSDLSASELAAAKAHLAGKNMQPSQLSYSSTASDN------
                                                                                                                                                                                                                                                                                                                       AHADNVRTKDEINRQKQEHVKDNE----KVNSNVAVARSQGRYTTNDGYVFNPADIIEDT
                                                                                           POPAPNLKIDSNSSLVSQLVRKVGEGYVFEEKGISRYVFAKDLPSETVKNLESKLSKQES
                                                                                                                            PNGVAIPHGDHYHFIPYSKLSALEEKIARMVP---
                                                                                                                                                                                          ----NTQSVAKGSTSKPANKSENLQSLLKELYDSPSAQRYSESDGLVFDPAKIISRT
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LTTSKELSSASDGYIFNPK-DIVEETATAYIVRHG--DHFHYIPK-----SNQIG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1999-03-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              28.9%; Score 1203.5; D
45.8%; Pred. No. 2e-78;
tive 77; Mismatches 1
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Best Local
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TOPOLOGY: linear;
; MOLECULE TYPE: protein;
; SEQUENCE DESCRIPTION: SEQ ID NO: 182: US-09-765-272-182
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Sequence 182, Application 05,000.

Patent No. US20020061545A1

GENERAL INFORMATION:
APPLICANT: Choice et. al.

TITLE OF INVENTION: Streptococcus pneumoniae Antigens and Vaccines.

11TLE OF OPCIENCES: 452
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INFORMATION FOR SEQ ID NO: 182:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb st
COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.2
SOFTWARE: ASCII Text
CURRENT APPLICATION NUMBER: US/09/765,272
FILING DATE: 22-Jan-2001
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity es 257; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: 08/961,083
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELECOMMUNICATION INFORMATION: TELEPHONE: (301) 309-8504
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
ADDRESSEE: Human Genome Sciences,
                                                                                                                                            124 DNYRTKEEINROKOEHSOHREGGTPRNDGAVALARSOGRYTTDDGYIFNASDIIEDTGDA 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  481
                            YIVPHGDHYHYIPKNELSASELAAAEAFLSGRGNLSNSRTYRRQNSDNTSRTNWVPSVSN 243
                                                                                                                                                                                                                         DHYHYYNGKVPYDAIISEELLMKDPNYKLKDEDIVNEVKGGYVIKVDGKYYVYLKDAAHA 123
                                                                                                                                                                                                                                                                                                                                       LGLYQARTVKENNRVSYIDGKQATQKTENLTPDEVSKREGINAEQIVIKITDQGYVTSHG 63
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                                                                                                                                                                                             DHYHYYNGKVPYDALFSEELLMKDPNYQLKDADIVNEVKGGYIIKVDGKYYVYLKDAAHA 120
                                                                                                                                                                                                                                                                                              LNQHRSQENKDNNRVSYVDGSQSSQKSENLTPDQVSQKEGIQAEQIVIKITDQGYVTSHG
YIVPHGGHYHYIPKSDLSASELAAAKAHLAGKNMQPSQLSYSSTASDN--
                                                                                                 DNVRTKDEINROKOEHVKDNE----KVNSNVAVARSOGRYTTNDGYVFNPADIIEDTGNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Brookes, A. Anders
REGISTRATION NUMBER: 36,373
REFERENCE/DOCKET NUMBER: PB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STREET: 9410 Key West Avenue
CITY: Rockville
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 447 amino acids
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46.3%;
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Pred. No. 2.5e-77;
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APPLICANT: Charland, Nathalie
APPLICANT: Charland, Nathalie
APPLICANT: Ouellet, Catherine
TITLE OF INVENTION: Streptococcus Antigens
FILE REFERENCE: 055190-0044
CURRENT APPLICATION NUMBER: US/09/884,465A
CURRENT FILING DATE: 2001-06-20
PRIOR APPLICATION NUMBER: 60/212,683
PRIOR FILING DATE: 2000-06-20
PRIOR FILING DATE: 2000-06-20
SOFTWARE: Patentin version 3.1
SEQ ID NO 384
SOFTWARE: Patentin version 3.1
SEQ ID NO 384
LENGTH: 913
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US-09-884-465A-384
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                                                                                                                                        Matches 189;
                                                                                                                                                        Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Shire Biochem, Inc.
                                                                                                                                                                                                                       NAME/KEY: MISC FEATURE
LOCATION: (344)...(344)
OTHER INFORMATION: Xaa = Glycine or nothing
NAME/KEY: MISC FEATURE
LOCATION: (345)...(345)
OTHER INFORMATION: Xaa = Proline or nothing
                                                                                                                                                                                                                                                                                                                             OTHER INFORMATION: Unknown Organism
NAME/KEY: MISC_FEATURE
LOCATION: (1)..(1)
OTHER INFORMATION: Xaa = Methionine or nothing
                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                       FEATURE:
                     547 TPHMGHSHWIGKDSLSDKEKVAAQAYTKEKGILPPSPDADVKANPTGDSAAAIYNRVKGE 606
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                                                                                          DLLAFLAPITHPERLGKPNSQIEYTEDEVRIAQLADKYTTSDGYIFDEHDIISDEGDAYV
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TPHMTHSHWIKKDSLSEAERAAAQAYAKEKGLTPPSTDHQDSGNTEAKGAEAIYNRVKAA
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Martin, Denis
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                                                                                                                                        Conservative
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Pred.
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                                                                                                                                                        991.5;
No. 1e-
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1e-62;
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US-09-884-465A-379
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                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: PRT
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 182
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                     YYVEHPDERPHSNDGWGNASEHVLGK-----KDHSE-----
                                                                                          KRIPLVRLPYMVEHTVEVKNGNLIIPHKDHYHNIKFAWFDDHTYKAPNGYTLEDLFATIK 666
                                                                                                                                        TPHMTHSHWIKKDSLSEAERAÄÄQÄYÄKEKGLTPPSTDHQDSGNTEAKGÄEÄIYNRVKAA 121
                                                                                                                                                                                                         DILAFLAPIRHPERLGKPNAQITYTDDEIQVAKLAGKYTTEDGYIFDPRDITSDEGDAYV
YYVEHPNERPHSDNGFGNASDHVRKNKADQDSKPDEDKEHDEVSEPTHPESDEKENHAGL
                                                                    KKVPLDRMPYNLQYTVEVKNGSLIIPHYDHYHNIKFEWFDEGLYEAPKGYSLEDLLATVK 181
                                                                                                                                                                   TPHMGHSHWIGKDSLSDKEKVAAQAYTKEKGILPPSPDADVKANPTGDSAAAIYNRVKGE
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Martin, Denis
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AMETLTGLKSSLLLGTKDNNTISAEVDSLLALLKESQPAPI 342
                                                          ATETLAGIRNNITLQIMDNNSIMAEAEKLLALIKGSNPSSV 790
                                                                                                                              NPSADNLYKPSTDTEETEEEAEDTTDEAEIPQVENSVINAKIADAEALLEKVTDPSIRQN
                                                                                                                                                                                                                                                                                                                              YYVEHPDERPHSNDGWGNASEHVLGK---
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                                                                                                                                                                                                                                                                                                                                                                                                                                 KRIPLVRLPYMVEHTVEVKNGNLIIPHKDHYHNIKFAWFDDHTYKAPNGYTLEDLFATIK 666
                                                                                                                                                                                            -----DPNKNFKADEEPVEETPAEPEVPOVETEKVEAQLKEAEVLLAKVTDSSLKAN
                                                                                                                                                                                                                                                                YYVEHPNERPHSDNGFGNASDHVRKNKADQDSKPDEDKEHDEVSEPTHPESDEKENHAGL
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OTHER INFORMATION: Unknown Organism NAME/KEY: MISC\_FEATURE LOCATION: (1)...(1)
OTHER INFORMATION: Xaa = Methionine o: NAME/KEY: MISC\_FEATURE LOCATION: (344)...(344)
OTHER INFORMATION: Xaa = Glycine or no NAME/KEY: MISC\_FEATURE LOCATION: (345)...(345) SOFTWARE: PatentIn version 3.1 SEQ ID NO 379 APPLICANT: Ouellet, Catherine
TITLE OF INVENTION: Streptococcus Antigens
FILE REFERENCE: 055190-0044
CURRENT APPLICATION NUMBER: US/09/884,465A
CURRENT FILING DATE: 2001-06-20 PRIOR APPLICATION NUMBER: 60/212,683 PRIOR FILING DATE: 2000-06-20 NUMBER OF SEQ ID NOS: 384 Charland, Nathalie Ouellet, Catherine Application US/09884465A
o. US20030077293A1 Proline or nothing Methionine or nothing or

Score 991.5; DB 1 Pred. No. 1.5e-62;

DB 11; 70;

Length 1152;

Mismatches

Indels

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US-09-884-465A-10
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SEQ ID NO 10
LENGTH: 840
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Shire Biochem, Inc.
APPLICANT: Hamel, Josee
APPLICANT: Brodeur, Bernard
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION NUMBER: US/09/884,465A CURRENT FILING DATE: 2001-06-20 PRIOR APPLICATION NUMBER: 60/212,683 PRIOR FILING DATE: 2000-06-20 NUMBER OF SEQ ID NOS: 384
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APPLICANT: Ouellet, Catherine
TITLE OF INVENTION: Streptococcus Antigens
FILE REFERENCE: 055190-0044
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                                      NKGRNSDFQALDKLLERLNDESTNKEKLVDDLLAFLAPITHPERLGKPNSQIEYTEDEVR
                                                                              YPHGDHHHADPIDEHKPVGIGHSHSNYELFKPEEGVAKKEG---NKVY---TGEELTNVV
                                                                                                                                                                                          GPQPAPNLKIDSNSSLVSQLVRKVGE--GYVFEEKGISRYVFAKDLPSETVKNLESKL--
                                                                                                                                                                                                                                    DESGFVMSHGDHNHYFFKKDLTEEQIKAAQKHLEEVKTSHNGLDSLSSHEQDYP-----
                                                                                                                                                                                                                                                                      TARGVAVPHGDHYHFIPYSQMSELEERIARIIPLRYRSNHWVPDSRPEQPSPQPTPEPSP
                                                                                                                                                                                                                                                                                                              LPINPGTSH-----EKH-EEDGYGFDANRIIAE
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Martin, Denis
                                                                                                                                                        -SNAKEMKDLDKKIEEKIAGIMKQYGVKR-----ESIVVNKEKNAII
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    --NNQNFTLANGQKRV----SFSFPPELEKKLG--
                                                                                                                  -SKQESVSHT----LTAKKENVAPRDQEFYDKAYNLLTEAHKALFX
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APPLICANT: He Page, Richard WF
APPLICANT: Wells, Jeremy M
APPLICANT: Hanniffy, Sean B
TITLE OF INVENTION: Proteins
FILE REFERENCE: PMC/P2108900
CURRENT APPLICATION NUMBER: US/09/769,736
CURRENT APPLICATION NUMBER: GB 9816335.5
PRIOR APPLICATION NUMBER: GB 9816335.5
PRIOR APPLICATION NUMBER: US/09/169,736
PRIOR FILING DATE: 1998-07-27
PRIOR APPLICATION NUMBER: US/09/16335.5
PRIOR FILING DATE: 1999-03-19
NUMBER OF SEQ ID NOS: 212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 18, Application US/09769736 Publication No. US20030138775A1 GENERAL INFORMATION:
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SEQ ID NO 18
LENGTH: 822
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Best Local
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TYPE: PRT
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QLYKLPLSQRHVESDGLVFDPAQITSRTARGVAVPHGDHYHFIPYSQMSELEERIARIIP 332
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                                                            TPAPGRRKAP - IPDVTPNPGQGHQPDNGGYHPAPPRPNDASQNKHQRDEFKGKTFKELLD
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                                                                                                                                                                                                                                        KDAAHADNVRTKEEINRQKQEHSQH-REGG-----TPRNDGAVALARSQGRYTTDDGY 169
                                                                                                                                                                                                                                                                                          YVTSHGDHYHFYNGKVPYDAIISEELLMTDPNYHFKQSDVINEILDGYVIKVNGNYYVYL
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                                                                                              QNSDNTSRTNWVPSVS-NPGTTNTNTSN-----NSNTNSQASQSND-----IDSLLK 272
                                                                                                                                                        IFNASDIIEDTGDAYIVPHGDHYHYIPKNELSASELAAAEAFLS---GRGNLSNSRTYRR 226
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ilarity 29.3%;
Conservative . 9
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; pred. No. 2.9e-58;
99; Mismatches 236;
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APPLICANT: HAMEL, Jose
APPLICANT: MARTIN, Denis
APPLICANT: MARTIN, Denis
TITLE OF INVENTION: NOVEL GROUP B STREPTOCCCCUS ANTIGENS
FILE REFERENCE: 8331-9002
CURRENT APPLICATION NUMBER: US/09/252,088
CURRENT FILING DATE: 1999-02-18
EARLIER APPLICATION NUMBER: US/60/075,425
EARLIER APPLICATION NUMBER: US/60/075,425
EARLIER FILING DATE: 1998-02-20
NUMBER OF SEQ ID NOS: 44
SOSTWARE: PATENTIN Ver. 2.0
SOSTWARE: PATENTIN Ver. 2.0
SEQ ID NO 15
LENGTH: 793
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 21
US-09-252-088-15
; Sequence 15, Application US/09252088
; Publication No. US20030031682A1
; Publication No. US20030031682A1
                                             Query Match
Best Local Similarity
Matches 265; Conserv
                                                                                                                               TYPE: PRT
ORGANISM: group
-09-252-088-15
                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: BRODEUR, Bernal
APPLICANT: RIOUX, Clment
APPLICANT: BOYER, Martine
APPLICANT: CHARLEBOIS, Isa
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      14 ENNRVSYID---GKQATQKTENLTPDEVSKREGINAEQIVIKITDQGYVTSHGDHYHYYN
                                                                                                                                                                                                                                                                                                                                                                                                                                              CHARLEBOIS, Isabelle
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                                             22.3%; Score 927; DB 11; ilarity 30.7%; Pred. No. 3.8e-58; Conservative 115; Mismatches 258;
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                                                                                    Length 793;
                                               Indels
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Sequence 24, Application US/09769736
Publication No. US20030138775A1
GENERAL INFORMATION:
APPLICANT: Microbial Technics Limited
APPLICANT: Le Page, Richard WF
APPLICANT: Hells, Jeremy M
APPLICANT: Hanniffy, Sean B
TITLE OF INVENTION: Proteins
FILE REFERENCE: PWC/P21089W0
CURRENT APPLICATION NUMBER: US/09/769,736
CURRENT FILING DATE: 2003-02-14
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                                                                                                                                                                                                                                                                                                                     EKQQADK---SNENQQPSEASKEE
                                                                                                                                                                                                                                                                                                                                                            IMAEAEKLLALLKGSNPSSVSKEK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HVLGKKDHSEDPNKNFKADEEPVEETPAE----PE----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HYHNIKFAWFDDHTYKAPNGYTLEDLFATIKYYVEHPDERPHSNDGW------GNASE 687
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APPLICANT: Martin, Denis
APPLICANT: Charland, Nathalie
APPLICANT: Coballet, Catherine
TITLE OF INVENTION: Streptococcus Antigens
FILE REFERENCE: 055190-0044
CURRENT APPLICATION NUMBER: US/09/884,465A
CURRENT FILING DATE: 2001-06-20
PRIOR APPLICATION NUMBER: 60/212,683
PRIOR APPLICATION NUMBER: 60/212,683
PRIOR FILING DATE: 2000-06-20
NUMBER OF 5E0 ID NOS: 384
SOFTWARE: Patentin version 3.1
SEO ID NO 369
LENGTH: 906
TYPE: PRT
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US-09-884-465A-369
; Sequence 369, Application US/09884465A
; Publication No. US20030077293A1
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TYPE: PRT
ORGANISM: Streptococcus agalactiae
-09-769-736-24
                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Shire Biochem, Inc. APPLICANT: Hamel, Josee APPLICANT: Brodeur, Bernard
                                                                                                                                                                ORGANISM: Artificial Sequence
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 43 GINAEQIVIKITDQGYVTSHGDHYHYYNGKVPYDAIISEELLMKDPNYKLKDEDIVNEVK 102
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Martin, Denis
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ilarity 49.6%;
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                                                                                                LGKKDHSEDPNKNFKADE--EPVEETPAEPE------VPQVETEKVEAQLK--
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                                                                KNKADQDSKPDEDKEHDEVSEPTHPESDEKENHAGLNPSADNLYKPSTDTEETEEEAEDT
                                                                                                                                IPHYDHYHNIKFEWFDEGLYEAPKGYSLEDLLATVKYYVE---
                                                                                                                                                             IPHKDHYHNIKFAWFDDHTYKAPNGYTLEDLFATIKYYVEHPDERPHSNDGWGNASEHV-
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US-09-884-465A-373

; Sequence 373, Application US/09884465A

; Bequence 373, Application US/09884465A

; GENERAL INFORMATION:

; APPLICANT: Shire Biochem, Inc.

; APPLICANT: Hamel, Josee

; APPLICANT: Brodeur, Bernard

; APPLICANT: Martin, Denis

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT FILING DATE: 2001-06-20
PRIOR APPLICATION NUMBER: 06/212,683
PRIOR APPLICATION NUMBER: 60/212,683
PRIOR FILING DATE: 2000-06-20
NUMBER OF SEQ ID NOS: 384
SOFTWARE: Patentin version 3.1
SEQ ID NO 373
LENGTH: 906
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local S
Matches 261
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APPLICANT: Ouellet, Catherine
TITLE OF INVENTION: Streptococcus Antigens
FILE REFERENCE: 055190-0044
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT
ORGANISM: Artificial Sequence
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Local Similarity 27.2%; Pred. No. 1e-42;
les 261; Conservative 105; Mismatches 291; Indels 303;
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AYAKEKGLTPPSTDHQDSGNTEAKGAEAIYNRVKAAKKVPLDRMPYNLQYTVEVKNGSLI
                    AYTKEKGILPPSPDADVKANPTGDSAAAIYNRVKGEKRIPLVRLPYMVEHTVEVKNGNLI
                                                                TDDEIQVAKLAGKYTTEDGYIFD-----
                                                                                     TEDEVRIAQLADKYTTSDGYIFDEHDIISDEGDAYVTPHMGHSHWIGKDSLSDKEKVAAQ
                                                                                                                                                                                                                                  TLTAKKENVAPRDQEFYDKAYNLLTEA-------HKALFXNKGRNSDFQALDKLL
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                                                                                                                                  EEAPAVDPVQEKLEKFTASYGLGLDSVIFNMDGTIELRLPSGEVIKKNLSDFIAGPQITY
                                                                                                                                                                ERLNDESTNKEKLVD------DLLAFLAPITHPERLG----KPN-----SQIEY
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| 문 | Ş   | B .5  | 9  | D Qy  | αd   | VQ  | B 8  | Db   | 8            | D 64                           | Query M<br>Best Lo<br>Matches   | Db 741  Oy 690  Db 790  Oy 733  Db 850  RESULT 25  US-09-884-465  Sequence 37  Publication  GENERAL INF APPLICANT: APPLIC | 80                                   |
|---|---|---|--|---|--|---|--|--|--------------|--------------------------------|---|--|--------------------------------------|
|   | 312 YHFIPYSOMSELEERIARIIPLRYRSNHWVPDSRPEOPS 350 | 93FTVPTSLAYKMASQTIFYPFHAGDTYLRVNPQFAVPKGTDALVRVFDE 34 | 63 OSNDIDSTIKOLYKI,BISOBHVESDGLVFDDAOTTSBTARGVAVDHGDH 31 | 212 LSGRGNLSNSRTYRRQNSDNTSRTNWVPSVSNPGTTNTNTSNNSNTNSQAS 262 | VVNILKNSTFNNONFTLANGOKRVSFSFPPELEKKLGINMLVKLITPDGKVLEKVSGKVF 2 | 173 ASDIIEDTGDAYIVPHGDHYHYIPKNELSASELAAAEAF 211 | 119 DAAHADNVRTKEEINRQKQEHSQHREGGTPRNDGAVALARSQGRYTTDDGYIFN 172 | 93 SSHEQDYPGNAKEMKOLDKKIEEKIAGIMKQYGVKRESIVVNKEKNAIIYPSG 145 | 79 ISEELLMKD | 43 GINAEQIVIKITDQGYVTSHGDHYHYY | / Match 17.1%; Score 710.5; DB 11; Length 906; .<br>Local Similarity 27.2%; Pred. No. 1.9e-42;<br>nes 264; Conservative 116; Mismatches 267; Indels 323; Gaps 42; | 741<br>790<br>790<br>790<br>790<br>733<br>350<br>71<br>71<br>71<br>71<br>71<br>71<br>71<br>71<br>71<br>71<br>71<br>71<br>71  | )HTYKAPNGYTLEDLFATIKYYVEHPDERPHSNDGW |

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APPLICANT: Charland, Nathalie
APPLICANT: Ouellet, Catherine
TITLE OF INVENTION: Streptococcus Antigens
FILE REFERENCE: 055190-0044
CURRENT APPLICATION NUMBER: US/09/884,465A
CURRENT FILING DATE: 2001-06-20
PRIOR APPLICATION NUMBER: 60/212,683
PRIOR APPLICATION NUMBER: 60/212,683
PRIOR FILING DATE: 2000-06-20
NUMBER OF SEQ ID NOS: 384
SOFTWARE: Patentin version 3.1
SEQ ID NO 33
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                               Matches
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APPLICANT:
                                                         Query Match
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                                                                                                    OTHER INFORMATION:
                                                                                                                 CRGANISM: Artificial Sequence FEATURE:
                                                                                                                                               TYPE: PRT
                                                                                                                                                           LENGTH: 900
                                             Local
                             cal Similarity
257; Conserv
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  43 GINAEQIVIKITDQGYVTSHGDHYHYYNGKVPYDAIISEELLMKDPNYKLKDEDIVNEVK 102
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                                                                                                                                                                                                                                                                                                                                 Brodeur, Bernard
Martin, Denis
                               Conservative 105; Mismatches 289;
                                                                                                  Unknown Organism
                                          16.2%; Score 675.5; DB 1 26.8%; Pred. No. 6.5e-40;
                                                        DB 11;
                             Indels 309;
                                                      Length
                                                         900;
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                                                                                                    US-09-252-088-16
                                                        Sequence 16, Application US/09252088 Publication No. US20030031682A1 GENERAL INFORMATION:
APPLICANT: BRODEUR, Bernard R. APPLICANT: RIOUX, Clment APPLICANT: BOYER, Martine APPLICANT: CHARLEBOIS, Isabelle
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CURRENT APPLICATION NUMBER: US/09/252,088
CURRENT FILING DATE: 1999-02-18
EARLIER APPLICATION NUMBER: US/60/075,425
EARLIER FILING DATE: 1998-02-20
NUMBER OF SEQ ID NOS: 44
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 16
LENGTH: 715
TYPE: PRT
ORGANISM: group B streptococcus
US-09-252-088-16
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APPLICANT: MARTIN, Denis
TITLE OF INVENTION: NOVEL GROUP B STREPTOCCCCUS
FILE REFERENCE: 8331-9002
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                                                                                 EKVEAQLKEAEVILAKVTDSSLKANATETLAGIRNNLTLQIMDNNSIMAEAEKILALIKG
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    SNPSSVSKEK 794
                                          DLSQAEWQQAQELLAKKN----TGDATDT---
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27.0%; Pred. No. 6e-39;
**** Mismatches 250;
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                                          -DKPKEKQQADK---SNEN
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US-09-884-465A-372
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US-09-884-465A-370
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APPLICANT: Ouellet, Catherine
TITLE OF INVENTION: Streptococcus Antigens
FILE REFERENCE: 055190-0044
CURRENT APPLICATION NUMBER: US/09/884,465A
CURRENT FILING DATE: 2001-06-20
PRIOR APPLICATION NUMBER: 60/212,683
PRIOR FILING DATE: 2000-06-20
NUMBER OF SEQ ID NOS: 384
                                                                                                                     Sequence 372, Application US/09884465A
Publication No. US20030077293A1
GENERAL INFORMATION:
APPLICANT: Shire Biochem, Inc.
APPLICANT: Hamel, Josee
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SEQ ID NO 370
LENGTH: 906
TYPE: PRT
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Best Local Similarity
                                                                APPLICANT:
                       APPLICANT:
TITLE OF I
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                                                                                 APPLICANT:
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    REFERENCE:
ANT: Brodeur, Bernard
ANT: Martin, Denis
ANT: Charland, Nathalie
ANT: Ouellet, Catherine
DF INVENTION: Streptococcus A
SFERENCE: 055190-0044
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Martin, Denis
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45.6%; Pred. No. 1e-37;
tive 40; Mismatches 74;
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Length Indels

Gaps

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989

102 626 42

267

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APPLICANT: Charland, Nathalie
APPLICANT: Ouellet, Catherine
TITLE OF INVENTION: Streptococcus Antigens
FILE REFERENCE: 055190-0044
CURRENT APPLICATION NUMBER: US/09/884,465A
CURRENT FILING DATE: 2001-06-20
PRIOR APPLICATION NUMBER: 60/212,683
PRIOR FILING DATE: 2000-06-20
NUMBER OF SEQ ID NOS: 384
SOFTWARE: Patentin version 3.1
SEQ ID NO 258
LENGTH: 272
TYPE: PRT
CRCANISM: Artificial Sequence
FEATURE:
COULDE THEOREMANTON: TILING DATE: 1000-06-00

NOTHING DATE: 2000-06-20

NUMBER OF SEQ ID NOS: 384
SOFTWARE: Patentin version 3.1
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CURRENT FILING DATE: 2001-06-20
PRIOR APPLICATION NUMBER: 60/212,683
PRIOR FILING DATE: 2000-06-20
NUMBER OF SEQ ID NOS: 384
SOFTWARE: Patentin version 3.1
SEQ ID NO 372
LENGTH: 906
TYPE: PRT
ORGANISM: Artificial Sequence
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                                                                        ; OTHER INFORMATION: US-09-884-465A-258
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Query Match 15.4%; Score 643; DB 11; Best Local Similarity 46.1%; Pred. No. 2.3e-38; Matches 140; Conservative 39; Mismatches 71;
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                                                                                       Unknown Organism
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US-09-884-465A-344
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SEQ ID NO 344
LENGTH: 895
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Best Local Similarity
                                                                                                                                                                                                                                                                                                              Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILE REFERENCE: 055190-0044
CURRENT APPLICATION NUMBER: US/09/884,465A
CURRENT FILING DATE: 2001-06-20
PRIOR APPLICATION NUMBER: 60/212,683
PRIOR FILING DATE: 2000-06-20
NUMBER OF SEQ ID NOS: 384
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Charland, Nathalie
APPLICANT: Ouellet, Catherine
TITLE OF INVENTION: Streptococcus Antigens
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APPLICANT: Hamel, Josee
APPLICANT: Brodeur, Bernard
APPLICANT: Martin, Denis
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                      152
                                                  687 EHV-LGKKDHSEDPNKNFKADE--EPVEETPAEPE-------VPQVETEKVEAQ 730
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o. US20030077293A1
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627 GNLIIPHKDHYHNIKFAWFDDHTYKAPNGYTLEDLFATIKYYVEHPDERPHSNDGWGNAS 686
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Pred. No. 1.4e-37;
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RESULT 33
US-09-884-465A-300
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US-09-884-465A-343
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APPLICANT: Ouellet, Catherine
: TITLE OF INVENTION: Strepbcoccus Antigens
:FILE REFERENCE: 055190-004
CURRENT APPLICATION NUMBER: US/09/884,465A
: CURRENT FILING DATE: 2001-06-20
PRIOR APPLICATION NUMBER: 60/212,683
: PRIOR FILING DATE: 2000-06-20
. NUMBER OF CEO. TO NO.
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SOFTWARE: PatentIn version 3.1
SEQ ID NO 343
LENGTH: 901
Type: """
                                               Sequence 300, Application US/09884465A Publication No. US20030077293A1 GENERAL INFORMATION:
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Best Local Similarity

Matches 140; Conserv
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                   APPLICANT: Shire Biochem, Inc. APPLICANT: Hamel, Josee
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      APPLICANT:
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ORGANISM: Artificial Sequence
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Martin, Denis
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; Pred. No. 1.4e-37;
39; Mismatches 71;
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                              ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Unknown Organism
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APPLICANT: Ouellet, Catherine
TITLE OP INVENTION: Streptococcus Antigens
FILE REFERENCE: 055190-0044
CURRENT APPLICATION UNMBER: US/09/884,465A
CURRENT FILING DATE: 2001-06-20
PRIOR APPLICATION NUMBER: 60/212,683
PRIOR FILING DATE: 2000-06-20
NUMBER OF SEQ ID NOS: 384
SOFTWARE: PatentIn version 3.1
SEQ ID NO 301
LENGTH: 272
TYPE: PRT
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SEQ ID NO 300
LENGTH: 272
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ORGANISM: Artificial Sequence
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Martin, Denis
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Ouellet, Catherine
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Ouellet, Catherine
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o. US20030077293A1
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APPLICANT: Martin, Denis
APPLICANT: Martin, Denis
APPLICANT: Charland, Nathalie
APPLICANT: Ouellet, Catherine
TITLE OF INVENTION: Streptococcus Antigens
FILE REFERENCE: 055190-0044
CURRENT APPLICATION NUMBER: US/09/884,465A
CURRENT FILING DATE: 2001-06-20
PRIOR APPLICATION NUMBER: 60/212,683
PRIOR FILING DATE: 2000-06-20
NUMBER OF SEQ ID NOS: 384
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Matches 140
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SEQ ID NO 336
LENGTH: 894
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Publication No. US20030077293A1
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APPLICANT: Hamel, Josee
                                                                                                                                                                                                                                                            TYPE: PRT ORGANISM: Artificial Sequence FEATURE:
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  GSLIIPSYDHYHNIKFEWFDEGLYEAPKGYSLEDLLATVKYYVE----PR----NAS
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46.1%; Pred. No. 3.2e-38;
tive 39; Mismatches 71;
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RESULT 37
US-09-884-465A-332
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; OTHER INFORMATION: Unknown Organism US-09-884-465A-335
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CURRENT FILING DATE: 2001-06-20
PRIOR APPLICATION NUMBER: 60/212,683
PRIOR FILING DATE: 2000-06-20
PRIOR FILING DATE: 2000-06-20
NUMBER OF SEQ ID NOS: 384
SOFTWARE: Patentin version 3.1
SEQ ID NO 335
LENGTH: 900
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Best Local Similarity
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APPLICANT: Hamel, Josee
APPLICANT: Brodeur, Bernard
APPLICANT: Martin, Denis
APPLICANT: Charland, Nathalie
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APPLICANT: Ouellet, Catherine
TITLE OF INVENTION: Streptococcus Antigens
FILE REFERENCE: 055190-0044
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ORGANISM: Artificial Sequence
FEATURE:
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Application US/09884465A

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APPLICANT: Brodeur, Bernard
APPLICANT: Martin, Denis
APPLICANT: Martin, Denis
APPLICANT: Charland, Nathalie
APPLICANT: Ouellet, Catherine
TITLE OF INVENTION: Streptcocccus Antigens
FILE REFERENCE: 055190-0044
CURRENT APPLICATION NUMBER: US/09/884,465A
CURRENT FILING DATE: 2001-06-20
PRIOR APPLICATION NUMBER: 60/212,683
PRIOR APPLICATION WHERE: 60/212,683
PRIOR FILING DATE: 2000-06-20
NUMBER OF SEQ ID NOS: 384
SOFTWARE: Patentin version 3.1
SEQ ID NO 293
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SOFTWARE: PatentIn version 3.1
SEQ ID NO 332
LENGTH: 906
Type: nom
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APPLICANT: Ouellet, Catherine
TITLE OF INVENTION: Streptococcus Antigens
FILE REFERENCE: 055190-0044
CURRENT APPLICATION NUMBER: US/09/884,465A
CURRENT FILING DATE: 2001-06-20
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Martin, Denis
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45.3%; Pred. No. 4.6e-37;
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SOFTWARE: PatentIn version 3.1
SEQ ID NO 294
LENGTH: 272
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Best Local Similarity
Matches 139; Conserv
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                                                                                                                                 Query Match
Best Local Similarity
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APPLICANT: Ouellet, Catherine
TITLE OF INVENTION: Streptococcus Antigens
FILE REFERENCE: 055190-0044
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                                                                                                                                                                                                                   ORGANISM: Artificial Sequence FEATURE:
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567 VAAQAYTKEKGILPPSPDADVKANPTGDSAAAIYNRVKGEKRIPLVRLPYMVEHTVEVKN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INFORMATION:
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Martin, Denis
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o. US20030077293A1
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ilarity 45.7%;
Conservative 39
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Pred. No. 1e-37;
Pred. No. 72;
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Pred. No. 1e-37;
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FILE REFERENCE: 055190-0044
CURRENT APPLICATION NUMBER: US/09/884,465A
CURRENT FILING DATE: 2001-06-20
PRIOR APPLICATION NUMBER: 60/212,683
PRIOR FILING DATE: 2000-06-20
NUMBER OF SEQ ID NOS: 384
SOFTWARE: Patentin version 3.1
SEQ ID NO 295
LENGTH: 272
TYPE: PRT
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US-09-884-465A-295
; Sequence 295, Application US/09884465A.
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APPLICANT: Ouellet, Catherine
TITLE OF INVENTION: Streptococcus Antigens
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Martin, Denis
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APPLICANT: Shire Biochem, Inc.
APPLICANT: Hamel, Josee
APPLICANT: Brodeur, Bernard
APPLICANT: Martin, Denis
APPLICANT: Charland, Nathalie
APPLICANT: Ouellet, Catherine
TITLE OF INVENTION: Streptococcus Antigens
FILE REFERENCE: 055190-0044
CURRENT APPLICATION NUMBER: US/09/884,465A
CURRENT FILING DATE: 2001-06-20
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US-09-884-465A-340
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CURRENT FILING DATE: 2001-06-20
PRIOR APPLICATION NUMBER: 60/212,683
PRIOR FILING DATE: 2000-06-20
NUMBER: CONTROL OF THE PRIOR FILING DATE: 2000-06-20
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APPLICANT: Hamel, Josee
APPLICANT: Brodeur, Berna
APPLICANT: Martin, Denis
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45.0%; Pred. No. 2e-36;
45.0%; Mismatches 76;
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                                                                                                          US-09-884-465A-339
                                                                                                                                                                         NUMBER OF SEQ ID NOS: 384
SOFTWARE: Patentin version 3.1
SEQ ID NO 339
LENGTH: 900
TYPE: PRT
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PRIOR FILING DATE: 2000-06-20
NUMBER OF SEQ ID NOS: 384
SOFTWARE: PatentIn version 3.1
SEQ ID NO 342
LENGTH: 894
                                                  Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 339, Application US/09884465A Publication No. US20030077293A1
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Best Local Similarity
                                    Matches 139;
                                                                                                                                                                                                                                                          APPLICANT: Charland, Nathalie
APPLICANT: Ouellet, Catherine
TITLE OF INVENTION: Streptococcus Antigens
FILE REFERENCE: 055190-0044
CURRENT APPLICATION NUMBER: U5/09/884,465A
CURRENT FILING DATE: 2001-06-20
PRIOR APPLICATION NUMBER: 60/212,683
PRIOR FILING DATE: 2000-66-20
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APPLICANT: Hamel, Josee
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ORGANISM: Artificial Sequence
                                                                                                                                        ORGANISM: Artificial Sequence FEATURE:
                                                                                                                        OTHER INFORMATION: Unknown Organism
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507 QIEYTEDEVRIAQLADKYTTSDGYIFDEHDIISDEGDAYVTPHMGHSHWIGKDSLSDKEK 566
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Martin, Denis
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                                    40; Mismatches
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Pred. No. 2e-36;
0; Mismatches 76;
                                                  Score 627; DB 1
Pred. No. 2e-36;
                                                                  DB 11; Length 900;
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                                    Indels
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US-09-884-465A-341
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SEQ ID NO 341
LENGTH: 900
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                                                                                                                                                                                                                                                                                                                                 Matches 139;
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TITLE OF INVENTION: Streptococcus Antigens
FILE REFERENCE: 055190-0044
CURRENT APPLICATION NUMBER: US/09/884,465A
CURRENT FILING DATE: 2001-06-20
PRIOR APPLICATION NUMBER: 60/212,683
PRIOR EPLICATION DATE: 2000-06-20
NUMBER OF SEQ ID NOS: 384
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LK----EAEVLLAKVTDSSLKANATETLAGLRNNLTLQIMDNNSIMAEAEKLLALLKGSN
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Brodeur, be-
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Ouellet, Catherine
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45.0%;
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Pred. No. 2e-36;
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Length 272;

Indels

54;

Gaps

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RESULT 46
US-09-884-465A-296
; Sequence 296, Application US/09884465A
; Publication No. US20030077293A1
; GENERAL INFORMATION:
; APPLICANT: Shire Biochem, Inc.
; APPLICANT: Hamel, Josee
; APPLICANT: Brodeur, Bernard
; APPLICANT: Martin, Denis
; APPLICANT: Charland, Nathalie
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APPLICANT: Ouellet, Catherine
TITLE OF INVENTION: Streptococcus Antigens
FILE REFERENCE: 055190-0044
CURRENT APPLICATION NUMBER: US/09/884,465A
CURRENT FILING DATE: 2001-06-20
PRIOR APPLICATION NUMBER: 60/212,683
PRIOR FILING DATE: 2000-06-20
NUMBER OF SEQ ID NOS: 384
SOFTWARE: Patentin version 3.1
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LENGTH: 270
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Best Local :
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TITLE OF INVENTION: Streptococcus Antigens
FILE REFERENCE: 055190-0044
CURRENT APPLICATION NUMBER: US/09/884,465A
CURRENT FILING DATE: 2001-06-20
PRIOR APPLICATION NUMBER: 60/212,683
PRIOR FILING DATE: 2000-06-20
NUMBER OF SEO ID NOS: 384
SOFTWARE: Patentin version 3.1
SEQ ID NO 296
LENGTH: 272
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                                                                                                                                   CURRENT APPLICATION NUMBER: US/09/884,465A
CURRENT FILING DATE: 2001-06-20
PRIOR APPLICATION NUMBER: 60/212,683
PRIOR FILING DATE: 2000-06-20
NUMBER OF SEQ ID NOS: 384
SOFTWARE: Patentin version 3.1
SEQ ID NO 298
LENGTH: 272
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Best Local Similarity
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APPLICANT: Hamel, Josee
APPLICANT: Brodeur, Bernard
APPLICANT: Martin, Denis
APPLICANT: Charland, Nathalie
                                                                                                                                                                                                                                                                                                         APPLICANT: Charland, Nathalie
APPLICANT: Ouellet, Catherine
TITLE OF INVENTION: Streptococcus Antigens
FILE REFERENCE: 055190-0044
                                                    OTHER INFORMATION: Unknown Organism
                                                                                   TYPE: PRT
ORGANISM: Artificial Sequence
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ORGANISM: Artificial Sequence
FEATURE:
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Pred. No. 4.6e-37;
9; Mismatches 73;
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APPLICANT: Charland, Nathalie
APPLICANT: Ouellet, Catherine
TITLE OF INVENTION: Streptococcus Antigens
FILE REFERENCE: 05519-0044
CURRENT APPLICATION NUMBER: US/09/884,465A
CURRENT FILING DATE: 2001-06-20
PRIOR APPLICATION NUMBER: 60/212,683
PRIOR FILING DATE: 2000-06-20
NUMBER OF SEQ ID NOS: 384
SOFTWARE: PatentIn version 3.1
SEQ ID NO 299
LENGTH: 272
TYPE: PRT
ORGANISM: Artificial Sequence
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; OTHER INFORMATION: Unknown Organism
US-09-884-465A-299
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                                                                                                                                                                                                                           Query Match
Best Local Similarity
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Best Local Similarity
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APPLICANT: Hamel, Josee
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                                                                                        AAAQAYAKEKGLTPPSTDHQDSGNTEAKGAEAIYNRVKAAKKVPLDRMPYNLQYTVEVKN 102
                                                                                                                                                    QITYTDDEIQVAKLAGKYTTEDGYIFD.
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    EHV-LGKKDHSEDPNKNFKADE--EPVEETPAEPE---
                               GSLIIPSYDHYSNIKFEWFDEGLYEAPKGYSLEDLLATVKYYVE----PR----NAS
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Martin, Denis
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Pred. No. 4.6e-37;
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Pred. No. 4.6e-37;
9; Mismatches 73;
                                                                                                                                                                                                               Mismatches
                                                                                                                                                                                                                                           Length 272;
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   -VPQVETEKVEAQ 730
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RESULT 50
US-09-884-465A-345
; Sequence 345, Application US/09884465A
; Publication No. US20030077293A1
; GENERAL INFORMATION:
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SEQ ID NO 346
LENGTH: 895
TYPE: PRT
ORGANISM: Artificial Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches 138;
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NUMBER OF SEQ ID NOS: 384
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OTHER INFORMATION: Unknown Organism
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                                                                                                                                  PSSV 790
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Martin, Denis
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APPLICANT: Charland, Nathalie
APPLICANT: Ouellet, Catherine
TITLE OF INVENTION: Streptococcus Antigens
FILE REFERENCE: 055190-004
CURRENT APPLICATION NUMBER: US/09/884,465A
CURRENT FILLING DATE: 2001-06-20
CURRENT FILLING DATE: 60/212,683
PRIOR APPLICATION NUMBER: 60/212,683
                                                                                                                                                                             687 EHV-LGKKDHSEDPNKNFKADE--EPVEETPAEPE------
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                                                          LK----EAEVLLAKVTDSSLKANATETLAGLRNNLTLQIMDNNSIMAEAEKLLALLKGSN 786
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Pred. No. 2.8e-36;
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APPLICANT: Brodeur, Bernard
APPLICANT: Brodeur, Bernard
APPLICANT: Charland, Nathalie
APPLICANT: Ouellet, Catherine
FILE REFERENCE: 005119-0044
CURRENT APPLICATION: Streptcoccus Antigens
CURRENT APPLICATION NUMBER: US/09/884,465A
CURRENT FILING DATE: 2001-06-20
PRIOR APPLICATION NUMBER: 60/212,683
PRIOR FILING DATE: 2000-06-20
NUMBER OF SEQ ID NOS: 384
SOFTWARE: Patentin version 3.1
SEQ ID NO 345
LENGTH: 901
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
COTHER INFORMATION: Unknown Organism
US-09-884-465A-345
Search completed: November 14, 2003, 10:50:45 Job time : 343 secs
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APPLICANT: Hamel, Josee
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score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

## 54419 59 103534 9 168601 9 171569 9 187517 9 188084 9 212941 21397 75248 98050 154101 194474 203434 214633 2647 22166 22290 22359 2359 2359 2457 2457 2517 2639 11931 11931 11931 11931 11931 11931 349980 10256 349980 Length 10320 20035 702 1342 1342 1446 2528 DB SPNEU1901 SPNEU1901 AX571762 AF340223 AR219123 AX343073 AF340222 AR120270 BD063279 BD003774 AE007418 AX571763 AC136885 AC137536 AX608407 AX343078 AX568780 AF318956 AX343114 AX343116 AR120328 BD063337 BD004035 AR120406 BD063415 AR120405 BD063414 AX569137 AF318955 AX568778 SPNEU1915 SPNEU1929 AF340221 HSBA192P3 AF225898 AE003719. AC015298 ATT5E8 AC123445 AC007811 AL732478 AC115959 AR218960 BD003872 AX343070 AX343071 AR219011 BD003923 BT005616 AY089131 AX602204 SAG766854 AE007403 AE008464 ij AF318954 AR218862 BT004286 AE014279 AX343074 AX569139 BD063414 Streptoco AX343115 Sequence AX343115 Sequence AR120328 Sequence AR120328 Sequence AR120328 Sequence AX343070 Sequence AX343070 Sequence AX343070 Sequence AX343071 Sequence AX343071 Sequence AX343071 Sequence AX362204 Sequence BD003872 Polynucle AE014779 Streptoco AX602204 Sequence AL7166854 Streptoco AX137536 Sus scrof AC137536 Sus scrof AC137536 Sus scrof AC137536 Mouse DNA AC015559 Mus muscu BT004286 Arabidops AY089111 Arabidops BT004286 Arabidops AX343072 Sequence AX343073 Sequence AF340222 Synthetic AR120270 Sequence BD063379 Streptoco AR219011 Sequence BD003923 Polynucle AF318954 Streptoco AX569137 Sequence AF318955 Streptoco AX569778 Sequence AF318954 Streptoco AX568778 Sequence AX3437074 Sequence AX3437074 Sequence AX3437075 Sequence AX3437075 Sequence AX3437075 Sequence AX3437075 Sequence AX3437075 Sequence AX3437075 Sequence AX571762 Sequence AF219123 Sequence AF219123 Sequence AF219123 Sequence AF2191035 Polynucle AR219106 Sequence Description Drosophil Humar Sequence Polynucle Sequence Streptoco Sequence Streptoco Sequence Streptoco Streptoco Streptoco Drosophil Arabidops Polynucle Streptoco Streptoco Streptoco Human DNA Homo sapi Sequence Sequence Sequence Sequence

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| 0.8 75668<br>0.8 77405<br>0.8 79676<br>0.8 91803<br>0.8 101981<br>0.8 103476                   | .8 60683<br>.8 61957<br>.8 64722         | .8 50354<br>.8 52144                      | .8 30799            | .8 11617<br>.8 21414                           | .8 10618<br>.8 10825                           | .8 6487<br>.8 10579                           | .8 6114               | .8 5158<br>.8 5215                         | .8 3501             | .8 2478<br>.8 2478                           | .8 2469               | .8 2313             | .8 670<br>.8 1910                             | .8 406<br>.8 501                               | .9 302417<br>.9 349980                         | .9 258290<br>.9 291061                         | .9 236764                                    | .9 223266<br>.9 226427                         | .9 207698<br>.9 219687                         | .9 193433<br>.9 193547  | .9 188307<br>.9 191750   | .9 184365                | .9 180643             | .9 177385<br>.9 180629  | .9 168544                 | .9 156526           | 9 150972                                 | .9 148348             | .9 139357           | .9 129559<br>.9 133237                             | .9 70046              | .9 58408                  | .9 29183                 | .9 2065                  | .9 231485<br>.9 29  | . 9 221952                        |
| 8 AP006097<br>2 AL353634<br>8 AB013396<br>9 AC092318<br>9 AC0923001<br>2 AC027350              | AL35631<br>AL13592<br>AC10047<br>AC12541 | AE01416<br>AC10421                        | SPBC19C             | AX60216<br>AE01424                             | AE01011<br>AE00662                             | AE01142<br>AF1776                             | AB03995               | AX30090<br>BD13683                         | AF06253             | AB07385                                      | AX60752               | AB031552            |   | G50086<br>AX30089                              |  | AC09587<br>AC09916                             | AC11243<br>AC13077                           | AC10634  | AC11449<br>AC11957                             | AP00152<br>AC02456  | AC12008<br>BX53731       | HS109M1                  | AC11725               | AC01088<br>AC10407  | AL51330                   | AC01066             | AL51238                                  | AC10225               | AC01090             | AC00555  | AC12084               | BX51094                   | AC01415                  | SIVM70                   |   |                                   |
| AP006097 Lotus AL353634 Homo s AL353636 Arabid AB013396 Arabid AC092318 Homo s AC003001 Homo s | lum<br>lum                               | AE014169 Strep AC104213 Mus m             | AL109731 S.pon      | AX602163 Seque<br>AE014248 Stren               | AE010110 Strep                                 | AE011427 Leptc<br>AF177668 Mus                | AB039951 Bacil        | AX300905 Seque<br>BD136831 Group           | AF062533 Strej      | AB073859 Strep                               | AX607520 Seque        | AB031552 Bacil      | AX602072 Seque<br>AJ290952 Strep              | G50086 SHGC-8<br>AX300897 Seque                | eq (   | AC095878 Rattu<br>AC099169 Rattu               | AC112436 Rattı<br>AC130777 Rattı             | AC098602 Rattu<br>AC106341 Rattu               | AC114491 Homo<br>AC119573 Mus m                | iom<br>m  | et)<br>an                | lom                      | aui                   |   | u i                       | 7 2 7               | 7 7                                      | 7 2                   | . E                 | 7 7  | 97,0                  | an)                       | ř                        | mian                     | lattu<br>legue  | _<br>G _ G                        |
| us jap<br>o sapi<br>bidops<br>o sapi<br>o sapi   | an DNA<br>an DNA<br>muscu<br>o sapi      | necu                                      | pe c                | nce<br>nce                                     | otoco<br>otoco                                 | muscu   | lus                   | ence<br>B s                                | otoco               | otoco  | nce                   | lus                 | otoco   | 12980<br>Ince                                  | phil<br>nce                                    | s no   | tus no                                       | is no  | sapi.<br>Nscu                                  | sapi<br>sapi  | rer                      | sapi                     | เนยตน                 | sapi<br>sapi  | DNA                       | cosophil            | DNA                                      | sapi                  | sapi                | n DNA<br>sapi                                      | muscu                 | rer                       | hil                      | immu                     | $\sim$  | ttus no                           |
| jap jap RESULT 1 sapi AR120265 togs LOCUS Sapi ACCESSION ACCESSION                             | DNA<br>DNA<br>USCU                       | 199 toco c 199                            | 19                  | C 19   | C 19   | · 19  | C 19                  | 18   | 1 8 8               | C 18   | C 18                  |                     | C 18  | c 17   | 00   | C 17   | C 17   | C 17   | C 16   | sapi 16   | rer   c 16               | sapi 16                  | c 16                  | зарі с 15<br>16   | DNA C 15                  | 2 (                 | 2 15                                     | C 15                  | 155                 | DNA C 14   | 18Cu C 14             | rer C 14                  | il c 14                  | mmu 14                   | no 14   | s no                              |
| RESULT 1 AR120265 LOCUS DEFINITION ACCESSION   | DNA<br>DNA<br>USCU                       | c 19<br>20                                | 197                 | 195<br>C 196                                   | C 193  | c 191<br>· 192                                | c 190                 | 188<br>189                                 | 187                 | 185<br>C 186                                 | C 184                 | 182                 | c 180   | c 178<br>c 179                                 | c 176<br>c 177                                 | c 174<br>c 175                                 | 172<br>C 173                                 | c 170<br>c 171                                 | c 168  | 3api 166<br>3api c 167  | rer 165                  | 163                      | C 161                 | sapi c 159  | DNA C 158                 | 156                 | C 154                                    | c 153                 | 151                 | DNA C 149  | 18Cu C 148            | rer c 146                 | il c 145                 | mmu 143                  | no 141<br>e 142   | s no 140                          |
| RESULT 1 AR120265 LOCUS AR120265 DEFINITION Sequence 55 fro                                    | DNA DNA USCU                             | c 199 20 0.8 205667<br>200 20 0.8 2056624 | 197 20 0.8 203223   | 195 20 0.8 200602<br>C 196 20 0.8 200602       | c 193 20 0.8 197658<br>c 194 20 0.8 199050     | c 191 20 0.8 196491<br>.192 20 0.8 197658     | c 190 20 0.8 196107   | 188 20 0.8 194785<br>189 20 0.8 194907     | 187 20 0.8 194425   | 185 20 0.8 193057<br>C 186 20 0.8 193301     | C 184 20 0.8 192410   | 182 20 0.8 192096   | 180 20 0.8 191231<br>C 181 20 0.8 191553      | C 178 20 0.8 186165<br>C 179 20 0.8 189350     | C 176 20 0.8 182658<br>C 177 20 0.8 185845     | C 174 20 0.8 182446<br>C 175 20 0.8 182632     | 172 20 0.8 180571<br>C 173 20 0.8 181584     | C 170 20 0.8 177623<br>C 171 20 0.8 180450     | C 168 20 0.8 175838<br>C 169 20 0.8 177071     | sapi     166     20     0.8     171370       sapi     c     167     20     0.8     174325         | rer 165 20 0.8 170167    | 163 20 0.8 168842        | c 161 20 0.8 163709   | sapi         c         159         20         0.8         161279           3api         160         20         0.8         161311 | DNA C 158 20 0.8 157850   | 156 20 0.8 156724   | 154 20 0.8 151857<br>C 155 20 0.8 152806 | c 153 20 0.8 148592   | 151 20 0.8 147829   | DNA C 149 20 0.8 137586 gapi 150 20 0.8 144722     | c 148 20 0.8 137519   | rer C 146 20 0.8 133418   | il c 145 20 0.8 131316   | mmu 143 20 0.8 119995    | no 141 20 0.8 110000<br>e 142 20 0.8 110590                       | s no 140 20 0.8 110000            |
| RESULT 1 AR120265 LOCUS AR120265 DEFINITION Sequence 55 ACCESSION AR120265                     | DNA<br>DNA<br>Jacu                       | C 199 20 0.8 2<br>200 20 0.8 2            | 197 20 0.8 203223 2 | 195 20 0.8 200602 10<br>c 196 20 0.8 200602 10 | c 193 20 0.8 197658 2<br>c 194 20 0.8 199050 1 | c 191 20 0.8 196491 9<br>.192 20 0.8 197658 2 | c 190 20 0.8 196107 8 | 188 20 0.8 194785 2<br>189 20 0.8 194907 2 | 187 20 0.8 194425 5 | 185 20 0.8 193057 9<br>C 186 20 0.8 193301 9 | C 184 20 0.8 192410 2 | 182 20 0.8 192096 2 | 180 20 0.8 191231 10<br>C 181 20 0.8 191553 2 | C 178 20 0.8 186165 9<br>C 179 20 0.8 189350 2 | C 176 20 0.8 182658 2<br>C 177 20 0.8 185845 9 | C 174 20 0.8 182446 2<br>C 175 20 0.8 182632 9 | 172 20 0.8 180571 9<br>C 173 20 0.8 181584 2 | C 170 20 0.8 177623 2<br>C 171 20 0.8 180450 3 | C 168 20 0.8 175838 2<br>C 169 20 0.8 177071 2 | sapi     166     20     0.8     171370     9       sapi     c 167     20     0.8     174325     2 | rer 165 20 0.8 170167 10 | sapi 163 20 0.8 168842 5 | c 161 20 0.8 163709 2 | sapi         c 159         20         0.8 161279         2           160         20         0.8 161311         2                  | DNA c 158 20 0.8 157850 9 | 156 20 0.8 156724 2 | 154 20 0.8 151857 9                      | c 153 20 0.8 150192 2 | 151 20 0.8 147829 2 | DNA C 149 20 0.8 137586 9 3api 150 20 0.8 144722 9 | c 148 20 0.8 137519 8 | rer C 146 20 0.8 133418 9 | il c 145 20 0.8 131316 2 | mmu 143 20 0.8 119995 10 | no 141 20 0.8 110000 2 PFMAL7P1<br>e 142 20 0.8 110590 2 BX001021 | s no 140 20 0.8 110000 2 PFMAL7P1 |

| Qy   | Oy dy   | φ φ  | Db Qy  | Qy<br>db   | Qy   | Qу<br>Db   | g<br>S   | Qy<br>Db  | Qy<br>Db  | Qy<br>Db   | Db Qy  | B Q   | Qy<br>Db  | Query Match<br>Best Local Sim<br>Matches 2389;  | source<br>BASE COUNT<br>ORIGIN                                  | TITLE<br>JOURNAL<br>FEATURES   | REFERENCE<br>AUTHORS   | KEYWORDS<br>SOURCE<br>ORGANISM   |
|--|---|--|--|--|--|--|--|---|---|--|--|---|---|---|---|--|--|--|
| 781 AGCAAGTCAAAGTAATGACATTGATAGTCTCTTGAAACAGCTCTACAAACTGCCTTTGAG 840   | 721 TGTAAGCAATCCAGGAACTACAAATACTAACACAAGCAACAACAACACTAACAGTCA 780   | 661 TTCAAGAACCTATCGCCGACAAAATAGCGATAACACTTCAAGAACAAACTGGGTACCTTC 720   | 601 ATCAGCTAGCGAGTTGGCTGCTGCAGAAGCCTTCCTATCTGGTCGAGGAAATCTGTCAAA 660   | 541 TGGTGATGCTTATATCGTTCCTCATGGAGATCATTACCATTACATTCCTAAGAATGAGTT 600 | 481 AGGACGCTATACTACAGATGATGGTTATATCTTTAATGCTTCTGATATCATAGAGGATAC 540 | 421 TCAACATCGTGAAGGTGGAACTCCAAGAAACGATGGTGCTGTTGCCTTGGCACGTTCGCA 480 | 361 TGCCCACGCGGATAACGTCCGTACAAAAGAGGAAATCAATC                        | 301 GGTCAAGGGTGGATATGTTATCAAGGTAGATGGAAAATACTATGTTTACCTTAAGGATGC 360  | 241 TGAAGAATTACTCATGAAAGATCCAAACTATAAGCTAAAAGATGAGGATATTGTTAATGA 300  | 181 TTCACATGGCGACCACTATCATTATTACAATGGTAAGGTTCCTTATGACGCTATCATCAG 240   | 121 GCGTGAAGGAATCAATGCTGAGCAAATCGTCATCAAGATAACAGACCAAGGCTATGTCAC 180 | 61 TATAGATGGAAAACAAGCGACGCAAAAAACGGAGAATTTGACTCCTGATGAGGTTAGCAA 120       | 1 TTCTTACGAGTTGGGACTGTATCAAGCTAGAACGGTTAAGGAAAATAATCGTGTTTCCTA 60   | tch 100.0%; Score 2389; DB 6; Length 2389; al Similarity 100.0%; Pred. No. 0; 2389; Conservative 0; Mismatches 0; Indels 0; Gaps 0; | Ф   | rannon, M.K. and kosen, C.A. Streptococcus pneumoniae antigens and vaccines Patent: US 6159469-A 55 12-DEC-2000; Location/Qualifiers | Unclassified.  1 (bases I to 2389) Choi,G.H., Kunsch,C.A., Barash,S.C., Dillon,P.J., Dougherty,B., | Unknown.   |
|  |   |  |  | <del></del>  |  |  |  |   |   |  |  |   |   |   |   | ·  |  |  |
| B &  | B &   | 8 8 8  | ₽ ₽ \$   | S B 8  | g dg cy  | , B &  | gg QY  | B 8   | 9 dd 9  | g dd (y  | B &  | B 6   | \$ \$ &   | Db Qy   | dg dy   | dg dy  | Db Db  | & B  |
| 1861 TACAGTTGAGGTTAAAAACGGTAATTTGATTATTCCTCATAAGGATCATTACCATAATAT 1920 | 01 CAATCGTGTGAAAGGGGAAAAACGAATTCCACTCGTTCGACTTCCATATATGGTTGAGCA 1 01 CAATCGTGTGAAAGGGGAAAAACGAATTCCACTCGTTCGACTTCCATATATGGTTGAGCA 1 | 1 TOCATO TO CAMAN CHAMA TO TAMADO CAMAT COME TOGAT AND COME THE COME THE COME THE COME THE COME THE COME THE COME THE COME THE COME THE COME COME THE COME COME COME COME COME COME COME COM | 61 CCITICIGAL ANGGANANGI INCACICANNOCIA ITAC LANGORAMANGIAN CUCACA (CITICIGAL ANGGANANGI INCACICA (CITICIGAL) (CIT | 621 TGAAGGAGATGCATATGTAACGCCTCATATGGGCCATAGTCACTGGATTGGAAAAGATAG 1   | 61 AGCTGATAAGTATACAACGTCAGATGGTTACATTTTTGATGAACATGATATAATCAGTGA 16   | 01 ACTTGGCAAACCAAATTCTCAAATTGAGTATACTGAAGACGAACTTCGTATTGCTCAATT 15   | 1441 TAAKSAAAATTGGTAGATGATTATTGGCATTCCTAGCACCAATTACCCATCCKAAGCG 1500 | BI TAMITCIGATITCCANGCCITAGACAAATTATTAGAACGCTTGAATGATGAATCGACTAA  1 TAMITCTGATTTCCAAGCCTTAGACAAATTATTAGAACGCTTGAATGATGAATCGACTAA | 21 TGATAAAGCATATAATCTGTTAACTGAGGCTCATAAAGCCTTGTTTGNAAATAAGGGTCG 21 TGATAAAGCATATAATCTGTTAACTGAGGCTCATAAAGCCTTGTTTGNAAATAAGGGTCG 21 TGATAAAGCATATAATCTGTTAACTGAGGCTCATAAAGCCTTGTTTGNAAATAAGGGTCG | 61 TGTTTCACACACTTTAACTGCTAAAAAAGAAAATGTTGCTCCTCGTGACCAAGAATTTTA 61 TGTTTCACACACTTTAACTGCTAAAAAAAAAATGTTGCTCCTCGTGACCAAGAATTTTA | OI GAAKGATITACCATCTGAAACTGTTAAAAATCTTGAAAGCAAGGTTATCAAAACAAGAGAG 1   | 1 ACGANANGI I GGGGANGGAI AI GIAI I CGANGANGGGCAIC I CICGI I AI GICCI I GG | BI CCCGCAACCTGCACCAATCTTAAAATAGACTCAAATTCTTCTTTGGTTAGTCAGCTGGT BI CCCGCACCTGCACCAATCTTAAAATAGACTCAAATTCTTCTTTTGGTTAGTCAGCTGGT BI CCCGCACCTGCACCAATCTTAAAATAGACTCAAATTCTTCTTTGGTTAGTCAGCTGGT BI CCCGCAACCTGCACAATCTTAAAATAGACTAAAATTCTTCTTTTGGTTAGTCAGCTGGT A CCAAAAATAGACTAAAATAGACTAAAATTCTTCTTTTGGTTAGTCAGCTGGT | 21 GGTACCAGATTCAAGGCCAGAACAAGTCCACAACCGCTCGGAACCTAGTCCAGG CTACHHILLHIHLHIHLHIHLHIHLHIHLHIHLHIHLHIHLHI                               | 61 GTCTGAATTGGAAGAACGAATCGCTCGTATTATTCCCCTTCGTTATCGTTCAAACCATTG | 901 AGCTAGAGGTGTTGCAGTGCCACAGGAGATCATTACCACTTCATCCTTACTCTCAAAT 960   | TCAACGACATGTAGAATCTGATGGCCTTGTCTTTGATCCAGCACAAATCACAAGTCGAAC                                       | 781 AGCAAGTCAAAGTAATGACATTGATAGTCTCTTGAAACAGCTCTACAAACTGCCTTTGAG 840<br>841 TCAACGACATGTAGAATCTGATGGCCTTGTCTTTGATCCAGCACAAATCACAAGTCGAAC 900 |

| Query Match Best Local Similarity 100.0%; Score 2389; DB 6; Length 2389; Best Local Similarity 100.0%; Pred. No. 0; Matches 2389; Conservative 0; Mismatches 0; Indels 0; Gaps Qy 1 TTCTTACGAGTTGGGACTGTATCAAGCTAGAACGGTTAAGGAAAATAATCGTGTTTCCTA | Key Locati 123 /orgar /mol t /db xx /db xx  | PR 31-CC1-1997 US 60/029960  PR 31-CC1-1996 US 60/029960  PI CHARLES A KUNSCH,GIL H CHOI,SYDNOR L JOHNSON,ALEX HROMOCKYJ  C12N15/31,C12N5/18,C12N1/21,C07K14/315,C12Q1/68,A61K39/09, PC  G01N33/569,  PC G01N33/68  PC G1N33/68  CC Strandedness: Double;  CC Topology: Linear; | REFERENCE 1 (bases 1 to 2389)  AUTHORS Kunsch, C.A., Choi, G.H., Johnson, S.L. and Hromockyj, A.  TITLE Streptococcus pneumoniae antigens and vaccines  JOURNAL Patent: JP 2001505415-A 28 24-APR-2001;  HUMAN GENOME SCIENCES INC  COMMENT PN JP 2001505415-A/28  PD 24-APR-2001 | BD063274 LOCUS LOCUS BD063274  DEFINITION Streptcoccus pneumoniae antigens and vaccines. ACCESSION BD063274 VERSION BD063274.1 GI:22608877 VERSION BD063274.1 GI:22608877 VERSION BD063274.1 GI:22608877 VERSION BD063274.1 GI:22608877 VERSION BD063274.1 GI:22608877 VERSION BD063274.1 GI:22608877 VERSION BD063274.1 GI:22608877 VERSION BD063274.1 GI:22608877 VERSION BD063274.1 GI:22608877 VERSION BD063274.1 GI:22608877 VERSION BD063274.1 GI:22608877 VERSION BD063274.1 GI:22608877 VERSION BD063274.1 GI:22608877 VERSION BD063274 Unidentified | Qy 2341 GTTGTTAAAAGGAAGTAATCCTTCATCTGTAAGGAAAAAAATAAAC 2389  | 2221 AGTAA<br>     <br>2221 AGTAA<br>2281 TTTGA                | 2101<br>2161<br>2161          | 2041<br>2041<br>2041<br>2101   |  |
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AF291695.1 GI:13345012
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Use of a whole genome approach to identify vaccine molecules affording protection against Streptococcus pneumoniae infection Infect. Immun. 69 (3), 1593-1598 (2001)
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TNSQASQSNDIDSLLKQLYKLPLSQHHVESGGLVFDPAQITSRTARGRAVPHGHYHY
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| 131 TRATANAGCATATAACTGTTAACTGAGACAATGTTGCTCCTCGTGACCAACAATTTTAACTGTTAACTGAGACATTTTAACTGATAAACGCTTGATAAAACCAAGAATTTTAACTGATAAACGCTTGATAAAACCAAGAATTTTAACTGAGGTCGATAAAACCCTTGATTGA | 1021 GGTACCAGATTCAAGGCCAGAACCAAGTCCACAACCGACTCCGGAACCTAGTCCAGG  |

| 318 GGTCAAGGGTGGATATGTTATCAAGGTAGATGGAAAATACTATGTTTACCTTAAGGATGC |   | OY 181 TTCACATGGCGACCACTATCATTATTACAATGGTAAGGTTCCTTATGACGCTATCATCAG   | Qy 121 GCGTGAAGGAATCAATGCTGAGCAAATCGTCAATCAAGATAACAGACCAAGGCTATGTCAC | 1 TATAGATGGAAAACAAGCGACGCAAAAAAACGGAGAATTTGACTCCTGATGAGGTTAGCAA  | TACGAGTTGGGACTGTATCAAGCTAGAACGGTTAAGGAAAATAATCGTGTT<br>                | Query Match 97.9%; Score 2338; DB 6; Length 2406;<br>Best Local Similarity 100.0%; Pred. No. 0;<br>Matches 2388; Conservative 0; Mismatches 1; Indels 0; Gaps |   | Chiron  | REFERENCE 1 AUTHORS Masignani, V., Tettelin, H. and Fraser, C. TITLE Streptococcus pneumoniae proteins and nucleic acids JOURNAL Patent: WO 02077021-A 2347 03-OCT-2002; | SOURCE Streptococcus pneumoniae ORGANISM Streptococcus pneumoniae Bacteria; Firmicutes; Lactobacillales; Streptococcaceae; Streptococcus | ITION Sequence 2347 from Patent W002077021.<br>SION AX569139<br>ON AX569139.1 GI:26002636<br>RDS |  | Qy 2341 GTTGTTAAAAGGAAGTAATCCTTCATCTGTAAGTAAGGAAAAATAAAC 2389             | Qy 2281 TTTGACTCTTCAAATTATGGATAACAATAGTATCATGGCAGAAGCAGAAAAATTACTTGC | Qy 2221 AGTAACGGATTCTAGTCTGAAAGCCAATGCAACAGAAACTCTAGCTGGTTTACGAAATAA | Qy 2161 TCAAGTAGAGACTGAAAAGTAGAAGCCCAACTCAAAGAAGCAGAAGTTTTGCTTGC     | Qy 2101 TAAGAACTTCAAAGCGGATGAAGACCAGTAGAGGAAACACCTGCTGAGCCAGAAGTCCC |
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| 377 Db   | 300 Db<br>317 Oy<br>360 Oy                              | 240 Db<br>257 Ov  | 180 Oy<br>197 Db   | 120 Qy<br>137 Db   | Oy Oy Db   | Qy<br>Db  | Qy<br>da  | Оу  | Qy<br>db   | . Db   | Db Qy  | one Db   | Qy  | 2340 Qy<br>2489 Db   | 2280. Qy<br>2429 Db  | 2320 Qy<br>2369 Db   | 2160 Qy<br>2309 Db  |
| 1398 TAATTCTGATTTCCAAGCCTTAGACACAAATTATTAGAACGCTTGAATGAA         | 38 TAATTCTGATTTCCAAGCCTTAGACAAATTATTATTAGAACGCTTGAATGAA | 1321 TGATATAAAGACTITAACTGCTAAAAAAGAAAATGITCCTCCTCGTGACCAAGAATTTTA 1337 1278 TGATATAAGCACTATAACTGCTAAAAAAAGAAATGTTGCTCCTCGTGACCAAGAATTTTA 1337 | GAAGATTTACCATCTGAAACTGTTAAAAATCTTGAAAGCTATGTTATCAAAACAAGGAG          | 141 ACGAAAAGTTGGGGAAGGATATGTATTCGAAGAAAAGGGCATCTCTCGTTATGTCTTTGC | 1081 CCCGCAACCTGCACCAAATCTTAAAATAGACTCAAATTCTTCTTTGGTTAGTCAGCTGGT 1140 | 1021 GGTACCAGATTCAAGGCCAGAACCAAGTCCACAACCGACTCCGGAACCTAGTCCAGG 1080<br>   | 61 GTCTGAATTGGAAGAACGAATCGCTCGTATTATTCCCCTTCGTTATCGTTCAAACCATTG 1<br> | 901 AGCTAGAGGTGTTGCAGTGCCACACGGAGATCATTACCACTTCATCCCTTACTCCAAAT 960<br> | 841 TCAACGACATGTAGAATCTGATGGCCTTGTCTTTGATCCAGCACAAATCACAAGTCGAAC 900   | 781 AGCAAGTCAAAGTAATGACATTGATAGTCTCTTGAAACAGCTCTACAAACTGCCTTTGAG 840<br>   | 721 TGTAAGCAATCCAGGAACTACAAATACTAACACAAGCAACAACAGCAACACTAACAGTCA 780<br>                         | 661 TTCAAGAACCTATCGCCGACAAAATAGCGATAACACTTCAAGAACAAACTGGGTACCTTC 720<br> | 601 ATCAGCTAGCGAGTTGGCTGCTGCAGAAAGCCTTCCTATCTGGTCGAGGAAATCTGTCAAA 660<br> | 541 TGGTGATGCTTATATCGTTCCTCATGGAGATCATTACCATTACATTCCTAAGAATGAGTT 600 | 481 AGGACGCTATACTACAGATGATGGTTATATCTTTAATGCTTCTGATATCATAGAGGATAC 540 | 421 TCAACATCGTGAAGGTGGAACTCCAAGAAACGATGGTGCTGTTGGCTTGGCACGTTCGCA 480 | 361 TGCCCACGCGGATAACGTCCGTACAAAGAGGAAATCAATC                        |

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1 (bases 1 to 8195)

Kunsch,-C.A., Choi,G.H., Dillon,P.S., Rose Fannon,M.R. and Dougherty,B.A.
Streptococcus pneumoniae polymucleotides
Patent: US 6420135-A 94 16-JUL-2002;
Location/Qualifiers
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Fannon,M. and Dougherty,B.A.
Polynucleotide of Streptococcus pneumoniae and seque
Patent: JP 200115101833-A 94 13-FEB-2001;
HUMAN GENOME SCIENCES INC
OS Unidentified
PN JP 2001501833-A/94
PD 13-FEB-2001
PF 30-OCT-1997 JP 1998520718
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CC Stran
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I MICHAEL FANNON, BRIAN A DOUGHERTY

C C11N15/09, A01K67/027, C07K14/315, C07K16/12, C12N1/15, C12N1/19,
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30-OCT-1997 JF 1998520718
31-OCT-1996 US 60/029960
CHARLES A KUNSCH,GIL H CHOI,PATRICK J
                                                                                                                                                                                                        Strandedness: Double;
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C12N5/10,C12P21/02,C12Q1/68,G06F17/30,C12N15/00,C12N5/00,
                                                                                                                                                                                       Topology: Linear;
                                              рJ
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/mol_type="genomic DNA"
/db_xref="taxon:32644"
1 1622 c 1777 g 210
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| 1021 GGTACCAGATTCAAGGCCAGAACAACCAAGTCCACAACCGACTCCGGAACCTAGTCCAGG 1080   | 961 GTCTGAATTGGAAGAACGAATCGCTCGTATTATTCCCCTTCGTTATCGTTCAAACCATTG 1020 | 901 AGCTAGAGGTGTTGCAGTGCCACACGGAGATCATTACCACTTCATCCCTTACTCTCAAAT 960<br>            | 841 TCAACGACATGTAGAATCTGATGGCCTTGTCTTTGATCCAGCACAAATCACAAGTCGAAC 900 | 781 AGCAAGTCAAAGTAATGACATTGATAGTCTCTTGAAACAGCTCTACAAACTGCCTTTGAG 840<br> | 721 TGTAAGCAATCCAGGAACTACAAATACTAACACAAGCAACAAGAGCAACACTAACAGTCA 780<br> | 661 TTCAAGAACCTATCGCCGACAAATAGCGATAACACTTCAAGAACAAACTGGGTACCTTC 720 | 601 ATCAGCTAGCGAGTTGGCTGCAGAAGCCTTCCTATCTGGTCGAGGAAATCTGTCAAA 660 | 541 TGGTGATGCTTATATCGTTCCTCATGGAGATCATTACCATTACATTCCTAAGAATGAGTT 600 | 481 AGGACGCTATACTACAGATGATGATTATATCTTTAATGCTTCTGATATCATAGAGGATAC 540   | 421 TCAACATCGTGAAGGTGGAACTCCAAGAAACGATGGTGCTGTTGCCTTTGGCACGTTCGCA 480  | 361 TGCCCACGCGGATAACGTCCGTACAAAAGAGGAAATCAATC                     | 301 GGTCAAGGGTGGATATGTTATCAAGGTAGATGGAAAATACTATGTTTACCTTAAGGATGC 360<br> | 241 TGAAGAATTACTCATGAAAGATCCAAACTATAAGCTAAAAGATGAGGGATATTGTTAATGA 300<br> | 181 TTCACATGGCGACCACTATCATTACTACAATGGTAAGGTTCCTTATGACGCTATCATCAG 240   | 121 GCGTGAAGGAATCAATGCTGAGCAAATCGTCATCAAGATAACAGACCAAGGCTATGTCAC 180 | 61 TATAGATGGAAAACAAGCGACGCAAAAAAACGGAGAATTTGACTCCTGATGAGGTTAGCAA 120<br> | GTTGGGACTGTATCAAGCTAGAACGGTTAAGGAAAATAATCGTGTTTCCTA 60<br>             | Best Local Similarity 100.0%; Pred. No. 0;<br>Matches 2388; Conservative 0; Mismatches 1; Indels 0; Gaps 0; |
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| g dg   | B &   | S B &   | S B &  | Db Qy  | g 4g   | S & &   | D Qy  | B &  | S B &  | S & &  | 2 B 5   | S B &  | S & &   | S B &  | 요 명 :  | o B 7  | o da Q   | Db  |
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| к з  | Umayam, I.A., White,O., Lewis,M.R., Radune,D., Holtzapple,E., Khouri,H., Wolf,A.M., Utterback,T.R., Hansen,C.L., McDonald,L.A. Feldblyum,T.V., Angiuoli,S., Gesuwan,P., Hickey,E.K., Holt,I.E., Loftus,B.J., Uywal,M.L., Yang,F., Smith,H.O., Venter,J.C., Dougherty,B.A., Morrison,D.A., Hollingshead,S.K. and Fraser,C.M. JOURNAL Submitseion JOURNAL Submitted (29-JUN-2001) The Institute for Genomic Research, 9712 Medical Center Dr, Rockville, MD 20850, USA FEATURES Location/Qualifiers source Jorganisms—"Strentcooccus pneumoniae TIGRA" | Venter, J.C., Dougherty, B.A., Morrison, I Fraser, C.M.  TITLE Complete genome sequence of a virulent pneumoniae Science 293 (5529), 498-506 (2001) MEDLINE 21357209 PUBMED 21357209 PUBMED 11463916 REFERENCE 2 (bases 1 to 10256) REFERENCE 2 (bases 1 to 10256) RETERENCE 3 (bases 1 to 10256) RETERENCE 2 (bases 1 to 10256) RETERENCE 3 (bases 1 to 10256) RETERENCE 3 (bases 1 to 10256) RETERENCE 4 (bases 1 to 10256) RETERENCE 5 (bases 1 to 10256) RETERENCE 7 (bases 1 to 10256) | SURCE Streptococcus pneumoniae TIGR4 ORGANISM Streptococcus pneumoniae TIGR4 Bacteria; Firmicutes; Lactobacillales; Streptococcaceae; Streptococcus. REFERENCE 1 (bases 1 to 10256) AUTHORS Tettelin, H., Nelson, K.E., Paulsen, I.T., Eisen, J.A., Read, T. Peterson, S., Heidelberg, J., DeBoy, R.T., Haft, D.H., Dodson, F. Durkin, A.S., Gwinn, M., Kolonay, J.F., Nelson, W.C., Peterson, Umayam, L.A., White, O., Salzberg, S.L., Lewis, M.R., Radune, D. Holtzapple, E., Khouri, H., Wolf, A.M., Utterback, T.R., Hansen McDonald, L.A., Feldblyum, T.V., Angluoll, S., Dickinson, T., Hickey, E.K., Holt, I.E., Leftus, B.J., Yang, F., Smith, H.O. | 5393 7 7 18/c AAE TION St TION AAE N AAE DS  | Oy 2161 TCAAGTAGAAGCTGAAAAAGTAGAAGCCCAACTCAAAGAAGCAGAAGTTTTGCTTGC  |
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| putat  | Radune_D., Holtrapple_E., R., Hansen,C.L., McDonald,L.A., R., Hansen,C.L., McDonald,L.A., an,P., Hickey,E.K., Holt,I.E., Smith,H.O., Venter,J.C., lingshead,S.K. and Fraser,C.M. ute for Genomic Research, 9712 0850, USA  | isolate of Streptococcus  Eisen,J.A., Read,T.D., Haft,D.H., Dodson,R.J.,  | Streptococcaceae;  Eisen,J.A., Read,T.D.,  Haft,D.H., Dodson,R.J.,  Ilson,W.C., Peterson,J.D.,  Lewis,M.R., Radune,D.,  terback,T.R., Hansen,C.L.,  terback,T.R., Hansen,C.L.,  Dickinson,T.,  ng.F., Smith,H.O.  | <br> GAAAAATAAAC 5441<br>  | GAAGCAGAAGITTTGCTTGCGAA 2220   |
| gene<br>CDS  |  | gene<br>CDS   | gene<br>CDS   | gene<br>CDS  | gene<br>CDS  |
| LRELYAKPLSERHVESDGLIF ERIGUSAR STRAMUPDSR PEEF FEENGVSRY1FAKDLSAETAA LARIHODLLDNKGRQVDFEAL LARIHODLLDNKGRQVDFEAL LARIHODLLDNKGRGLTPPST TVEVKNGSLIIFHYDHYHNIK TVEVKNGSLIIFHYDHYHNIK EPEESPEESEEEQVETEKVE QDNNTIMAEAEKLLALLKEK QDNNTIMAEAEKLLALLKES Complement (5346775 /gene="Sp1175" complement (5346775 | similarity; putative similarity; putative /codon_start=1 /transl_table=11 /transl_table=11 /product="conserved c /protein_id="AAK75283 /db_xref="GI:14972659 /translation="MKINKKY DQAGQKAENLTPDEVSKREGJ ELLMKDPNYQLKDSDIVNEIF SHNHNSRADNAVAARAQGRV SASRI_AABAEAVMGKYGGSDS   | T="CONSETVE n id="AAK75 f="G:"14972 f="G:"14972 ation="MES3] RVVSENPADTI LSVIQTQLAEI LSVIQTQLAEI LSVIQTQ1729. SP1174" ent (2729.  | /transl_table=11 /product="hypothetica /product="hypothetica /protein_id="AAK75281 /protein_id="AAK75281 /db_xref="G:14972652 /translation="MLYAVPF complement(1933230 /gene="SP1173" complement(1933230 /gene="SP1173" /gene="SP1173" /gene="SP1173" /codon_start=1 /transl_table=11   | /db_xref="G1:14972651 /translation="MFYKFLL VPMNKALWKDLELKKISKQBL GAHDLLDSLIERDYNLYAATN YEKIGQQIAGFSKEKTLMIGE SYQDLLDCLDKNILEKITF" complement (1724 184 /gene="SP1172" /gene="SP1172" /gene="SP1172" /gene="identified by /codon_start=1 | /translation="MSEVDFN TWKSPSLVKEGDYIGRRDSQV DIYLDHVAKYAYEQKVNNIKE VSKETPFSEMDERMFKNISEK Complement (760 . 1473 Gene="SP1171" complement (760 . 1473 /gene="Sp1171" /note="identified by PF00702" /transl_table=11 /product="hydrolase, /protein id="AAK75280 |

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INKYLAGSVAVLALSVCSYELGRYQAGODKKESNRVAYIDG
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VNEIKGGYVIKVNGKYYVYLKDAAHDNIRTKEEIKRÖKOE
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TEKVEEKLREAEDLLGKIQDPIIKSNAKETLITGLKNNLLFGT
TEKVEEKLREAEDLLGKIQDPIIKSNAKETLITGLKNNLLFGT
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TNGITTAIQTGRLAQSGLAFYFNQVFISEOLOTQKFDALF
GDSLTADIQGGNNAGIDTIWYNPHHLENHTQAQPTYEVY
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KBYYPLRRAILHQBNALFRFFSNFDDFLEKNYLKTIWQ
EKIIFERGSKMLNDLKSNYKK"
                                                                                                                                                                                                                                                                                                                                                                                                                                        domain protein"
83.1"
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BASE COUNT
ORIGIN
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Best Local Similarity
Matches 2388; Conserv
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                                                GCGTGAAGGAATCAATGCTGAGCAAATCGTCATCAAGATAACAGACCAAGGCTATGTCAC 180
                                                                                                                               TATAGATGGAAAACAAGCGACGCAAAAAAACGGAGAATTTGACTCCTGATGAGGTTAGCAA
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IAHDLTPSDTAQLDKNEVKAFTUNIGGRAADIRDVTKRVLALLKDAQTVTADGKHFELAAN
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8 2089 c 1850 g 3475 t
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complement (9788.
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HSNDGWGNAS EHVLGKKDHSEDPNKNFKA DEE PVEETPA EPEVPQVETEKVEA QLKEA
EVLLAKVTDSSLKANATETLAGLRNNLTLQIMDNNS IMA EA EKLLALLKGSNPSSVSK
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complement (8049.
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similarity; putative"
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  TGTTTCACACACTTTAACTGCTAAAAAAGAAAATGTTGCTCCTCGTGACCAAGAATTTTA 1320
                                                                                  GAAAGATTTACCATCTGAAAACTGTTAAAAATCTTGAAAAGCAAGTTATCAAAAACAAGAGAG 1260
                                                                                                                                                ACGAAAAGTTGGGGAAGGATATGTATTCGAAGAAAAGGGCATCTCTCGTTATGTCTTTGC 1200
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| ξ Q                        | 1 GTTGTTAAAAGGAA   | 234                      |
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| . אַנ<br>אַנ               | 1 TITGACICTTCAAATTAIGGATAACAATAGTAICATGGCAGAAGCAGAAAAATTACTIGC 2340<br>  | 228<br>545               |
| S B S                      | 1 AGTAACGGATTCTAGTCTGAAAGCCAATGCAACAGAAACTCTAGCTGGTTTACGAAATJ            |                          |
| ? B Q                      | I TCAAGTAGAGACTGAAAAAGTAGAAGCCCAACTCAAAGAAGCAGAAGTTTTGCTTGC              | 2161<br>5577             |
| S B S                      | 11 TAAGAACTTCAAAGCGGATGAAGAGCCAGTAGAGGAAACACCTGCTGAGCCAGAAGTCCC 2160<br> | 210:<br>563 <sup>-</sup> |
| S B &                      | 11 TGGATGGGGCAATGCCAGTGAGCATGTGTTAGGCAAGAAGACCACAGTGAAGATCCAAA 2100<br>  | 569                      |
| S B &                      |  | 1981<br>5757             |
| 5 g 5                      | 1 TAAATTTGCTTGGTTTGATGATCACACATACAAAGCTCCAAATGGCTATACCTTGGAAGA 1980<br>  | 1921<br>5817             |
| S B &                      | 1 TACAGTIGAGGITAAAAACGGTAAITTGAITATTCCTCATAAGGAICAITACCAIAATAI 1920<br>  | 1861<br>5877             |
| Best<br>Matc               | 1 CAATCGTGTGAAAGGGAAAAACGAATTCCACTCGTTCGACTTCCATATATGGTTGAGCA 1860<br>   | 1801<br>5937             |
| BASE<br>ORIG               | 11 TCCATCTCCAGACGCAGATGTTAAAGCAAATCCAACTGGAGATAGTGCAGCTAGTTTA 1800<br>   | 74                       |
|                            | 11 CCTTTCTGATAAGGAAAAGTTGCAGCTCAAGCCTATACTAAAGAAAAAGGTATCCTACC 1740<br>  | 168:                     |
|                            | 1  | 162:<br>611:             |
| т<br>н                     | 31 AGCTGATAAGTATACAACGTCAGATGGTTACATTTTTGATGAACATGATATAATCAGTGA 1620<br> | 156:<br>617:             |
| AUTH<br>TITI<br>JOUR       | 1 ACTTGGCAAACCAAATTCTCAAATTGAGTATACTGAAGACGAAGTTCGTATTGCTCAATT 1560<br>  | 150:<br>623:             |
|                            | 1 TAAAGAAAAATTGGTAGATGATTTATTGGCATTCCTAGCACCAATTACCCATCCAGAGCG 1500<br>  | 144:<br>629:             |
| ACCESS<br>VERSIC<br>KEYWOR | 1  | 138:<br>635:             |
| T & R                      | 11 TGATAAAGCATATAATCTGTTAACTGAGGCTCATAAAGCCTTGTTTGNAAATAAGGGTCG 1380<br> | 132:                     |
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Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Masignani, V., Tettelin, H. and Fraser, C. Streptococcus pneumoniae proteins and nucleic acids Patent: WO 02077021-A 4982 03-0CT-2002; Chiron Spa (IT); THE INSTITUTE FOR GENOMIC RESEARCH
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                                                  TCAACATCGTGAAGGTGGAACTCCAAGAAACGATGGTGCTGTTGCCATTCGCACGTTCGCA
                                                                                                                                                     GGTCAAGGGTGGATATGTTATCAAGGTAGATGGAAAATACTATGTTTACCTTAAGGATGC
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AGGACGCTATACTACAGATGATGGTTATATCTTTAATGCTTCTGATATCATAGAGGATAC
                                                                              TCAACATCGTGAAGGTGGAACTCCCAAGAAACGATGGTGCTTTGCCTTTGGCACGTTCGCA
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//db xref="taxon:1313"
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/note="seq 4979 too long: 2.162.598 bases~replaced by
/note="seq 4979 too long: 2.162.598 bases~replaced by
following seq:-seq 4979: from 0.000.001 to 0.349.980-seq
4980: from 0.300.001 to 0.649.980-seq 4981: from 0.600.001
to 0.949.980-seq 4982: from 0.900.001 to 1.249.980-seq
4983: from 1.200.001 to 1.549.980-seq 4984: from 1.500.001
to 1.849.980-seq 4985: from 1.800.001 to 2.149.980-seq
4986: from 2.100.001 to 2.162.598"
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| Norris, F.H., O'Gara, M., Pee<br>Sun, PM., Winkler, M.E., Ya  | 105390 AGCTGATAAGTATACAACGTCAGATGGTTACATTTTTGATGAACATGATATAATCAGTGA 105331   | 망     |
|---|--|-------|
| Gilmour, K., Giass, J.S., Kic<br>LeeBlanc, D.J., Lee, L.N., Lef<br>McAhren, S., McHennev, M., Mc    | 1561 AGCTGATAAGTATACAACGTCAGATGGTTACATTTTTGATGAACATGATATAATCAGTGA 1620       | Qy .  |
| REFERENCE 1 (bases 1 to 10320) AUTHORS Hoskins, J.A., Alborn, W. Jr. DeHoff, B.S., Estrem, S., Fri  | 1501 ACTTGGCAAACCAAATTCTCAAATTGAGTATACTGAAGACGAAGTTCGTATTGCTCAATT 1560       | g Qy  |
| SOURCE Streptococcus pneumoniae Re ORGANISM Streptococcus pneumoniae Re Bacteria; Firmicutes; Lacto | 1441 TAAAGAAAATTGGTAGATGATTTATTGGCATTCCTAGCACCAATTACCCATCCAGAGCG 1500        | D Q   |
|   | 1381 TAATTCTGATTTCCAAGCCTTAGACAAATTATTAGAACGCTTGAATGATGAATCGACTAA 1440       | ° ₽ & |
| RESULT 9 AE008479/c AE008479 LOCUS DEFINITION Streptococcus pneumoniae Ré                           | 1321 TGATAAAGCATATAATCTGTTAACTGAGGCTCATAAAGCCTTGTTTGNAAATAAGGGTCG 1380       | D Qy  |
| Db 104610 GTTGTTAAAAGGAAGTAATCCTTC  | 1261 TGTTTCACACACTTTAACTGCTAAAAAAAGAAAATGTTGCTCCTCGTGACCAAGAAATTTTA 1320<br> | Qу    |
| 104670  | 1201 GAAAGATTTACCATCTGAAACTGTTAAAAATCTTGAAAGCAAGTTATCAAAACAAGAGAG 1260<br>   | D Q   |
| 104730  | 1141 ACGAAAAGTTGGGGAAGGATATGTATTCGAAGAAAAGGGCATCTCTCGTTATGTCTTTGC 1200       | B 8   |
| 104790  | 1081 CCCGCAACCTGCACCAAATCTTAAAATAGACTCAAATTCTTCTTTGGTTAGTCAGCTGGT 1140       | d dd  |
| 104850  | 1021 GGTACCAGATTCAAGGCCAGAACAACCAAGTCCACAACCGACTCCGGAACCTAGTCCAGG 1080       | Db Qy |
| 104910  | 961 GTCTGAATTGGAAGAACGAATCGCTCGTATTATTCCCCTTCGTTATCGTTCAAACCATTG 1020        | 9g 9g |
| 104970  | 901 AGCTAGAGGTGTTGCAGTGCCACACGGAGATCATTACCACTTCATCCCTTACTCTCAAAT 960<br>     | 용왕    |
| 1.05030   | 841 TCAACGACATGTAGAATCTGATGGCCTTGTCTTTGATCCAGCACAAATCACAAGTCGAAC 900         | 당 왕   |
| 105090  | 781 AGCAAGTCAAAGTAATGACATTGATAGTCTCTTGAAACAGCTCTACAAACTGCCTTTGAG 840         | g Q   |
| 105150  | 721 TGTAAGCAATCCAGGAACTACAAATACTAACACAAGCAACAGCAACAGCAACACTAACAGTCA 780      | B 8   |
|   | 661 TTCAAGAACCTATCGCCGACAAAATAGCGATAACACTTCAAGAACAGAACTGGGTACCTTC 720        | g &   |
| 105270  | 601 ATCAGCTAGCGAGTTGGCTGCTGCAGAAGCCTTCCTATCTGGTCGAGGAAATCTGTCAAA 660<br>     | gg Qg |
| 1621  | 541 TGGTGATGCTTATATCGTTCCTCATGGÁGAFCATTACCATTACATTCCTAAGAATGAGTT 600         | g Q   |
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AGCCAGTAGAGGAAACACCTGCTGAGCCCAGAAGTCCC 2160
                                                                                                                                                                                                                                                                                                        ATGTGTTAGGCAAGAAAGACCACAGTGAAGATCCAAA 2100
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ATTTGATTATTCCTCATAAGGATCATTACCATAATAT 105031
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AGCCAGTAGAGGAAACACCTGCTGAGCCAGAAGTCCC
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Streptococcus pneumoniae R6 section 95 of 184 of the complete

genome.

AEOOB479 AEOO7317

LENOMA79.1 GI:15458677

RESION

AEOOB479.1 GI:15458677

AEOOBA79.1 GI:15458677

Streptococcus pneumoniae R6

Bucteria; Firmicutes; Lactobacillales; Streptococcaceae;

Breptococcus.

1 (bases 1 to 10320)

HOKins,J.A., Alborn,W.Jr., Arnold,J., Blaszczak,L., Burgett,S.,

Gilmour,R., Glass,J.S., Khoja,H., Kraft,A., LaGace,R.,

LeBlanc,D.J., Lee,L.N., Lefkowitz,E.J., Lu.J., Matsushima,P.,

McAhren,S., FH., O'Gara,M., Peery,R., Robettson,G.T., Rockey,P.,

Sun,P.-M., Winkler,M.E., Yang,Y., Young-Bellido,M., Zhao,G.,

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PUBMED
REFERENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Genome of the bacterium Streptococcus pneumoniae strain R6 J. Bacteriol. 183 (19), 5709-5717 (2001)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /translation="mfykfllfdldhtlldfdaaedvaltqllkeegvadiqaykdyy
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                                                                                   'gene="spr1059"
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transl_table=
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transī_table=11
label=spr1059
                                                                                                                                                                                                                         cranslation="MNLKMVTDFSDKSIIINRVPIVEGAYNAAALLQAGAELSVIQTQ
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aGace,R.,
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GDSAAAIYNRVKGEKRIPLVRLPYMVEHTVEVKNGNLIIPHKDHYHNIKFAWFDDHTY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AKQBSLISHKLGAKKTDLPSSDREFYNKAYDLLARIHQDLLDNKGRQVDFEALDNLLER
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NTEAKGAEAIYNRVKAAKKVPLDRMPYNLQYTVEVKNGSLIIPHYDHYHNIKFEWFDE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GLYEAPKGYSLEDLLATVKYYVEHPNERPHSDNGFGNASDHVQRNKNGQADTNQTEKP
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                                                                                                                                                                                                                                                                             complement (8122.
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complement(2725.
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EC_number="
                                                                                                                                                                                                                                                'gene="ptsI"
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transl_table=11
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                                                                                                                                        number="2.7.3.9"
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lement(2725. .5292)
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Microb. I
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2 (bases 1 to 20035)
Dopazo, J., Mendoza, A., Herrero, J., Caldara, F., Polissi, A.,
Humbert, Y., Friedli, L., Guerrier, M., Grand-Schenk, E., Gandin, C.,
Francesco, M., Buell, G., Feger, G., Garcia, E., Peitsch, M. and
                                                                                and Garcia-Bustos, J.F.
Annotated draft genomic sequence from a Streptococcus
type 19F clinical isolate
Microb. Drug Resist. 7 (2), 99-125 (2001)
                                                                                                                                                                                                            Streptococcus pneumoniae
Streptococcus pneumoniae
Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
                                                                                                                                                                                                                                                          SPNEU1915
Streptcocccus pneumoniae clone (
AL449937
AL449937.1 GI:11545162
HTG: HTGS_PHASE2.
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Direct Submission
Submitted (31-OCT-2000) Research Department, Gl
Severo Ochoa 2, 28760 Tres Cantos, SPAIN
* NOTE: This is a 'working draft' sequence.
* This sequence will be replaced
* by the finished sequence as soon as it is ava
* the accession number will be preserved.

Location/Qualifiers
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/db_xref="taxon:1313"
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 Annotated draft genomic sequence from a Streptococcus pneumoniae type 19F clinical isolate Microb. Drug Resist. 7 (2), 99-125 (2001)
                                           Dopazo, J., Mendoza, A., Herrero, J., Caldara, F., Humber Friedll, L., Guerrier, M., Grand-Schenk, E., Gandin, C., Francesco, M., Polissi, A., Buell, G., Feger, G., Garcia, and Garcia, Bustos, J.F.
                                                                                                                               Streptococcus pneumoniae
Streptococcus pneumoniae
Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
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2D 11442348
CE 2 (bases 1 to 702)
CE 2 (bases 1 to 702)
RS Dopazo, J., Mendoza, A., Herrero, J., Caldara, F., Polissi, A., Humbert, Y., Friedli, L., Guerrier, M., Grand-Schenk, E., Gandin, (Francesco, M., Buell, G., Feger, G., Garcia, E., Peitsch, M. and Garcia-Bustos, J.F.
Direct Submission
Submitted (31-OCT-2000) Research Department, Glaxo Wellcome, Severo Ochoa 2, 28760 Tres Cantos, SPAIN
* NOTE: This is a 'working draft' sequence.
* This sequence will be replaced
* by the finished sequence as soon as it is available and
* the accession number will be preserved.
* the accession number will be preserved.
* Location/Qualifiers
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/mol_type="genomic DNA"
/serotype="19F"
/db_xref="taxon:1313"
/clone="G54"
a 144 c 147 g 176
   pneumoniae
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99.1%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Green, B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                protein from Streptococcus pneumoniae, protects mice intranasal pneumococcal challenge Infect. Immun. 69 (6), 3827-3836 (2001)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bacteria; Firmicutes; Lactobacillales; Streptococcaceae
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AAACTGCCTTTGAGTCAACG
                                                               AACACTAACAGTCAAGCAAGTCAAAGTAATGACATTGATAGTCTCTTGAAACAGCTCTAC
                                                                                                   AACTGGGTACCTTCTGTAAGCAATCCAGGAACTACAAATACTAACACAAGCAACAACAGC
                                                                                                                    GGAAATCTGTCAAATTCAAGAACCTATCGCCGACAAAATAGCGATAACACTTCAAGAACA
                                           AACACTAACAGTCAAGCAAGTCAAAGTAATGACATTGATAGTCTCTTGAAACAGCTCTAC
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EDLLATVKYYVEHPNER PHSDNGFGNASDHVQRNKNGQADTNGTEKPEEEFDQTEKPE
EETPREEKPQSEKPESPKFTERPEESSPESPERPEESEFDQVETEKVKEKLREAEDLLGK
IQNPI I KSNAKETLTGLKNNLLFGTQDNNT IMAEAEKLLALLKESK"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             protein_id="AAK26629.1"
/db_xref="GI:13447094"
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/transl_table=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /gene="phpA"
/note="histidine motif-containing protein"
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Pred. No. 8.6e-96;
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AX343072
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                                                                                                                                                                     Streptococcus antigens
Streptococcus antigens
Patent: WO 0198334-A 4 27-DEC-2001;
SHTRE BIOCHEM INC. (CA)
                                                                                                                                                                                                                                                                                                 2647 bp
Sequence 4 from Patent W00198334.
AX343073
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Patent: WO 0198334-A 3 27-DEC-2001;
SHIRE BIOCHEM INC. (CA)
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AX343072
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/mol_type="genomic DNA"
/db_xref="taxon:32644"
/note="BVH-11"
                                                                                                                                                Location/Qualifiers
1. .2647
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/mol_type="genomic DNA"
/db_xref="taxon:32644"
/note="BVH-11"
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Synthetic construct PhpA-79 (phpA-79) gene, complete cds
AF340222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (25-JAN-2001) Department of Bacteriology, Wyeth Lederle Vaccines, 211 Bailey Road, West Henrietta, NY 14586, USA Location/Qualifiers
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Zhang, Y., Masi, A., B
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IDEKLVKEAVRKVGDGYVFEENGVSRYIPAKDLSAETNAGIISKLAKQESLSHKLGAK
KTDLPSSDREFYNKAYDLLARIHQDLLDNKGRQVDEFALDULLERLKDVPSDKVKLVD
DILAFLAPIRHEERLGKRNAQITYTDDBIQVAKLAGKYTTEDGYIFDPRDITSDEGDA
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VKAAKKVPLDRWPYNLQYTVEVCNGSLIIPHYDHYHNIKFEWFDEGLYEAFKGYTLED
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YHQNGGENISSLLRELYAKPLSERHVESDGLIFDPAQITSRTARGVAYPHGNHYHFIP
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/mote="N-terminal truncated
/note="N-terminal protein"
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/transl_table=11
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/db_xref="taxon:32630"
/note="derived from Streptococcus
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L. .2166
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PC G01N33
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Choi,G.H., Kunsch,C.A., Ba
Fannon,M.R. and Rosen,C.A.
                                                                                                                                                                                                                                                       PF PN
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Kunsch, C.A., Choi, G.H.,
                                                                                                                                                                                                                                                                                                                                                                                 unidentified
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D 24-APR-2001
D 39-APR-2001
F 30-OCT-1997 JP 1998520667
R 31-OCT-1996 US 60/029960
I CHARLES A KUNSCH,GIL H CHOI,SYDNOR L JOHNSON,ALEX HROMOCKYJ
C12N15/31,C12N5/18,C12N1/21,C07K14/315,C12Q1/68,A61K39/09, PC
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/db_xref="taxon:32644"
474 c 498 g 54
                                                                                                                     Location/Qualifiers.
Location/Qualifiers
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474 c 498 g
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                                 STEVEN C BARASH,
PI MICHAEL FANNON
PC C12N15/09,A01K
PC C12N1/21,
PC C12N5/10,C12P2
G06F15/40
CC Strandedness:
CC Topology: Line
FH Key
FT Source
FT Source
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AR219011
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Streptococcus pneumoniae polynucleotides and Patent: US 6420135-A 243 16-JUL-2002;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Kunsch, C.A., Choi, G.H., Dillon, P.S., Fannon, M.R. and Dougherty, B.A.
                                                                                                                                                                                                                                                     Fannon,M. and Dougherty,B.A.

Polynucleotide of Streptococcus pneumoniae
Patent: JP 2001501833-A 243 13-FEB-2001;
HUWAN GENOME SCIENCES INC
                                                                                                                                                                                                                                                                                                                                                             unidentified
                                                                                                                                                                                                                                                                                                                                                                                                              Polynucleotide of Streptococcus
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                                                                                                                                    MICHAEL FANNON, BRIAN A DOUGHERTY C12N15/09, A01K67/027, C07K14/315, C07K16/12, C12N1/15, C12N1/19,
                                                                                                             C12N5/10, C12P21/02, C12Q1/68, G06F17/30, C12N15/00, C12N5/00,
                                                                                                                                                                           CHARLES A KUNSCH, GIL H CHOI, PATRICK J DILLON, CRAIG A ROSEN, PI
                                                                                                                                                                                         30-OCT-1997 JP 1998520718
31-OCT-1996 US 60/029960
                                                                                     Strandedness: Double;
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                                                                                                                                                                                                                                             Unidentified
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/organism="unidentified"
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53; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Adamou, J.E., Heinrichs, J.H., Erwin, A.L., Walsh, W., Gayle Dormitzer, M., Dagan, R., Brewah, Y.A., Barren, P., Lathigra Langermann, S., Koenig, S. and Johnson, S. Identification and characterization of a novel family of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Streptococcus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (03-NOV-2000) Molecular Microbiology, MedImmune, West Watkins Mill Road, Gaithersburg, MD 20878, USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      pneumococcal proteins that are protective against sepsis Infect. Immun. 69 (2), 949-958 (2001)
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                                     /protein_id="AAK06759.1"
//db_xref="G1:12744742"
//db_xref="G1:12744742"
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/translation="MKINKKYLAGSSVAVLAGSVTSHGDHYHYYNGKVPYDAIISE
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EDAGQKAENLTPDEVSKREGINAEQIVIKINGKYYVYLKDAAHADNITTKEBIKRQKQER
ELLMKDPNYQLKDSDIVNEIKGGYVIKVNGKYYVYLKDAAHADNITTKEBIKRQKQER
SHNHNSRADNAVAAARAQGRYTTDDGYIFNASDIIEDTGDAYIVPTTYHQNQGENISSI
LRELYAKPLSERHVBSDGLIFDPAQITSRTARQVAVPHGHYHFIPYEQNSELEKRIA
RIIPLRYRSNHWVPDSRPEBPSQPTPESPSPPQPAFSNPIDGKLVKEAVRKVGDGYV
FEENGVSRYIFAKDLSAETAAGIDSKLAKQESLSHKLGTKKTDLFSDREFYNKAVDL
LARIHQDLLDNKGRQVDFBALDNLLERLKDVSSDKVKLVEDIIAFLAFIRHPERLGKP
NAQITYTDDBIQVAKLAGKYTAEDGYIFDAKGAEAIYNRVKAXKVPLDRWYNLQY
EARRAAAQAYAXEKGLTPPSTDHQDGSUTEAKGAEAIYNRVKAXKVPLDRWYNLQY
EARRAAAQAYAXEKGLTPSTDHQDSGNTEAKGAEAIYNRVKAXKVPLDRWYNLQY
TVEVKNGSLIIPHYDHYNIKFEWFDEGLYEARKGYTLEDGLATVKYYVEHPNERPHS
TVEVKNGSLIIPHYDHYNIKFEWFDEGLYEARKGYTLEDGLATVKYYVEHPNERPHS
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DNGFGNASDHVQRNKNGQADTNQTEKPSEEKPQTEKPEEETPREEKPQSEKPESPKPT
EEPEESPEESEEPQVETEKVEEKLREAEDLLGKIQDPIIKSNAKETLTGLKNNLLFGT
                                                                                                                                                                                                                                                                                                                                                                                      precursor"
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/transI_table=11
/product="pneumococcal histidine"//product="pneumococcal  histidine"//product="pneumococccal histidine"//pneumococccal histidine
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/db_xref="taxon:32644"
_451 c 511 g 6
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/mol_type="genomic DNA"
/serotype="4"
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Barren,P., Lathigra,
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AX569137
                                                                                                                                                                                                                                                                                                                Streptococcus pneumoniae proteins and nucleic Patent: WO 02077021-A 2345 03-OCT-2002; Chiron Spa (IT) ; THE INSTITUTE FOR GENOMIC RE
                                                                                                                                                                                                                                                                                                                                                                                                                                       Streptococcus pneumoniae
Streptococcus pneumoniae
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larity 100.0%; I
Conservative 0;
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larity 100.0%; Pred. No.
Conservative 0; Mismatch
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/note="Region: l
718. .792
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616. .633
                                                                                                                                                                                                        /mol_type="genomic DN
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_497 c 531 g
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1. .2457
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496 c 533
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|578. 1758
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|396. .1488
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657. .1674
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Pred. No. 2e-
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Adamou,J.E., Heinrichs,J.H., Erwin,A.L., Walsh,W., Gayle, Dormitzer,M., Dagan,R., Brewah,Y.A., Barren,P., Lathigra, Langermann,S., Koenig,S. and Johnson,S. Identification and characterization of a novel family of pneumococcal proteins that are protective against sepsis Infect. Immun. 69 (2), 949-958 (2001)
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AF318955
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Direct Submission
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amou,J.E., Heinrichs,J.H.,
/gene="phtD"
/note="Region: |
1417. .1509
                                                                                                                                                                                                                                                                                            ARIIPLRYRSNHWVPDSRPEQPSPQSTPEPSDSPQPAPNPQPAPSNPIDEKLVKEAVR KVGDGYVFEENGVSRYIPAKDLSAETAAGIDSKLAKQESLSHKLGAKKTDLPSSDREF YNKA YDLLARIHQDLLDNKGRQVDFEALDNLLERLKOVPSDKYLVDDILAFLAPIRH PERLGKPNAQITYTDDEIQVAKLAGKYTTEDGYIFDRDTIFDEGDAYVTPHMTHSHWIKKDSLSEAERAAAQAYKEKGLTPPSTDHQDSGNTEAKGAEAIYNRVYAAKKYVPLDR MPYNLQYTVEVKNGSLIPHYDHYHNIKFEWFDEGLYEAPKGYTLEDLLATVKYYVEH PNERPHSDNGFGNASDHVRXKKVDQDSKPDEDKEHDEVSEPTHPESDEKENHÄGLNPS
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SHNHGGGSNDQAVVAARAQGRYTTDDGYIFNASDIIEDTAIVPHGPHYHYIFNE
LSASELAAAEAYWNGKQGSRÞSSSSSYNANPAQPRLSSNHNLTVTPTYHQNQGENISS
LKRELYAKPLSERHVESDGLIFDPAQITSRTJARGVAVPHGNHYHFIPVEQMSELEKRI
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                                                  /note="Region: 943. .960
                                                                                                                                                                                                            /gene="phtD"
247. .264
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                                                                                     'gene="phtD"
                                                                                                                                                                    /gene="phtD"
/note="Region:
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/transl_table=11
/product="pneumococcal histidine
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mol_type="genomic DNA"
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                                                                                                                     note="Region:
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Molecular Microbiology, Gaithersburg, MD 20878,

MedImmune, USA

pneumoniae"

triad protein

Erwin, A.L., Walsh, W.,

Dormitzer, M.

Gayle, T.,

BCT 31-AUG-2001

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Sequence 5 from Patent WO0198334.
AX343074
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Sequence 1985 from Patent
AX568778
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            Streptococcus antigens
Patent: WO 0198334-A 5 27-DEC-2001;
SHIRE BIOCHEM INC. (CA)
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                                                           Hamel, J., Ouellet, C.,
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/note="Region: coiled-coil domain"
1678. . 1695
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1597. .1779
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/gene="phtD"
                                                                                                                                                                                                                                                                                                                                                                                                                                                /mol_type="genomic DNA"
/db_xref="taxon:1313"
509 c 545 g 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    organism="Streptococcus
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                                                                                                                                                                                                                                                                                                                                                                Score 53; DB Pred. No. 2e-0; Mismatches
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                                                                                                                                                                                                                                                                                                            Tettelin, H., Nelson, K.E., Paulsen, I.T., Eisen, J.A., Read, T.D., Peterson, S., Heidelberg, J., DeBoy, R.T., Haft, D.H., Dodson, R.J., Durkin, A.S., Gwinn, M., Kolonay, J.F., Nelson, W.C., Peterson, J.D., Umayam, L.A., White, O., Lewis, M.R., Radune, D., Holtzapple, E., Khouri, H., Wolf, A.M., Utterback, T.R., Hansen, C.L., McDonald, L.A., Feldblyum, T.V., Angiuoli, S., Gesuwan, P., Hickey, E.K., Holt, I.E., Loftus, B.J., Ujwal, M.L., Yang, F., Smith, H.O., Venter, J.C., Dougherty, B.A., Morrison, D.A., Hollingshead, S.K. and Fraser, C.M. Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Tettelin, H., Nelson, K.E., Paulsen, I.T., Eisen, J.A., Read, T.D., Peterson, S., Heidelberg, J., DeBoy, R.T., Haft, D.H., Dodson, R. J., Durkin, A.S., Gwinn, M., Kolonay, J.F., Nelson, W.C., Peterson, J.D., Umayam, L.A., White, O., Salzberg, S.L., Lewis, M.R., Radune, D., Holtzapple, E., Khouri, H., Wolf, A.M., Utterback, T.R., Hansen, C.L., McDonald, L.A., Feldblyum, T.V., Angiuoli, S., Dickinson, T., Hickey, E.K., Holt, I.E., Loftus, B.J., Yang, F., Smith, H.O., Venter, J.C., Dougherty, B.A., Morrison, D.A., Hollingshead, S.K. and Fraser, C.M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Streptococcus pneumoniae TIGR4
                                                                                                                                                                                                                                                           Submitted (29-JUN-2001) The Institute for Genomic Research, Medical Center Dr. Rockville, MD 20850, USA Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Streptococcus pneumoniae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Complete genome sequence of a virulent isolate
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AE007403.1 GI:14
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/mol_type="genomic DNA"
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/note="BVH-11-2"
                                           /note="This region contains a match to at least one other gene that is not full length, and is not the result of a sequencing artifact; similar to GP:5019533; identified by sequence similarity; putative; IS630-Spn1, transposase
             Orf2, truncation"
956. .1156
                                                                                                                                                               /db_xref="taxon:170187"
129. 476
                                                                                                                                                                                             /organism="Streptococcus
/mol_type="genomic DNA"
/strain="TIGR4"
                                                                                                                                              'gene="SP0995"
                                                                                                               'gene="SP0996"
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/pros
                                                                                                                                                          YFTYGYKHSTIEE"
5016. .5933
                                                                                   GLIRLRKEKGMPKAGEFKTPLVPLLPILSIIICLSFMLQYNMNTWIAFLVALLVGSII
                                                                                                         GVVHYSHLNVDDAVAFALRSVGISWAANYVSLVAILTLITVCISMTYALSRMIYSLAR
DGLVPAAFKELTKTSKIPKNATILTGLASAVAAGMFPLASIAAFLNICTLAYLIMLAY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /translation="mkkvmfaglsllslvvlmacgebetkktqaaqqpkqqttvqqia
vgkdapdftlqsmdgkevklsdfkgkkvylkfwaswcgpckksmpelmelaakpdrdf
eiltviapgiqgektveqfpqwfqeqgykdipvlydtkattfqayqirsipteylids
qgkigkiqfgaismadaeaafkemn"
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HQMEIFHLKKLEVQKSFTFKKSDSNRYWSAFLLGITFSFGWTPCIGPVLSSVLALAAS
GGNGAWQGAIYTLIYTLGMALFFLVLALASGLVMPYFSKIKRHMMLLKKIGGFLIVLM
                                                                                                                                                                                                                                                                                                       /transl_table=11
/product="amino acid permease family protein"
/protein id="AAK/5118.1"
/db_xref="GI:14972474"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GILLLLGQVNVLAGIFE"
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similarity; putative"
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KVLGQLDAEKADKKVLAKAQNLLQETLDFVKEENGSAETETKLVEELKAILDKLK"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /gene="SP1001"
3482. .4873
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/trans| table=11
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/protein_id="AAK75117.1"
/db_xref="GI:14972473"
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/db_xref="GI:14972472"
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1833. .2540
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1303. .1602
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Query Match
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SHNHGGGSNDOA VVAARAOGRYTTDOOY I FNASDI I EDTGDAY I VPHGDHYHY I PKNE
LSASELAAAEA YWNGKOGSR PSSSS SYNANPAOPRI LSENHNLTVT PTYHQNOGENI SS
LLAELYAKFLSERHVESDGLI FDPAQI TSRTNAGVA VPHGNHYHF I PYEOMSELEKRI
ARI I PLRYRSNHWVPDSR PEQPSPQSTPEPSPS PQPAPNQPAPSNP I DEKLVKEAVR
KVGDGYVFEENGVSRY I PAKDISAETAAGI DSKLAKOESLHKLGAKKTOLPSSDREF
YNKAYDLLARI HODLLDNKGRQVDFEALDNLLERLKDVPSDKVKLVDDI LAFLAFI RH
PERLGKPNAQI TYTDDEI QVAKLAGKYTTEDGY I FDRROI TSDEGDAYVTPHMTHSHW
I KKDSLSAAERAAQAYAKEKGLTPPSTDHQDSGNTEAKGAEAI YNR VKAAKKVPLDR
MPYNLQYTVBVKNGSLI I PHYDHYNN I KFEWFDEGLYEAPKGYTLEDLLATVKYAVVEH
PMERPHSDNGFGNASDHYKKNKVVODOSK PDEDLYEAPKGYTLEDLLATVKYAKYVPLH
PMERPHSDNGFGNASDHYRKNKVVODOSK PDEDLYEAPKGYTLEDLLATVKYYKYVBH
PMERPHSDNGFGNASDHYRKNKVVODOSK PDEDLYEAPKGYTLEDLLATVKYYKNAKAGINPS
ADNLYKPSTDTEETEEBAEDTTDEAEI PQVENS Y INAKI ADAEALLEKVTDPS I RQNA
METLTGLKSSLLLGTKDNNTI SAEVDSLLAALLKESQPAPIQ"
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                                                                                                                                      VBVPILEKENQTDKPSILPQFKRNKAQENLKLDEKVEEPKTSEKVEKEKLSETGNSTS
NSTLEEVPTVDPVQEKVAKFAESYGMKLENVLFNMDGTIELYLPSGEV IKKMADFTG
EAPQGNGENKPSENGKVSTGTVENQDTENKFADSLFBEAPUKFPNKFENTDNGMLNPE
GNVGSDPMLDPALEEAPAVDPVQEKLEKFTASYGLGLDSVIFNMDGTIELRLPSGEVI
                                                                                                                                                                                                                                          DSPSAQRYSESDGLVEDPAKLI SRTENGVAI PHODHYHFI PYSKLSALEEKI ARMVPI
SGTGGTVSTNAK PREVVSSLGSLSSNPSSLTTSKELSSASDGY I FRPKDI VEETATAY
I VRHGDHFHYI PKSNQI GQPTL PNNSLATPS PSL PI NPGTSHEKHEEDGYGFDANRI I
AEDESGFVNSHGDHHYF FFKUDLTEEQI KAAQKHLEEVKTSHNGLDSLSSHEQD YSN
AKEMKDLDKKI EEKI AGIMKQYGVKRES I VVNKEKNAI I YPHGDHHHAD PI DEHKPVG
IGHSHSNY BL FK DEGVAKKEGNKVYTGEBLINVNALLKNSTFUNQNFTLANGQKRVS
FSFPDELEKKLGINNLVKLIT PDGKVLEKVGSKVFGEGGVSHI ANFELDQPYLDGQTFK
YTI ASKDYPEVSYDGTFTVPTSLAYKMASQTI FY PFHAGDTYLRVNPQFAVPKGTDAL
URVPDEFHGNAYLENNYKVGEI KLP I PKLNQGTTRZAGNK, I PVTFANAN YLDNQSTYI

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VKDNEKVNSNVAVARSQGRYTTNDGYVFNPADI I EDTGNAY I VPHGGHYHY I PKSDLS
ASELAAAKAHLAGKNMQPSQLSYSSTASDNNTQSVAKGSTSKPANKSENLQSLLKELY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /protein_id="AAK75121.1"
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SQSSQKSENLTPDQVSQKEGIQAEQIVIKITDQGYVTSHGDHYHYYNGKVPYDALFSE
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/db_xref="GI:14972475"
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/transI_table=11
/product="conserved hypothetical protein"
/protein_id="AAK75120.1"
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REFERENCE
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AUTHORS
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JOURNAL
MEDLINE
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53; Conserv
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21429245
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Streptococcus pneumoniae R6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            and Glass, J.I.
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AE008464.1 GI:15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              d (27-JUL-2001) Infectious Diseases Lilly Research Labs, Indianapolis, Location/Qualifiers
                                                                                                                        /protein_id="AAK99709.1"
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; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              12372 bp
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184 of the
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              gene="phtE"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    'gene="lmb"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /translation="MykelpmkkqNlflyllsyfllcigacgqkesqtgkgmkiytsf
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product="Pneumococcal histidine triad protein
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transl_table=
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transl_table≈11
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                    3682
                                                        983
                                                                                          53;
                                                                                                         Similarity
                                           GCTCGTATTATTCCCCTTCGTTATCGTTCAAACCATTGGGTACCAGATTCAAG 1035
                                                                                        Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /transl +=+*
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              product="Pneumococcal histidine triad
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                                                                                        Score 53; DB 1; Li
Pred. No. 1.8e-16;
0; Mismatches 0;
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                                                                                                                                                                                                                                                                         SPNEU1901 232807
Streptococcus pneumoniae clor
AL449923
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            l Similarity
53; Conserv
Annotated draft genomic sequence from a Streptococcus pneumoniae type 19F clinical isolate Microb. Drug Resist. 7 (2), 99-125 (2001) 21335329
                                                                                  Dopazo,J., Mendoza,A., Herrero,J., Caldara,F., Humbert,Y. Friedli,L., Guerrier,M., Grand-Schenk,E., Gandin,C., de Francesco,M., Poliss,A., Buell,G., Feger,G., Garcia,E.,
                                                                                                                                                                                                  AL449923.1 GI:11545148
HTG; HTGS_PHASE2.
Streptococcus pneumoniae
Streptococcus pneumoniae
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* NOTE: This is a 'working draft' sequence.

* This sequence will be replaced
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Dopazo,J., Mendoza,A., Herrero,J., Caldara,F., Polissi,A., Humbert,Y., Friedli,L., Guerrier,M., Grand-Schenk,E., Gandin,C., Francesco,M., Buell,G., Feger,G., Garcia,E., Peitsch,M. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Dopazo,J., Mendoza,A., Herrero,J., Caldara,F., Humbert,Y.,
Friedli,L., Guerrier,M., Grand-Schenk,E., Gandin,C., de
Francesco,M., Polissi,A., Buell,G., Feger,G., Garcia,E., Peitsch,M.
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Streptococcus pneumoniae
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                                                                         and Garcia-Bustos,J.F
                                                                                                                                                                                     Bacteria;
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/mol_type="genomic DNA"
/serotype="19F"
/db_xref="taxon:1313"
                                                                                                                                                                                 Firmicutes; Lactobacillales;
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12-JUL-2001

Peitsch, M

1035 75109

Gaps

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Severo Ochoa 2, 28760 Tres Cantos, SPAIN
* NOTE: This is a 'working draft' sequence.
* This sequence will be replaced
* by the finished sequence as soon as it is
* the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                Streptococcus pneumoniae proteins and nucleic acids Patent: WO 02077021-A 4981 03-OCT-2002; Chiron Spa (IT); THE INSTITUTE FOR GENOMIC RESEARCH
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Streptococcus pneumoniae
Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
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/note="seq 4979 too long: 2.162.598 bases-replaced by note="seq 4979 too long: 2.162.598 bases-replaced by following seq:-seq 4979: from 0.000.001 to 0.349.980-seq 4980: from 0.300.001 to 0.649.980-seq 4981: from 0.600.001 to 0.949.980-seq 4982: from 0.900.001 to 1.249.980-seq 4983: from 1.200.001 to 1.549.980-seq 4983: from 1.200.001 to 1.549.980-seq 4984: from 1.500.001 to 1.849.980-seq 4985: from 1.800.001 to 2.149.980-seq 4986: from 2.100.001 to 2.162.598"
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/mol_type="genomic DNA"
/serotype="19F"
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/mol_type="genomic DNA"
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/clone="G54"
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1 (bases 1 to 492)
Zhang,Y., Masi,A.W., Barniak,V., Mountzouros,K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          492
Synthetic construct PhpA-20 (
AF340223
                                            1 (bases 1 to 973)
Kunsch, C.A., Choi, G.H., Dillon
Fannon, M.R. and Dougherty, B.A.
                                                                                                                                                                                   Sequence 355 from patent AR219123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       protein from Streptococcus pneumoniae, protects mice intranasal pneumococcal challenge Infect. Immun. 69 (6), 3827-3836 (2001)
              Streptococcus pneumoniae polynucleotides Patent: US 6420135-A 355 16-JUL-2002;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (25-JAN-2001) Department of Bacteriology, Vaccines, 211 Bailey Road, West Henrietta, NY 14586,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Recombinant PhpA protein, a unique histidine motif-containing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         synthetic construct
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                                                                                                                                                                  AR219123.1
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                                                                                                Unclassified
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                                                                                                                                                                                                                                                                                                    TCGTATTATTCCCCTTCGTTATCGTTCAAACCATTGGGTACCAGATTCAA
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/transT table=11
/product="PhpA-20"
/protein id="AAK26631.1"
/db_xref="GI:13447098"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /translation="mssllrelyakplserhvesdglifdpaqitsrtangvavphgd
hyhfipysqlspleeklvvlfpfvivqtigyqiqrpeqpvhnrlrepspspkpapnpq
papsnpideklvkeavrkvgdgyvfeengvaslypkprilqqkqqqalianwpsrkvy
Location/Qualifiers
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/mol_type="genomic DNA"
/db_xref="taxon:32630"
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note="histidine
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                                                             Choi, G.H., Dillon, P.S.,
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9.5e-15;
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                                                               Rosen, C.A.,
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, USA
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VERSION
KEYWORDS
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AUTHORS
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SOURCE
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BD004035
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AR120406/c
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ORGANISM
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Best Local Similarity
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Best Local
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                                            AR120406
Sequence
AR120406
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Polynucleotide of Streptococcus pneumoniae and sequence Patent: JP 2001501833-A 355 13-FEB-2001;
HUMAN GENOME SCIENCES INC
                                                                                                                                                                                                                                                                                                                                                                                                                                 PR PR PR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Polynucleotide of Streptococcus BD004035
         Unknown.
                                   AR120406.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     unclassified
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                                                                                                                                                                                                                                                                                                                                                                                                                      STEVEN C BARASH
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ilarity 100.0%;
Conservative (
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30-OCT-1997 JP 1998520718
31-OCT-1996 US 60/029960
CHARLES A KUNSCH,GIL H CHOI, PATRICK J DILLON, CRAIG A ROSEN,
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ilarity 100.0%;
Conservative (
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C12N15/09, A01K67/027, C07K14/315, C07K16/12, C12N1/15, C12N1/19,
                                                                                                                                                                                                                                                                                                                                                 Strandedness: Double;
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282 from patent US (
                                                                                                                                                                                                                                                                                      /organism='Unidentified'
                                                                                                                                                                                                                              /organism="unidentified"
/mol_type="genomic DNA"
/db_xref="taxon:32644"
178 c 211 g 25
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178 c 211 g
                                   GI:14103982
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Pred. No. 1.6e-1
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Pred. No.
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hes 0;
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AUTHORS
TITLE
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DEFINITION
                                                                              RESULT 35
AR120405
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ORIGIN
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Query Match
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              AR120405
Sequence
AR120405
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Runsch.C.A., Choi.G.H., Johnson,S.L. and Hromockyj,A.

Streptococcus pneumoniae antigens and vaccines
Patent: JP 2001505415-A 169 24-APR-2001;

HUMAN GENOME SCIENCES INC
PN JP 2001505415-A/169
PN JP 2001505415-A/169
PD 24-APR-2001
PF 30-OCT-1996 US 60/029960
PR 31-OCT-1996 US 60/029960
PR 31-OCT-1996 US 60/029960
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l Similarity 100.0%;
30; Conservative
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Streptococcus pneumoniae
BD063415
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Choi,G.H., Kunsch,C.A.,
Fannon,M.R. and Rosen,C
AR120405.1
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                                                                                                                                             CCTTCATCTGTAAGTAAGGAAAAAATAAAC 2389
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I CHARLES A KUNSCH,GIL H CHOI,SYDNOR L JOHNSON,ALEX HROMOCKYJ
C12N15/31,C12N5/18,C12N1/21,C07K14/315,C12Q1/68,A61K39/09, PC
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                               281 from patent
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6 c 7 g
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/db_xref="taxon:32644"
6 c 7 g
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 GI:14103981
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Pred. No. 0.00073;
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Pred. No.
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hes 0;
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1 (bases 1 to 37)
1 (bases 1 to 37)
1 TILE
1 Streptococcus pneumoniae antigens and vaccines
1 Patent: JP 2001505415-A 168 24-APR-2001;
1 HUMAN GENOME SCIENCES INC
1 PN JP 2001505415-A/168
24-APR-2001
PF 30-0CT-1997 (TP
PR 31-0CT-1997 (TP)
PR 31-0CT-1997 (TP)
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                                        AX343114 33 bp
Sequence 45 from Patent WO0198334.
AX343114
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Choi, G.H., Kunsch, C.A.,
Fannon, M.R. and Rosen, C.
unidentified unidentified
                               AX343114.1 GI:18152294
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                                                                                                                                                                        Similarity
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F 31-OCT-1996 US 60/029960

I CCHARLES A KUNSCH,GIL H CHOI,SYDNOR L JOHNSON,ALEX HROMOCKYJ PC C12N15/31,C12N5/18,C12N1/21,C07K14/315,C12Q1/68,A61K39/09, PC
                                                                                                                   TTCTTACGAGTTGGGACTGTATCAAGC 37
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/mol_type="genomic DNA"
/db_xref="taxon:32644"
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AR120328
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AX343116.
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AX343116
Streptococcus pneumoniae antigens and vaccines Patent: US 6159469-A 181 12-DEC-2000; Location/Qualifiers
                                    1 (bases 1 to 1342)
Choi, G.H., Kunsch, C.A., Ba
Fannon, M.R. and Rosen, C.A.
                                                                                                                                                                                                                                                                                 l Similarity
25; Conserv
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Patent: WO 0198334-A 47 27-DEC-2001;
SHIRE BIOCHEM INC. (CA)
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Patent: WO 0198334-A 45 27-DEC-2001;
SHIRE BIOCHEM INC. (CA)
                                                                                                                                         Sequence 181 from patent AR120328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 unidentified unidentified
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larity 100.0%;
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/mol_type="genomic DNA"
/db_xref="taxon:32644"
/note="HAMJ 284"
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/mol_type="genomic DNA"
/db_xref="taxon:32644"
/note="HAMJ 282"
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                                                 Dillon, P.J.,
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                                 Glaser, P.,
                                                                       Streptococcus agalactiae
Streptococcus agalactiae
Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
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24; Conserv
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Sequence 6336 from Patent WO02092818.
AX608407
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Kunsch,C.A., Choi,G.H., Johnson,S.L. and Hromockyj,A.
Streptococcus pneumoniae antigens and vaccines
Patent: JP 2001505415-A 91 24-APR-2001;
HUMAN GENOME SCIENCES INC
Streptococcus agalactiae genome sequence, use
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R 31-0CT-1996 US 60/029960
I CHARLES A KUNSCH,GIL H CHOI,SYDNOR L JOHNSON,ALEX HROMOCKYJ
C12N15/31,C12N5/18,C12N1/21,C07K14/315,C12Q1/68,A61K39/09, PC
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                        Rusniok, C., Couve, E., B
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100.0%; Pred. No. 0.
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AX343078
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Streptococcus pneumoniae
Bacteria; Firmicutes; Lactobacillales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             vaccines, diagnostic tools, and for identifying therapeutic targets patent: WO 02092818-A 6336 21-NOV-2002; INSTITUT PACTEUR (FR) , CENTRE NATIONAL DE LA RECHERCHE SCIENTIFIQUE (CNRS) (FR)
              Masignani,V., Tettelin,H. and Fraser,C.
Streptococcus pneumoniae proteins and nucleic acids
Patent: WO 02077021-A 1987 03-OCT-2002;
Chiron Spa (IT); THE INSTITUTE FOR GENOMIC RESEARCE
Location/Qualifiers
1. .3117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Streptococcus antigens
Patent: WO 0198334-A 9 27-DEC-2001;
SHIRE BIOCHEM INC. (CA)
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l Similarity 100.0%;
24; Conservative
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AF318956
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Streptococcus pneumoniae Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
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Watkins Mill Road, Gaithersburg, MD 20878, USA
Location/Qualifiers
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                                    DSPSAQRYSESDGLVFDPAKIISRTPNGVAIPHGDHYHFIPYSKLSALEEKIARMVPI
SGTGSTVSTNAKENEVVSSLGSLSSNESSLTTSKELSSASDGYLFNFKDIVEETATAY
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L. .3120
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   24;
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Sequence 1 from Patent W00198334.
AX343070
                                                                                                                                         Streptococcus antigens
Patent: WO 0198334-A 1 27-DEC-2001;
SHIRE BIOCHEM INC. (CA)
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247. .264
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1648. .1665
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1186. .1203
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0; Mismatches
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RESULT 48
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 BD003872 6867 bp Polynucleotide of Streptococcus
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                                                                                                                                                                                        Streptococcus pneumoniae polynucleotides Patent: US 6420135-A 192 16-JUL-2002;
                                                                                                                                                                                                                                                                                        Sequence 192 from patent AR218960
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Fannon,M.R. and Dougherty,B.A.
                                                                                                                                                                                                                                                   Unknown
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1325 c 1212 g
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/mol_type="genomic DNA"
/db_xref="taxon:32644"
/note="BVH-3"
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                                       Tettelin,H., Masignani,V., Cieslewicz,M.J., Eisen,J.A., Peterson,S., Wessels,M.R., Paulsen,I.T., Nelson,K.E., Margarit,I., Read,T.D., Madoff,L.C., Wolf,A.M., Beanan,M.J., Brinkac,L.M., Daugherty,S.C., DeBoy,R.T., Durkin,S., Kolonay,J.F., Umayam,L.A., Madupu,R., Lewis,M.R., Radune,D., Fedorova,N.B., Scanlan,D., Khouri,H., Mulligan,S., Carty,H.A., Cline,R.T., Gill,J., Scarselli,M., Mora,M., Iacobini,E.T., Brettoni,C., Galli,G., Mariani,M., Vegni,F., Maione,D., Rinaudo,D., Rappuoli,R., Telford,J.L., Kasper,D.L., Grandi,G. and Fraser,C.M., Complete genome sequence and comparative genomic analysis of an emerging human pathogen, serotype V Streptococcus agalactiae proc. Natl. Acad. Sci. U.S.A. 99 (19), 12391-12396 (2002)
                                                                                                                                                                                                                                                                                                                                       Streptococcus agalactiae 2603V/R Streptococcus agalactiae 2603V/R Bacteria; Firmicutes; Lactobacil
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Streptococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Polynucleotide of Streptococcus pneumoniae and Patent: JP 2001501833-A 192 13-FEB-2001;
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JP 2001501833-A/192.
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Fannon,M. and Dougherty,B.A.
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Kunsch, C.A., Choi, G.H.,
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R 31-OCT-1996 US 60/029960
I CHARLES A KUNSCH,GIL H CHOI, PATRICK J DILLON, CRAIG A ROSEN,
STEVEN C BARASH,
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JP 2001501833-A/192
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/mol_type="genomic DNA"
/db_xref="taxon:32644"
1325 c 1212 g 2433
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/product="PTS system, IIC component, putative"
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SGTMIAPFATELAKKVGAFPAGARAGSLITHSTLEGPMEKIFGYVIGKATTGQLSAII
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/gene="SAG1933"
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complement (155. .2605)
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                                                                                                                                                                        complement (4332. .4637)
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VLGDSDSQEKLSPPLKSEIATEENRKQANLAELNATQPNNRTTYIIPESSHSIAEQQR
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                                                                                                              sequence similarity; putative
                                                                                                                                                                                                                                                                                                TLIIFATAYLGLFMWYAKQMKRRNAEYAANQK"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TLWEKMAANWHVLFKFYL"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  codon_start=1/transl_table=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ILSNGEKIHSLTMDNKKEQNTESVPVQLKNGDIKLFMRNLTGNLEVATSKDGGETWQN
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                           putative"
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                                                                                                                                                                                                                                /note="identified by match to PFAM protein family HMM PF02580; The product of this gene was detected by Western blot analysis. For details on the method see Tettelin et
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /translation="MKRIRKSLIFVLGVVTLICLCACTKQSQQKNGLSVVTSFYPVYS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            triad family protein, complement (8936. .985
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /translation="MLKRERLQKIIEKVNINGIVTVNEIMEELDVSDMTVRRDLDELD
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INSIKSLNFSKAFVSSNGVFEKSIATYDEGEGEIQRIALNNSFEKFLLVDSQKFGKYD
                                                                                                                                                                                                                                                                                                                                                            complement (10114.
                                                                                                                                                                                                                                                                                                                                                                                                                        complement (10114. .10557)
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/transl_table=11
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                                                                                                                  function TIGR00256"
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Best Local
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                                                                                                                                                                                                                                                          Streptococcus agalactiae genome sequence, use for developing vaccines, diagnostic tools, and for identifying therapeutic targets Patent: WO 02092818-A 133 21-NOV-2002; INSTITUT PASTEUR (FR); CENTRE NATIONAL DE LA RECHERCHE
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Zouine, M., Couve, E., Bu
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                                                 Conservative 0;
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RIYVFTPNGAVQELPRESGPIDFAYAIHTQVGEKATGAKVNGRMVPLTAKLKTGDVVE
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DGVTKLGKVEYKSHEEQLAENHRKMLMAMSKDIRVILVKLADRLHNMRTLKHLRKDKQ
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14447 c 11608 g 24847 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SNATKLVSTVNAQPTKDMKFANIHVSFGISNLAQLTTVVDKIKIIPDVYSVKRTNG"
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complement(10567. .12783)
                                                                                                                                                                                                                        Location/Qualifiers
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/(rransT table=11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    translation="MVKEINLTGEEVVAITSQYMSETDVAFVKFALNYATAAHYYQAR
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                                                                                                                                                                                                            .75248
                                                                                     1.0%;
                                                                 Score 24; DB 6;
Pred. No. 0.7;
                                                                                                                                                                                                                                                                                                                                            Buchrieser, C., Poyart, C., Trieu-Cuot, P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 24;
Pred. No.
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t WO02092818
                                                   Mismatches
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0.78;
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                                                                                 Length 75248;
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AUTHORS
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ACCESSION
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LOCUS
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MEDLINE
PUBMED
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                                 gene
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   complement (1983.
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22369 CGCTATACTACAGATGATGGTTAT 22346
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Submitted (31-MAY-2002) Glaser P., Institut Pasteur,
Microorganismes Pathogenes, 25, rue du Docteur Roux,
Cedex 15, FRANCE. E-mail: pglaser@pasteur.fr Phone: +
89 96, Fax: +33 (0)1 45 68 87 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Genome sequence of Streptococcus agalactiae, a pathogen causing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Zouine, M., Couve, E., Lalioui, L., Trieu-Cuot, P. and Kunst, F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Glaser, P., Rusnick, C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Streptococcus agalactiae NEM316 Streptococcus agalactiae NEM316
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Streptococcus agalactiae AL766854 AL732656
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bacteria; Firmicutes; Lactobacillales; Streptococcaceae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AL766854.1 GI:24413438
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                                                                        /trānsiation="MTSVVVVGTQWGDEGKGKITDFLSADAEVIARYQGGDNAGHTIV
ITDRKKERLHLIPSGIFFKEKISVIGKGVVVWPKSLVKELAYLHEGGVTTDNLEISDRA
HVILPYHIKLDQLQEDAKGDNKIGTIKGIGPAYNDKAARVGIRIADLLDREWFAERL
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FEGAQGYMLDIDQGTYFVTSSNPVAGGVTIGSGVGESKINKVVGVCKAYTSRVGDGP
FPTELFDEVGGNIDIDGKRIDYYPASLEQLKRCKFIYEELPGWSEDITACRSLDDLPEN
SGLDTVKICVAYDLDGKRIDYYPASLEQLKRCKFIYEELPGWSEDITACRSLDDLPEN
                         complement (1983. .3130)
                                                 ARNYVRRVGELVGVRISTFSVGPGREQTNILESVWSNI"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                complement (405. .424)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              complement (405. .1725)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ILTVVSLVLLHTLIHNINSLLFLSITVVLLISGKSLSLISIYLLKRKSKHQKV"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /gene="gbs1858"
117. .410
/gene="gbs1860"
                                                                                                                                                                                                                                                                                                                                                                                                                                                   /gene="purA"
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                                                                                                                                                                                                                                                                                                                                                                              note="Similar to adenylosuccinate synthase"
                                                                                                                                                                                                                                                                                                                                                                                                  'gene="purA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             translation="MILINLIALPICFLVELSAGLLLKLEMHKQHGYYPLERLLMTGN/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    protein_id="CAD47517.1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /product="Unknown"
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terminator
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                                                                                                                                                                                                                                                    /Translation="MIIGRLQRSHSHLPILQATFGLERESLRIHQPTQRVAQTPHPK
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TIGGTEYRFFYLEGDCIAVLERVAANNVGDGHTSGLLKKKNQNFLKGYDHRSPLEV
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VNDTPGTATPIAGFAVMFAYNPMIKVLITALGCIILSLLAGYFGGIVFKDYKLVTKEE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3465.
                                                   /gene="gbs1863"
6700. .7518
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="similar to gamma-glutamylcysteine synthetase (for
the N_terminal part) and to cyanophycinsynthetase
(C-terminal part)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4188.
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HISGRTISSPLTTFALDLIKNKVYKEKDFVTNYKAIVSBLVGHVEGSTFFIKNAQNEL
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6700. .7518
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3465. .3470
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5700. .7518
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 'gene="gbs1862"
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transl_table=
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/note="Similar to unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /gene="gbs1860"
}465. .4209 •
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/note="Similar to transcriptional regulators and to PTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         'gene="gbs1861"
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AC136885 154101 bp DNA linear F
Sus scrofa clone RP44-473J11, WORKING DRAFT SEQUENCE.
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                                                                                                                                                                                                      CGCTATACTACAGATGATGGTTAT 508
                                                                                                                                                       CGCTATACTACAGATGATGGTTAT 77473
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MAANVVKQEDTLARNIVSAEMLIEDNTKSIENLIGVIAFIELSOSAEAANARASHLQVEI
LALDSQTSEYQIKSNOLARMTEVINTLEQQHTEYVSRLYVAMATTPQMRNLVKVSSDM
ROKLGMLRRNTIFTMKLSIAQLGMMQQSVKSGVTADAIVNANNAALQMLAETSKEAIP
ROKLGMLRRNTIFTMKLSIAQLGMMQQSVKSGVTADAIVNANNAALQMLAETSKEAIP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /translation="MDKIIKSISTSGSFRAYVLDCTETVRTAQEKHQTLSSSTVALGR
TLIANQILAANQKNSKVTVKVIGDSSFRAYVLDGTEGNVKGYLQNTGYDIKKTATG
EULVGPFMGMHFVVITDXATGQPYTSTTPLITGEIGEDFAYYLTESEGTPSAVGLNV
LLDDEDKVKVAGGFMLQVLPGASDEEISRYEKRIQEMPSISSLLESENHIESLLSAIY
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QLDLIRNEANQLQKAIEPNIYKRITKKANTFSNEINEQLIKLHASPELEPISDQEDEM
IRIAPELKPFYHNIQDDHFAILKKIEEADNKAELAAIHQANMKRFTDVLAGYIRIKQS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /gene="gbs1866"
9770. .10747
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VKIRDKKIVEALLNEGKSTQEKVDES"
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                                                                                                                                                                                                                                                                                                                                                           /product="Unknown"
/protein_id="CAD47!
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/gene="gbs1865"
/note="Similar to
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/transl_table=
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/db_xref="GI:24413446"
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/note="Similar to other proteins"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The sequence data in this record represents an 'enhanced' version of a Phase 2 submission. Specifically, the indicated order and orientation of each sequence contig has been established using one or more of the following: read-pair data from individual subclones, overlaps with neighboring clones, alignment with available reference sequence (e.g., human), and/or confirmation by PCR testing. In addition, the sequence assembly is based on at least 8X average coverage in Q20 bases and has been reviewed to rule out gross misassemblies, the low-quality ends of sequence contigs have been trimmed away, and each base is associated with a phran-derived resilier.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (26-NOV-2002) NIH Intramural Sequencing Center, 8 Grovemont Circle, Gaithersburg, MD 20877, USA On Nov 26, 2002 this sequence version replaced gi:24819761.
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NOTE: This is a 'working draft' sequence. It currently consists of 1 contigs. Gaps between the contigs are represented as runs of N. The order of the pieces is believed to be correct as given, however the sizes of the gaps between them are based on estimates that have provided by the submittor.

This sequence will be replaced by the finished sequence as soon as it is available and the accession number will be preserved.
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Contact: nisc_zoo@nhgri.nih.gov
------ Project Information
                                                                                                                                                                                                                                                                                                                                                    Insert size: 148000; agarose-fp
Insert size: 154101; sum-of-contigs
Quality coverage: 12.16x in Q20 bases; agarose-fp
Quality coverage: 11.68x in Q20 bases; sum-of-cont
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Center clone name: 473J11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  776
                                                                                                                                                                                                                                                                                                                                                                                Benjamin, B., Blakesley, R. W., Bouffard, G.G., Brinkley, C., Brooks, S. Cariaga, K., Coleman, B., Engle, J., Granite, S., Guan, X., Gupta, J., Haghighi, P., Han, J., Hansen, N., Ho, S.-L., Idol, J.R., Karlins, E., Laric, P., Lee-Lin, S.-Q., Legaspi, R., Maduro, Q. L., Maduro, V. B., Margulies, E. H., Masiello, C., Maskeri, B., McDowell, J., Paguirigan, C., Pearson, R., Portnoy, M.E., Prasad, A., Paguirigan, C., Pearson, R., Portnoy, M.E., Prasad, A., Schandler, K., Schueler, M.G., Sison, C., Stantripop, S., Thomas, J. W., Thomas, P.J., Touchman, J. W., Vogt, J. L., Wetherby, K. D., Wiggins, L., Young, A., and Green, E.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          23;
                                                                                                     Submitted (18-DEC-2002) NIH Intramural Sequencing Center, Grovemont Circle, Gaithersburg, MD 20877, USA On Dec 18, 2002 this sequence version replaced gi:2570011
                                                                                                                                                                                                                                   Direct Submission
Submitted (22-NOV-2002) NIH Intramural Sequencing Center,
Grovemont Circle, Gaithersburg, MD 20877, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.

1 (bases 1 to 19474)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AC137536 194474 bp DNA linear H
Sus scrofa clone RP44-254B17, WORKING DRAFT SEQUENCE,
                                                                                                                                                                                             Green, E.D
                                                                                                                                                                                                                                                                                                   Green, E.D.
                                                                                                                                                                                                                                                                                                                                                                NISC Comparative Sequencing Initiative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Akhter, N., Antonellis, A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sus scrofa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sus scrofa (pig)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HTG; HTGS_PHASE2; HTGS_DRAFT
                                                                                                                                                                         Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AC137536.3
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                                                                                                                                                                                                               (bases 1 to 194474)
                                                                                                                                                                                                                                                                                                                      (bases 1 to 194474)
Contact: nisc_zoo@nhgri.nih.gov
                      Web site: http://www.nisc.nih.gov
                                         Center: NIH Intramural Sequencing Center Center code: NISC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
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/note="clone overlaps with GenBank Accession Number
AC137536 clone RP44-254B17 (center project name dbo)
a 33945 c 34061 g 43739 t 1 others
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           clone_end:T7
vector_side:
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/db_xref="taxon:9823"
/clone="RP44-473J11"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  note="assembly_fragment/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               clone_lib="RP44"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                organism="Sus scrofa"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GI:27228817
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                                                                                      Genome Center
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Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ayele, K., Beckstrom-Sternberg, S.M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              bp in length.
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                                                                                                         gi:25700111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HTG 18-DEC-2002
E, 7 ordered
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FEATURES
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misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      * by the finished sequence as soon as it is available and

* the accession number will be preserved.

* 10381 10381: contig of 10381 bp in length

* 10482 10481: gap of unknown length

* 10482 36866: contig of 26385 bp in length

* 36867 36966: gap of unknown length

* 36867 100817: contig of 63851 bp in length

* 100918 100917: gap of unknown length

* 100918 125399: contig of 24482 bp in length

* 125400 125499: gap of unknown length

* 125401 129483: contig of 3984 bp in length

* 12984 160266: contig of 30683 bp in length

* 12984 160266: gap of unknown length

* 160267 160366: gap of unknown length

* 160267 194474: contig of 30683 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The sequence data in this record represents an 'enhanced' version of a Phase 2 submission. Specifically, the indicat order and orientation of each sequence contig has been established using one or more of the following: read-pair data from individual subclones, overlaps with neighboring clones, alignment with available reference sequence (e.g., human), and/or confirmation by PCR testing. In addition, the sequence assembly is based on at least & average the reference assembly is based on at least & average.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             gross misassemblies, the low-quality ends of sequence contigs have been trimmed away, and each base is associated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        with a Phrap-derived quality score.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               coverage in Q20 bases and has been reviewed to rule
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NOTE: This is a 'working draft' sequence. It currently consists of 7 contigs. Gaps between the contigs are represented as runs of N. The order of the pieces is believed to be correct as given, however the sizes of the gaps between them are based on estimates that I provided by the submittor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This sequence will be replaced
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequencing vector: plasmid; n/a; 100% of reads chemistry: Dye-terminator Big Dye; 100% of reads Assembly program: Phrap; version 0.990319
Consensus quality: 192852 bases at least Q40
Consensus quality: 193282 bases at least Q30
Consensus quality: 193289 bases at least Q20
Consensus quality: 193599 bases at least Q20
Insert size: 175000; agarose-fp
Insert size: 193874; sum-of-contigs
Quality coverage: 12.57x in Q20 bases; sgarose-fp
Quality coverage: 11.34x in Q20 bases; sum-of-contigs
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Center clone name: 254B17
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                                                                                                                                                                                                                                                                                                                                                                                                                             /note="clone overlaps with GenBank Accession Number AC136885 clone RP44-473J11 (center project name dbn)"
                                                                                                                                                                                                    36967.
                                                                                                                                                                                                                                                                                                                                                                                                        1. .10381
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /mol_type="genomic DNA"
/db_xref="taxon:9823"
/clone="RP44-254B17"
                                                             /note="assembly_fragment"
125500 .129483
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   note="assembly_fragment"
129584. .160266
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REFERENCE
AUTHORS
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AL732478/c
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                                                                                                                                 FEATURES
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ORGANISM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (09-JUL-2002) Wellcome Trust Sanger Institute, Hinxton, Cambridgeshire, CBLO 15A, UK. E-mail enquiries: humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk on Jul 1, 2002 this sequence version replaced gi:21615720.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     23;
                                                                                                                                                                                                                                                                                                            regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest. The following abservations are used to associate primary accession numbers given in the feature table with their source databases: Em:, EMBL; Sw:, SWISSRROT; Tr:, TREMBL; Wp:, WORMPEP; Information on the WORMPEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.

This sequence was finished as follows unless otherwise noted: all
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AL732478 203434 bp DNA linear ROD 09 Mouse DNA sequence from clone RP23-42N14 on chromosome 2,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mus musculus (house mouse)
                                                                                                                                                                                constructed by the group of Pieter de Jong.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       During sequence assembly data is compared from overlapping clones.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: humquery@sanger.ac.uk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Web site: http://www.sanger.ac.uk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Center code: SC
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HTG.
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                                                                                                                                                                                                                                       http://www.sanger.ac.uk/Projects/C_elegans/wormpep
from the RPCI-23 Mouse PAC Library
                                                                                                                                                                                                                                                                                            database can be found at
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    vector_side:right"
161455. .194474
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/mol_type="genomic DNA
/db_xref="taxon:10090"
/chromosome="2"
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                                                                             organism="Mus musculus"
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                                                                                                                                 ocation/Qualifiers
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                                                                                                                                                                                   http://www.chori.org/bacpac/home.htm
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TITLE
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                         Birren, B., Nusbaum, C., Lander, E., Abouelleil, A., Allen, N.,
Anderson, S., Arachchi, H.M., Barna, N., Bastien, V., Bloom, T.,
Boguslavkiy, L., Boukhgalter, B., Camarata, J., Chang, J., Choepel, Y.,
Collymore, A., Cook, A., Cooke, P., Corum, B., DeArellano, K.,
Diaz, J.S., Dodge, S., Dooley, K., Dorris, L., Erickson, J., Faro, S.,
Ferreira, P., FitzGerald, M., Gage, D., Galagan, J., Gardyna, S.,
Graham, L., Grand-Pierre, N., Hafez, N., Hagopian, D., Hagos, B.,
Graham, L., Grand-Pierre, N., Lafez, N., Lavine, R., Jones, C.,
Kamat, A., Karatas, A., Kells, C., Landers, T., Levine, R.,
Lindbiad-Toh, K., Liu, G., Lui, A., Mabbitt, R., MacLean, C.,
Lindbiad-Toh, K., Liu, G., Lui, A., Mabbitt, R., MacLean, C.,
Macdonald, P., Major, J., Manning, J., Matthews, C., McCarthy, M.,
Meldrin, J., Meneus, L., Mihova, T., Mlenga, V., Murphy, T., Naylor, J.,
Nguyen, C., Nicol, R., Norbu, C., O'Connor, T., O'Donnell, P.,
O'Neil, D., Oliver, J., Peterson, K., Phunkhang, P., Pierre, N.,
Rachupka, A., Ramasamy, U., Raymond, C., Retta, R., Rise, C., Rogov, P.,
Porman, T., Change, C., Cohunback, B., Camar, C., Carter, B., College, C., Rogov, P.,
Rochan, C., Rogov, P., Carter, M., Carter, R., C., Rogov, P.,
Rochan, C., Rogov, P., Carter, M., Carter, R., C., Rogov, P.,
Rochan, C., Rogov, P., Carter, M., Carter, R., C., Rogov, P.,
Rochan, C., Rogov, P., Carter, R., Carter, R., C., Rogov, P.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (22-MAR-2002) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA (1998) 1, 1998 1, 1998 1, 1998 1, 1998 1, 1998 1, 1998 1, 1998 1, 1998 1, 1998 1, 1998 1, 1998 1, 1
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Direct Submission
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Mus musculus, clone RP24-65D16
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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HTG; HTGS_PHASE1; HTGS_DRAFT
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/clone lib="RPCI-23"
44643 c 45404 g
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Smith, C.
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Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
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Talamas, J., Tesfaye, S., Theodore, Topham, K., Travers, M.,
Vassliev, H., Venkstearaman, V.S., Viel, R., Vo, A., Wilson, B., Wu, X
Wyman, D., Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NOTE: This is a 'working draft' sequence. It currentl consists of 24 contigs. The true order of the pieces is not known and their order in this sequence record
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Insert size: 212333; sum-of-contigs
Quality coverage: 10.6 in Q20 bases; agarose-fp
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Sequencing vector: Plasmid; n/a; 100% of Chemistry: Dye-terminator Big Dye; 100% of Chemistry: Dye-terminator Big Dye; 100% of Chemistry: Dye-terminator Big Dye; 100% of Chemistry: Dye-terminator Big Dye; 100% of Chemistry: Dye-terminator Big Dye; 100% of Chemistry: Dye-terminator Big Dye; 100% of Chemistry: Dye-terminator Big Dye; 100% of Chemistry: Dye-terminator Big Dye; 100% of Chemistry: Dye-terminator Big Dye; 100% of Chemistry: Dye-terminator Big Dye; 100% of Chemistry: Dye-terminator Big Dye; 100% of Chemistry: Dye-terminator Big Dye; 100% of Chemistry: Dye-terminator Big Dye; 100% of Chemistry: Dye-terminator Big Dye; 100% of Chemistry: Dye-terminator Big Dye; 100% of Chemistry: Dye-terminator Big Dye; 100% of Chemistry: Dye-terminator Big Dye; 100% of Chemistry: Dye-terminator Big Dye; 100% of Chemistry: Dye-terminator Big Dye; 100% of Chemistry: Dye-terminator Big Dye; 100% of Chemistry: Dye-terminator Big Dye; 100% of Chemistry: Dye-terminator Big Dye; 100% of Chemistry: Dye-terminator Big Dye; 100% of Chemistry: Dye-terminator Big Dye; 100% of Chemistry: Dye-terminator Big Dye; 100% of Chemistry: Dye-terminator Big Dye; 100% of Chemistry: Dye-terminator Big Dye; 100% of Chemistry: Dye-terminator Big Dye; 100% of Chemistry: Dye-terminator Big Dye; 100% of Chemistry: Dye-terminator Big Dye; 100% of Chemistry: Dye-terminator Big Dye; 100% of Chemistry: Dye-terminator Big Dye; 100% of Chemistry: Dye-terminator Big Dye; 100% of Chemistry: Dye-terminator Big Dye; 100% of Chemistry: Dye-terminator Big Dye; 100% of Chemistry: Dye-terminator Big Dye-terminator Big Dye-terminator Big Dye-terminator Big Dye-terminator Big Dye-terminator Big Dye-terminator Big Dye-terminator Big Dye-terminator Big Dye-terminator Big Dye-terminator Big Dye-terminator Big Dye-terminator Big Dye-terminator Big Dye-terminator Big Dye-terminator Big Dye-terminator Big Dye-terminator Big Dye-terminator Big Dye-terminator Big Dye-terminator Big Dye-terminator Big Dye-terminator 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The Salk, Stanford, PGEC (SSP) Consortium members constructed and sequenced the pUNI (ORF) clones using the RAFI CDNAs: Yamada,K., Chan,M.M., Chang,C.H., Dale,J.M., Hue,J.M., Lee,J.M., Onodera,C.S., Quach,H.L., Tang,C.C., Toriumi,M., Wong,C., Wu,H.C., Yu,G., Yuan,S., Chen,H., Cheuk,R., Jones,T., Kim,C.J., Nguyen,M., Palm,C.J., Southwick,A., Tripp,M.G., Wu,T., Davis,R.W.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (15-MAR-2003) Plant Gene Expression Center, 800 Buchanan Street, Albany, CA 94710, USA
The RIKEN Genomic Sciences Center (GSC) members carried out the
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Yamada, K., Chan, M.M., Chang, C.H., Dale, J.M., Hsuan, V.W., Lee, J.M., Onodera, C.S., Quach, H.L., Tang, C.C., Toriumi, M., Wong, C., Wu, H.C., Yu, G., Yuan, S., Carninci, P., Chen, H., Cheuk, R., Hayashizaki, Y., Ishida, J., Jones, T., Kamiya, A., Kawai, J., Kim, C.J., Narusaka, M., Nguyen, M., Palm, C.J., Sakurai, T., Satou, M., Seki, M., Shinn, P., Southwick, A., Tripp, M.G., Wu, T., Shinozaki, K., Davis, R.W., Direct Submission
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Palm,C.J., Shinn,P., Southw
Ecker,J.R. and Theologis,A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 collection and clustering of RAFL cDNAs (RAFL cDNA : 'RIKEN Arabidopsis Full-Length cDNA'): Seki,M', Marusaka,M', Isi Satou,M', Kamiya,A', Sakurai,T', Carninci,P', Kawai, J', Hayashizaki,Y', and Shinozaki,K'
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                           ecotype: Columbia"
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/gene="At5g09300"
                                                                                                 clone="U50137"
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'db_xref="taxon:3702"
'chromosome="5"
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Submitted (11-MAR-2002) Ceres, Inc, 3007 Malibu Canyon Road, Malibu, CA 90265, USA
This clone sequence is one of 5,000 Ceres full-length cDNAs made available to TIGR and Genbank. The following quality assessment of this set was done by comparison with known proteins: two percent of the clones are estimated to be 5'-truncated; less than one percent are 3'-truncated; approximately two percent represent alternative splice variants, including unspliced introns and spliced exons; one percent may contain premature stop codons; five percent may have frame shifts in a coding region. A sequence is considered to be 5'-truncated if it lacks the translation initiation start (ATG). A sequence is considered to be 3'-truncated if it lacks the considered to be 3'-truncated if it lacks the considered to be 3'-truncated if it lacks the considered to be 3'-truncated if it lacks the considered to be 3'-truncated if it lacks the considered to be 3'-truncated if it lacks the considered to be 3'-truncated if it lacks the considered to be 3'-truncated if it lacks the considered to be 3'-truncated if it lacks the considered to be 3'-truncated if it lacks the considered to be 3'-truncated if it lacks the considered to be 3'-truncated if it lacks the considered to be 3'-truncated if it lacks the considered to be 3'-truncated if it lacks the considered to be 3'-truncated if it lacks the considered to be 3'-truncated if it lacks the considered to be 3'-truncated if it lacks the considered to be 3'-truncated if it lacks the considered to be 3'-truncated if it lacks the considered to be 3'-truncated if it lacks the considered to be 3'-truncated if it lacks the considered to be 3'-truncated if it lacks the considered to be 3'-truncated if it lacks the considered to be 3'-truncated if it lacks the considered to be 3'-truncated if it lacks the considered to be 3'-truncated if it lacks the considered to be 3'-truncated if it lacks the considered to be 3'-truncated if it lacks the considered to be 3'-truncated if it lacks the considered to be 3'-
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Haas, B.J., Volfovsky, N., Town, C.D., Troukhan, M., Alexandrov, N., Feldmann, K.A., Flavell, R.B., White, O. and Salzberg, S.L. Feldmann, K.A., Flavell, R.B., White, O. and Salzberg, S.L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3 (bases 1 to 1547)
Brover, V., Troukhan, M., Alexandrov, N., Lu, Y.-P.,
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Arabidopsis thaliana clone 3693
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Full-Length cDNA from Arabidopsis thaliana
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dehydrogenase El alpha subunit"
/protein id="Ano64036.1"
/db_xref="GI:28973423"
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YSAVHTAREMAIREQRPILIEALTYRVGHHSTSDDSTRYRSAGEIEWWNKARNPLSRF
RTWIESNGWWSDKTESDLRSRIKKEMLEALRVAEKTEKPNLQNWFSDVYDVPPSNLRE
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/codon_start=1
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Pred. No.
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JOURNAL REFERENCE
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BT004286
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                                                                                                                                                                                                                                              2 (bases 1 to 1603)
Yamada, K., Chan, M.M., Chang, C.H., Dale, J.M., Hsuan, V.W., Lee, J.M. Onodera, C.S., Quach, H.L., Tang, C.C., Toriumi, M., Wong, C., Wu, H.C. Yu, G., Yuan, S., Carninci, P., Chen, H., Cheuk, R., Hayashizaki, Y., Ishida, J., Jones, T., Kamiya, A., Kawai, J., Kim, C.J., Narusaka, M., Nguyen, M., Palm, C.J., Sakurai, T., Satou, M., Seki, M., Shinn, P., Southwick, A., Tripp, M.G., Wu, T., Shinozaki, K., Davis, R.W.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 (bases 1 to 1603)
Yamada, K., Chan, M.M., Chang, C.H., Dale, J.M., Hsuan, V.W., Lee, J.M. Onodera, C.S., Quach, H.L., Tang, C., Toriumi, M., Wong, C., Wu, H.C., Yu, G., Yuan, S., Carninci, P., Chen, H., Cheuk, R., Hayashizaki, Y., Ishida, J., Jones, T., Kamiya, A., Kawai, J., Kim, C.J., Narusaka, M., Nguyen, M., Palm, C.J., Sakurai, T., Satou, M., Seki, M., Shinn, P., Southwick, A., Tripp, M.G., Wu, T., Shinozaki, K., Davis, R.W., Ecker, J.R. and Theologis, A. Arabidopsis Full Length cDNA Clones
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    sequences are derived from the Ws or LAer ecotypes and therefore may contain polymorphisms when compared to sequences from Col-0. Genset carried out the library production and sequencing of the full-length clones. Ceres, Inc. carried out the clustering of the 5' sequences, selection of clones, and sequence assembly.
collection and clustering of RAFL cDNAs (RAFL cDNA : 'RIKEN Arabidopsis Full-Length cDNA'): Seki,M., Narusaka,M., Ishida,J., Satou,M., Kamiya,A., Sakurai,T., Carninci,P., Kawai,J., Hayashizaki,Y. and Shinozaki,K.
                                                                                                                Street, Albany, CA 94710, USA RIKEN Genomic Sciences Center (GSC) members carried out the
                                                                                                                                                                Direct Submission
Submitted (14-FEB-2003) Plant Gene Expression Center,
                                                                                                                                                                                                                                                                                                                                                                                                                                         Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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Arabidopsis thaliana
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/db_xref="taxon:3702"
/clone="3693"
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                                                                                                                                                                         800 Buchanan
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Wu, H.C.,
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The Salk, Stanford, PGEC (SSP) Consortium members carried out sequencing and annotation of the RAFL cDNAs: Yamada,K., Chan, Chang,C.H., Dale,J.M., Hsuan,V.W., Lee,J.M., Onodera,K.S., Quach,H.L., Tang,C.C., Toriumi,M., Wong,C., Wu,H.C., Yu,G., Yuan,S., Chen,H., Cheuk,R., Jones,T., Kim,C.J., Nguyen,M., Palm,C.J., Southwick,A., Tripp,M.G., Wu,T., Davis, Palm,C.J., Shinn,P., Southwick,A., Tripp,M.G., Wu,T., Davis,

Chan, M.M.,

out the

Yamada,K. (SSP/PGEC) and Seki,M. (RIKEN GSC) contributed equally to

(SSP/PGEC)

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REFERENCE
AUTHORS
TITLE
JOURNAL
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DEFINITION
ACCESSION
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AC015298
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                                                                                                                                                         HTG; PHASE2.

Drosophila melanogaster (fruit fly)

Drosophila melanogaster

Drosophila melanogaster

Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;

Meoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;

Ephydroidea; Drosophilidae; Drosophila.

1 (bases 1 to 54419)
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                                                     Rockville, MD, USA
This sequence was identified as CDM:10213547 by
                                                                                                 Submitted (16-NOV-1999) Celera Genomics, 45 West Gude Drive,
                                                                                                                                                                                                                                                                                                     AC015298
AC015298.1 GI:6436037
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                                                                                                                                     Adams, M. and Venter, J.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity
                                                                                                                       Direct Submission
or further information on this sequence e-mail to fly@celera.com. NOTE: This is a 'working draft' sequence.
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/dehydrogenase E1 alpha subunit"
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/db_xref="G1:28393751"
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RVPCYRVLDDNGQLITNSQFVQVSEEVAVKIYSDMVTIQIMDNIFYEAQRQGRUSFYA
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ALNIAAVMEAPVLFICRNNGWALSTFDSQFRSDGVVVKGRAVGIRSIRVDGNUSALAM
XSAVHTAREMAIREQRFILEBALTYRVGHHSTSDDSTRYRSAGETEWNINGANISRF
ETWITCHNGWALSTFED
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/note="artifact within poly A tail"
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67. .1485
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/note="This clone is in a modified pBluescript vector2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Information on performance of analysis and a more detailed annotation of this entry and other sequences of chromosomes 3, 4 and 5 can be viewed at: http://www.mips.biochem.mpg.de/proj/thal/.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EU Arabidopsis sequencing, project. Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bevan, M., Murphy, G., Ridley, P., Hudson, S., Bancroft, I., Mewes, H.W., Rudd, S., Lemcke, K. and Mayer, K.F.X.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Unpublished
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PWKRRKLPAIPTKNDDDAKGRDHAKSSWLLDLSRGDEFYTQEQMQQRLKEHSQDERPM
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12728 c 10928 g 14786
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chromosome="5"
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'variety="Columbia"
                                                                                                                                                                 note="similarity to GCF2 fusion
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| = "TSEB 20" = "Contains I hment site I hment site I n_start=1 n_st | /gene="T5B8_20"<br>join(7652 .7793,7900 .8133,8215 .8308,8403 .8617,<br>j698 .8837.8992 .9648) | /gene="15E8 10" /gene="15E8 10" /number=7 complement (56356144) /gene="15E8 10" /number=8 76529648  | •   | Complement (52755397) /gene="T5E8_10" /number=6 complement (53985441)                                     | /number=5<br>complement(52275274)<br>/gene="7588_10"<br>/number=5  | /number=4<br>complement(49105226)<br>/gene="T5B8_10" | /gene="T5E8_10"<br>/number=4<br>complement(46864909)<br>/gene="T5E8 10" | complement (43074411) /gene="T5E8_10" /number=3 complement (44124685) | / number=2<br>complement(4011. 4306)<br>/gene="75E8_10"<br>/number=3 | /number=2<br>complement(36344010)<br>/gene="75E8_10" . | /number=1<br>complement(35253633)<br>/gene="T5E8_10" | /number=1<br>complement(34523524)<br>/gene="T5E8_10" | VPTWDPOVSKUVENAPOVAAYRFOTSVELMKNICMKKDYMELPYLEKLALSDLLFGKV LPHVRSIASESNIHDAVTKTERIVASLSGVWTGPSVTRTHSHLLQPLVDCTLTLGRIL EKKVCLGTGRYGNHWSRPQEDVDLQLTDPFSVKIKVI" complement(33953451) /gene="T5E8_10" | AYEEARDSLLQRADKIFSDASVVYSELSRVKSIFKRGARHPSPAFRAAYTSLTVPSMY<br>SPYLRLELLRWDPLHQDVDFSDMNWHGLLFHSRIVCGSTPVCTNPNFVSELVKYVAVP<br>ILHHRIVRCWDILSTRETRNVVAATSLVARYVFPSSEALAELSLAIHARLVEAIIAIS | YAGRPEELAKEPDENLTMSIAAAESCPSAPVYKYASLQEISDFKSVFRNFMQGICVAF<br>VCVSGAFISIKRLLSIFFLSQKWGYLITAIEDQWKVDGYSLIVEGDSSTDDESDCETS |
| intron 1199612105 /gene="TSE8 30" /number=1 exon 1210612214 /gene="TSE8 30" /number=2 intron 1221512603 /gene="TSE8 30" /number=3 intron 12604 .12841 /gene="TSE8 30" /number=3 intron 1292412923 /gene="TSE8 30" /number=3  | exon 1184011995<br>/gene="T588_30"<br>/number=1  | LYRLFEQSSRLTILITGAGVSTECGIPDYRSPNGAYSSGFKPITHQEFTRSSRARRRYW ARSYAGWRRFTAAQPGPAHTALASLEKAGRINFMITQNVDRLHHRAGSDPLELHGTVY TVWCLECGFSFPRDLFQDQLKAINFKASWAEA ESIDHGDPGSEKSFGNKQRPDGDIE IDEKFWEEGFHIPVCEKCKGVLKPDVIFFGDNIFKERATQAMEVAKQSDAFLVLGSSL MTMSAFRLCRAAHEAGAMTAIVNIGETRADDIVPLKINARVGEILHRVLDVGSLSVPA | /product= SIRS_INITED   PRODUCT=   /protect= in_id= "CACO5449.1" /db_xref="GI:9955510" /translation="MKLHQDKNRRESHERIFDRELTRSSSRERDRSEGEIEAKERELR /translation="MKLHQDKNRRESHERIFDRELTRSQDLFPSRSMYRPLQS PORENKIDTSDFCHLYPNNNKKFMKIKKKTERISFTPRTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT | /gene="T5E8 30" /note="similarity to sirtuin type 4 (SIRT4) - Homo sapiens, EMBL:AF083109" /codon start=1 | /gene="1558_30"<br>join(1184011995,1210612214,1260412841,1292412989<br>1309013135,1324513405,1348213617,1369113855,<br>1392914056.1412914228.1434814398) | /gene="T5E8_20"<br>/number=6<br>11840.114398         | Intron 8838. 8991 //gene="TSE8_20" /number=5 /number=5 exon 8992. 9648  | ) ~ ~ B ~   | /gene="1558_20" /number=4 intron 8618.8697 /gene="T558_20"           | , 1,   | I <sub>N</sub>                                       | ="T5E8_2<br>er=2<br>.8308                            | exon 79008133<br>/gene="T5E8_20"<br>/number=2<br>intron 81348214  |  | exon 76527793<br>/gene="T558_20"   |

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Allen, C., Allen, H., Alsbrooks, S., Adams, C., Alder, J., Allen, C., Allen, H., Alsbrooks, S., Anin, A., Angulano, D., Allen, H., Alsbrooks, S., Anin, A., Angulano, D., Anyalebechi, V., Aoyagi, A., Ayodeji, M., Baca, E., Baden, H., Baladwin, D., Bandaranaike, D., Barber, M., Barnstead, M., Benahmed, F., Biswalo, K., Blair, J., Blankenburg, K., Blyth, P., Brown, M., Cher, J., Cherelans, V., Carrer, K., Cavazos, I., Ceasar, H., Center, A., Chen, Z., Chu, J., Cleveland, C., Cockrell, R., Cox, C., Coyle, M., Cree, A., D., Scher, G., Chen, Y., Chen, Y., Chen, Z., Chu, J., Claves, D., Chen, G., Chen, R., Chen, Y., Chen, Z., Chu, J., Claveland, C., Decrano, C., Ding, M., Durbin, K., Duvall, B., Eaves, K., Egan, A., Escotto, M., Eugene, C., Evans, C.A., Falls, T., Fan, G., Frinley, M., Flagg, N., Forbes, I., Foster, M., Foster, M., Gabisi, A., Gantar, R., Garcia, A., Garner, T., Garza, M., Gebregoorgis, B., Geer, K., Gill, R., Grady, M., Guerra, W., Gunaratne, P., Haaland, M., Hamil, C., Hamilton, C., Hamilton, K., Harvey, Y., Havlak, P., Hawes, A., Henderson, N., Hernandez, J., Havlak, P., Hawes, A., Henderson, N., Hernandez, M., Harvey, Y., Havlak, P., Hawes, A., Henderson, N., Hernandez, J., Liu, W., London, P., Longare, S., Lopez, J., Liu, V., London, P., Longare, S., Lopez, J., Liu, V., London, P., Longare, S., Lopez, J., Liu, V., London, P., Longare, S., Lopez, J., Liu, V., London, P., Mortens, S., Manner, S., Manner, S., Manner, S., Manner, S., Manner, S., Manner, S., Manner, S., Manner, S., Manner, S., Manner, S., Manner, S., Manner, S., Manner, S., Manner, S., Manner, S., Manner, S., Manner, S., Manner, S., Manner, S., Manner, S., Manner, S., Pers, Y., Reter, Y., Retter, M., Richards, S., Reigh, R., Reily, M., Ren, Y., Retter, M., Rose, M., Rais, S., Shen, H., Sander, M., Sodergren, S., Soott, G., Shatsman, S., Shen, H., Sander, M., Sodergren, S., Soott, G., Shatsman, S., Shen, H., Shen, H., Shen, H., Shen, H., Shen, H., Shen, H., Shen, H., Shen, H., Shen, H., Shen, H., Shen, H., Shen, H., Shen, H., Shen, H.,
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AC123445.4 GI:25137917
HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_ENRICHED.
Rattus norvegicus (Norway rat)
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
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100.0%; Pred. No.
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FEATURES

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.4155

/note="wgs\_end\_extension clone\_end:Sp6" /note="wgs\_end\_extension
clone\_end:Sp6"

/organism="Rattus norvegicus" /mol\_type="genomic DNA" /db\_xref="taxon:10116"

clone="CH230-403G9"

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On Nov 20, 2002 this sequence version replaced gi:23907751.
The sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequencing reads assembled using Atlas (http://www.hgsc.bcm.tmc.edu/projects/rat/). Each contig described in the feature table below represents a scaffold in the Atlas assembly (a 'contig-scaffold'). Within each contig-scaffold, individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (29-MAY-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA 3 (bases 1 to 168601)
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Direct Submission
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Direct Submission
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                                                                                                                                                                                                                                                                                       NOTE: Estimated insert size may differ from sequence length (see http://www.hggc.bcm.tmc.edu/docs/Genbank_draft_data.) NOTE: This is a 'working draft' sequence. It currently consists of 3 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will
                                                                                                                                                                                                                                                   be preserved
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Center project Information
Center project name: GXID
Center clone name: CH230-403G9
Center clone name: CH230-403G9
Consensus quality: 159374 bases at least Q40
Consensus quality: 160849 bases at least Q30
Consensus quality: 161918 bases at least Q30
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165292: contig of 165292 bp in length 165392: gap of unknown length 166779: contig of 1387 bp in length 166879: gap of unknown length 168611: contig of 1722 bp in length.

    Genome Center

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                                                                                                                                                      Celniker, S.E., Agbayani, A., Arcaina, T.T., Baxter, E., Blazej, R.G. Butenhoff, C., Champe, M., Chavez, C., Chew, M., Classiolka, L., Doyle, C.M., Farfan, D.E., Galle, R., George, R.A., Harris, N. L., Hoskins, R.A., Houston, K.A., Hummasti, S.R., Karra, K., Kearney, L., Kim, E., Lee, B., Lewis, S., Li, P., Lomotan, M.A., Mazda, P., Moshrefi, A.R., Moshrefi, M., Nixon, K., Pacaleb, J.M., Park, S., Pfeiffer, B., Poon, L., Sequeira, A., Sethi, H., Snir, E., Svirskas, R.R., Wan, K.H., Weinburg, T., Zhang, R., Zieran, L.L. and
                                        Submitted (14-JUN-1999) Drosophila Genome Center, Lawrence Berkeley Laboratory, MS 64-121, Berkeley, CA 94720, USA On Feb 15, 2001 this sequence version replaced gi:5822638.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Drosophila melanogaster (fruit fly)
Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
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22; Conserv
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1 (bases 1 to 171569)
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BACR45M04, complete seque
Berkeley Drosophila Genome Project
                                                                                                                                                                                                                                                                                                                                                                      Unpublished
                                                                                                                                                                                                                                                                                                                                                                                             Sequencing of Drosophila chromosome 3R, region 90C-90D
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                                                                                                             Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.

The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases:

Em: RMBL; Sw. SWISSPROT; Tr:, TREMBL; Wp:, WORMPEP; Information on the WORMPEP database can be found at http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence was generated from part of bacterial clone contigs of human chromosome 10, constructed by the Sanger Centre Chromosome 10 Mapping Group. Further information can be found at http://www.sanger.ac.uk/HGP/Chr10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (04-MAR-2003) Wellcome Trust Sanger Institute, Hinxton, Cambridgeshire, CB10 1SA, UK. B-mail enquiries: humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk Clone sequence version replaced gi:5931851. On Sep 30, 1999 this sequence version replaced gi:5931851. During sequence assembly data is compared from overlapping clones.
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Contact: humquery@sanger.ac.uk
                                                   Center code:
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/clone=lib="RPCI-98 (Roswell Park Cancer Institute
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This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >=

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RP11-192P3 is from the library RPC1-11.1 constructed by the group of Pieter de Jong. For further details see
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Homo sapiens BAC clone 13d21, complete sequence.
AF225898
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Fitzpatrick,E.S., Hammond,H.A., DeAngelis,D.M., Sodermaritzpatrick,E.S., Liu,X., Diame,L., McGowan,J., Ziegler,S., Todd,J., Caskey,C.T. and Metzker,M.L.
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/db_xref="taxon:9606"
/chromosome="10"
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/mol_type="genomic DNA"
/db_xref="taxon:9606"
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160946. .161130,163685. .165932)
jproduct="two-handed zinc finger protein ZEB"
/note="corresponds to mRNA sequence deposited in GenBank
Accession Number U19969"
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97612. .97702
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/rpt_family="Alu"
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/rpt_family="L1"
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/rpt_family="Alu"
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|8377. 48660
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rpt_family="L1"
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/rpt_family="Alu"
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/rpt_family="Alu"
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/rpt_family="L1"
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complement(120797.
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147695. .147897,151625. .151727,157139. .158949,
160946. .161126,163685. .164393)
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160946. .161126,163685. .164819)
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/note="corresponds to mRNA sequence deposited in
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RRS Adams, M.D., Celniker, S.E., Holt, R.A., Evans, C.A., Gocayne, J.D., Adams, M.D., Celniker, S.E., Li, P.W., Hoskins, R.A., Galle, R.F., George, R.A., Lewis, S.E., Richards, S., Ashburner, M., Henderson, S.N., Sutton, G.G., Wortman, J.R., Yandell, M.D., Zhang, O., Chen, L.X., Sutton, G.G., Wortman, J.R., Yandell, M.D., Zhang, O., Chen, L.X., By Change, M., Pfeiffer, B.D., Wan, K.H., Doyle, C., Baxter, E.G., Helt, G., Nelson, C.R., Gabor, G.L., Abril, J.F., Agbayani, A., An, H.J., Andrews-Pfannkoch, C., Baldwin, D., Ballew, R.M., Baxu, A., Baxendale, J., Bayraktaroglu, L., Beasley, E.M., Beeson, K.Y., Benos, P.V., Berman, B.P., Bhandari, D., Bolshakov, S., Busam, D.A., Butler, H., Cadieu, E., Center, A., Chandra, I., Cherry, J.M., Cawley, S., Dahlke, C., Davenport, L.B., Davies, P., de Pablos, B., Delcher, A., Deng, Z., Mays, A.D., Dew, I., Dietz, S.M., Dodson, K., Doup, L.E., Downes, M., Dugar-Rochla, S., Dankov, B.C., Dunn, P., Durbin, K.J., Evangelista, C.C., Ferraz, C., Ferriera, S., Fleischmann, W., Fosler, C., Gabrielian, A.E., Garg, N.S., Gelbart, W.M., Glasser, K., Glodek, A., Gong, F., Gorrell, J.H., Gu, Z., Guan, P., Harris, M., Harris, N.L., Harvey, D., Heiman, T.J., Wei, M.H., Ibegwam, C., Jalali, M., Kalush, F., Karpen, G.H., Ke, Z., Kravitz, S., Kulp, D., Lai, Z., Liasko, P., Lei, Y., Levitsky, A.A., Li, J., Li, Z., Liang, Y., Lin, X., Liu, X., Mattei, B., Windon, K.A., Nusskern, D.R., Pacleb, J.M., Palazzolo, M., Pittman, G.S., Pan, S., Pollard, J., Puri, V., Reese, M.G., Reinert, K., Remington, K., Sapleron, M., Strong, R., Sun, E., Svirskas, R., Tector, C., Turner, R., Venter, E., Wang, A.H., Wang, X., Wallson, D.A., Weinstock, G.M., Weinstock, G.M., Shou, Y., Shou, N., Spier, E., Spier, E., Spier, E., Spier, E., Spier, E., Spier, E., Spier, E., Spier, R., Sun, E., Svirskas, R., Tector, C., Turner, R., Zhong, F., Chang, M., Zhang, G., Zho, X., Sanith, H.O., Glbbs, R.A., Wyers, E.M., Rubin, G.M. and Venter, J.C.
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AE003719.3 GI:23171576
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/rpt_family="THE1"
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complement(182278.
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181513. .181648
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COMMENT
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Submitted (06-SEP-2002) University of California Berkeley, 539 Life
Sciences Addition, Berkeley, CA 94720, USA
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On Sep 18, 2002 this sequence version replaced gi:10726587
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (13-FEB-2003) University of California Berkeley, 539 Life Sciences Addition, Berkeley, CA 94720, USA
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Adams, M.D., Celniker, S.E., Gibbs, R.A., Rubin, G.M. and Venter, C.J.
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                                                                                                                                                                                                                                                                                                                                                                        /locus tag="CG7660"
/notes="last curated on Mon Aug
/notes="last curated on Mon Aug
/maps="90C2-90C2"
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                                                                                                            /locus_tag="CG7660"
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join(583 ..845,1140 ..1927,2060.
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3241. .3399,3454. .3773,3829. .4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Drosophila melanogaster"
/mol_type="genomic DNA"
'locus_tag="CG7660"
                                                                         241. .3399,3454. .3773,3829.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 note="genotype: y[1]; cn[1] bw[1] sp[1]; Rh6[1]"
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                                          gene="pxt"
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                                                                                                            .2486,2615. .2942,3004.
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                                                                                                                .3178,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RAHSSDGTPLLGARKISRTLLSDUDRRHPKYNLMVMODGQVLAHDISQTSSIRLEDGS
LVQCCSPEGKVALSPQOSHFACMPIHVEPDDEFFSAFGVRCLNFVRLSLVPSSPDCQLS
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VIAEMCHITYNEFLPIIIGPQMKRFRLVPLHGGYSHDYNMVPAITNEFSGAAYRM
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ISGGLSRFLFRGDNPFGLDLAAINIQRGRDQGLRSYNDYLELMGAPKLHSFEQFPIEI
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PLAHHGQPPPVCGNIRSVYRSMDGTCNNPEPQRSLMGAAGQPMERMLPPAYEDGIWTP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /product="CG12334-RA"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PLAAFVRADHPGNQMIGCDDPNLPSVNLEAWRA"
join(680. .845,1140. .1927,2060. .2486,2615.
3241. .3399,3454. .3773,3829. .3895)
                                                                                                                                                                                                                                                                                                                                                                                                                                           complement (5533...61)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AQKLSRVYRTPDDIDLMVGGLLEKAVEGGVVGVTFAEIIADQFARFKQGDRYYYEYDN
GINPGAFNPLQLQEIRKVTLARLLCDNSDRLTLQAVPLAAFVRADHPGNQMIGCDDPN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NDYLELMGAPKLHSFEQFPIEIAQKLSRVYRTPDDIDLMVGGLLEKAVEGGVVGVTFA
EIIADQFARFKQGDRYYYEYDNGINPGAFNPLQLQEIRKVTLARLLCDNSDRLTLQAV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GALHELNPSASDETLFQEARRIVIAEMQHITYNEFLFIIIGPQQMKRFRLVPLHQGYS
HDYNVNVNPAITNEFSGAAYRMGHSSVDGKFQIRQEHGRIDEVVNIPDVMFNPSRMRK
REFYDDMLRTLYSQPMQQVDSSISQGLSRFLFRGDNPFGLDLAAINIQRGRDQGLRSY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EEAGKSCFHSGKSLLSNVFLIINSLITYLTRLGDGRTNQIISLITLQILLAREHNRVA
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LVQCCSPEGKVALSPQQSHFACMPIHVEPDDEFFSAFGVRCLNFVRLSLVPSPDCQLS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             complement (5533.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /protein_id="AAF55458.2"
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complement(5533. .6153)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LPSVNLEAWRA"
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|note="pxt gene product from transcript CG7660-RB'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   'gene="pxt"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Allen, C., Allen, Mettker, M.Lee, Abramzon, S., Adams, C., Alder, J., Allen, C., Allen, H., Alabrooks, S., Amin, A., Angulano, D., Allen, C., Allen, H., Alabrooks, S., Amin, A., Angulano, D., Baden, H., Baldwin, D., Bandaranaike, D., Barber, M., Barnstead, M., Benahmed, F., Bliswalo, K., Blair, J., Blankenburg, K., Blyth, P., Brown, M., Bryant, N., Buhay, C., Burch, P., Burrell, K., Calderon, E., Cardenas, V., Carter, K., Cavazos, J., Ceasar, H., Center, A., Chu, J., Chacko, J., Chavez, D., Chen, G., Chen, Y., Chen, Y., Chen, Z., Chu, J., Chacko, J., Chavez, D., Chen, G., Chen, M., Chen, Y., Chen, Z., Chu, J., Chacko, J., Chavez, D., Chen, G., Chen, M., Chen, Y., Chen, Z., Chu, J., Davila, M.L., Davis, C., Davy-Carroll, L., De Anda, C., Dederich, D., Davila, M.L., Davis, C., Davy-Carroll, L., De Anda, C., Dederich, D., Davila, M., Locate, S., Dunn, A., Durbin, K., Duval, B., Eaves, K., Draper, H., Dugan-Rocha, S., Dunn, A., Durbin, K., Duval, B., Eaves, K., Egan, A., Escotto, M., Eugene, C., Evans, C.A., Falls, T., Fan, G., Fraeer, C.M., Gabisi, A., Ganta, R., Garcia, A., Garrar, M., Guevara, W., Gerra, W., Guevara, W., Harley, Y., Haalland, W., Hamil, C., Hamilton, C., Hamilton, C., Hamilton, C., Hamilton, C., Hamilton, C., Hamilton, C., Hamilton, C., Hamilton, C., Hamilton, C., Hamilton, C., Hamilton, C., Hamilton, C., Harlyk, S., Hune, J., Idebird, D., Jackson, A., Hernandez, M., Hernandez, M., Johnson, B., Johnson, R., Jolivet, A., Kowis, C., Kraft, C.L., Lebow, H., Levan, J., Lewis, L., Li, Z., Liu, J., Liu, W., Liu, Y., London, P., Longacre, S., Lopez, J., Love, J., Liu, J., Liu, W., Liu, Y., London, P., Longacre, S., Lopez, J., Mangum, B., Mapua, P., Martin, K., Martin, R., Martinez, E., Mundasa, M., Murphy, M., Nair, L., Markon, M., Mahindara, M., Martin, R., Martinez, E., Mangum, A., Martinez, B., Montenayor, J., Moore, S., Mangum, A., Petz, J., Fannkoch, C., Parks, K., Parks, K., Parks, K., Parks, K., Parks, K., Parks, K., Parks, K., Parks, M., Reigh, R., Lagg, F., Lagg, F., Lagg, F., Lagg, F., Lagg, 
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Taylor,T., .... Vera,V., v.... Warren,J.
                           Reilly, B., Reilly, M., Ren, Y., Reuter, M., Richards, S., Riggs, F., Rives, C., Rodkey, T., Rojas, A., Rose, M., Rose, R., Ruiz, S.J., Sanders, W., Savery, G., Scherer, S., Scott, G., Shatsman, S., Shen, H., Shetty, J., Shvartsbeyn, A., Sisson, I., Sitter, C.D., Smajs, D., Shetty, J., Sheat, A., Sodergren, E., Song, X.-Z., Sorelle, R., Sosa, J., Steimle, M., Strong, R., Sutten, A., Svatek, A., Tabor, P., Taylor, C., Taylor, T., Thomas, N., Tingey, A., Trejos, Z., Usmani, K., Valas, R., Vera, V., Villasana, D., Waldron, L., Walker, B., Wang, J., Wang, O., Wang, S., Warren, J., Warren, R., Wei, X., White, F., Walliam, S., Wang, S., Warren, J., Warren, R., Wei, X., White, F., Walliam, Walliam, Walliam, Walliam, Walliam, Walliam, Walliam, Walliam, Walliam, Walliam, Walliam, Walliam, Walliam, Walliam, Walliam, Walliam, Walliam, Walliam, Walliam, Walliam, Walliam, Walliam, Walliam, Walliam, Walliam, Walliam, Walliam, Walliam, Walliam, Walliam, Walliam, Walliam, Walliam, Walliam, Walliam, Walliam, Walliam, Walliam, Walliam, Walliam, Walliam, Walliam, Walliam, Walliam, Walliam, Walliam, Walliam, Walliam, Walliam, Walliam, Walliam, Walliam, Walliam, Walliam, Walliam, Walliam, Walliam, Walliam, Walliam, Walliam, Walliam, Walliam, Walliam, Walliam, Walliam, Walliam, Walliam, Walliam, Walliam, Walliam, Walliam, Walliam, Walliam, Walliam, Walliam, Walliam, Walliam, Walliam, Walliam, Walliam, Walliam, Walliam, Walliam, Walliam, Walliam, Walliam, Walliam, Walliam, Walliam, Walliam, Walliam, Walliam, Walliam, Walliam, Walliam, Walliam, Walliam, Walliam, Walliam, Walliam, Walliam, Walliam, Walliam, Walliam, Walliam, Walliam, Walliam, Walliam, Walliam, Walliam, Walliam, Walliam, Walliam, Walliam, Walliam, Walliam, Walliam, Walliam, Walliam, Walliam, Walliam, Walliam, Walliam, Walliam, Walliam, Walliam, Walliam, Walliam, Walliam, Walliam, Walliam, Walliam, Walliam, Walliam, Walliam, Walliam, Walliam, Walliam, Walliam, Walliam, Walliam, Walliam, Walliam, Walliam, Walliam, Walliam, Walliam, Walliam, Walliam, Walliam, Walliam, Wall
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Rattus norvegicus clone CH230-166D21, WORKING DRAFT SEQUENCE.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Rattus norvegicus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HTG; HTGS_PHASE2; HTGS_DRAFT; HTGS_FULLTOP
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/note="last curated on Mon Jan 21 21:08:19 PST
/map="90C2-90C2"
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100.0%; Pred. No.
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7.8;
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FEATURES
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JOURNAL
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                                                                                                                                                          misc_feature
                                                                                                                                                                                                                                                                                                                                     source
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On May 10, 2003 this sequence version replaced gi:25089200.
The sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequencing reads assembled using Atlas (http://www.hgsc.bcm.tmc.edu/projects/rat/). Each contig described in the feature table below represents a scaffold in the Atlas assembly (a 'contig-scaffold'). Within each contig-scaffold, individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence may extend beyond the ends of the clone and there may be sequence contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         of Molecular and Human Genetics,
Baylor Plaza, Houston, TX 77030,
3 (bases 1 to 221952)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (05-NOV-2001) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   wases 1 to 221952)
Worley,K.C.
Direct
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             table.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       shotgun sequence only contigs will be indicated in the feature
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NOTE: Estimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).

NOTE: This is a 'working draft' sequence. It currently consists of 1 contigs. Gaps between the contigs are represented as runs of N. The order of the pieces is believed to be correct as given, however the sizes of the gaps between them are based on estimates that have
                                                                                                                                                                                                                                                                                                                                                                          the accession number will be preserved.

1 221952: contig of 221952 bp in length.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       provided by the submittor.
This sequence will be replaced by the finished sequence as so
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Center project name: GINS
Center clone name: CH230-166D21
Center clone name: CH230-166D21
Center Summary Statistics
Assembly program: Atlas 3.0;
Consensus quality: 213950 bases at least Q40
Consensus quality: 215107 bases at least Q30
Consensus quality: 2158107 bases at least Q20
Consensus quality: 215809 bases at least Q20
Estimated insert size: 225832; sum-of-contigs estimation
Quality coverage: 7x in Q20 bases; sum-of-contigs estimation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Web site: http://www.hgsc.bcm.tmc.edu/Contact: hgsc-help@bcm.tmc.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Center: Baylor College of Medicine Center code: BCM
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   end_sequence:BH279251"
47344 c 43902 q 61
                                                                      site: EcoRI
                                                                                                                                                                complement (217689
                                                                                                 /note="clone_boundary
clone_end:T7
                                                                                                                                                                                                  /clone="CH230-166D21"
                                                                                                                                                                                                                          /mol_type="genomic DNA'
/db_xref="taxon:10116"
                                                                                                                                                                                                                                                                                                organism="Rattus norvegicus"
                                                                                                                                                                                                                                                                                                                                                                location/Qualifiers
                                                                                                                                                                                                                                                                                                                                     .221952
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43902 g 61410 t
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BASE COUNT ORIGIN

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  TITLE
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                                     Allen, C., Allen, H., Albirocks, S., Amin, A., Adams, C., Aller, J., Allen, C., Allen, H., Albirocks, S., Amin, A., Angulano, D., Anyalebechi, V., Aoyagi, A., Ayodeji, M., Baca, E., Badden, H., Anyalebechi, V., Aoyagi, A., Ayodeji, M., Baca, E., Badden, H., Anyalebechi, V., Aoyagi, A., Ayodeji, M., Baca, E., Badden, H., Balawin, D., Bandzer, M., Benahmed, F., Bladwin, D., Bardzer, M., Burnstead, M., Benahmed, F., Blawalo, K., Blair, J., Blankenburg, K., Blyth, P., Brown, M., Benahmed, F., Blawalo, K., Blair, J., Blankenburg, K., Blyth, P., Brown, M., Brown, M., Buhay, C., Burch, P., Burcell, K., Cadderon, E., Chu, J., Claveland, C., Cockreil, R., Coxacos, I., Casar, H., Center, A., Chen, Z., Chen, Z., Chen, Z., Chen, Z., Chen, C., Coyle, M., Cree, A., D'Souza, L., Davila, M., Davis, C., Davy-Carroll, L., De Anda, C., Dederich, D., Delgado, O., Denson, S., Dermo, C., Ding, Y., Dinh, H., Divya, K., Darper, H., Dugan-Rocha, S., Dunn, A., Durbin, K., Duval, B., Eaves, K., Egan, A., Escotto, M., Espen, C., Evans, C.A., Falls, T., Fan, G., Ferrandez, S., Finley, M., Flagg, N., Forbes, L., Foster, M., Foster, P., Ferrandez, S., Hally, M., Flagg, N., Forbes, L., Foster, M., Foster, P., Ferrandez, R., Hines, S., Haldun, S. L., Hodgson, N., Heryes, M., Herrandez, R., Hines, S., Haldun, S. L., Hodgson, A., Hogues, M., Herrandez, R., Hines, S., Haldun, S. L., Hodgson, A., Hogues, M., Hallins, B., Johnson, R., Johnson, R., Johnson, R., Johnson, R., Johnson, R., Johnson, R., Johnson, R., Johnson, R., Johnson, R., Johnson, R., Johnson, R., Johnson, R., Johnson, R., Johnson, R., Johnson, R., Johnson, R., Johnson, R., Johnson, R., Johnson, R., Johnson, R., Johnson, R., Johnson, R., Johnson, R., Johnson, R., Johnson, R., Johnson, R., Johnson, R., Johnson, R., Johnson, R., Johnson, R., Johnson, R., Johnson, R., Johnson, R., Johnson, R., Johnson, R., Johnson, R., Johnson, R., Johnson, R., Johnson, R., Johnson, R., Johnson, R., Johnson, R., Johnson, R., Johnson, R., Johnson, R., Johnson, R., Johnson, R., Johnson, R., Johnson, R., J
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Rattus norvegicus (Norway rat)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AC098902.7 GI:30521241
HTG; HTGS_PHASE2; HTGS_DRAFT; HTGS_FULLTOP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (bases 1 to 221952)
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                             Submission
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100.0%; Pred. No. 7.8;
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Submitted (10-MAY-2003) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
On May 10, 2003 this sequence version replaced gi:25089200.
The sequence in this assembly is a combination of BAC based reads and whole genome shorgun sequencing reads assembled using Atlas (http://www.hgsc.bcm.tmc.edu/projects/rat/). Each contig described in the feature table below represents a scaffold in the Atlas assembly (a 'contig-scaffold'). Within each contig-scaffold, individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome
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Baylor Plaza, Houston, TX 77030, USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NOTE: Estimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/docs/Genbank draft data./ NOTE: This is a 'working draft' sequence. It currently consists of 1 contigs. Gaps between the contigs are represented as runs of N. The order of the pieces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This sequence will be replaced
by the finished sequence as soon as it is available
the accession number will be preserved.
1 221952: contig of 221952 bp in length.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       is believed to be correct as given, however the sizes of the gaps between them are based on estimates that have provided by the submittor.
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Center clone name: CH230-166D21

Center clone name: CH230-166D21

Center clone name: CH230-166D21

Center Summary Statistics

Assembly program: Atlas 3.0;

Consensus quality: 213950 bases at least Q40

Consensus quality: 215107 bases at least Q40

Consensus quality: 215109 bases at least Q20

Consensus quality: 215809 bases at least Q20

Estimated insert size: 225832; sum-of-contigs estimation

Quality coverage: 7x in Q20 bases; sum-of-contigs estimation
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clone_end:T7
site:EcoRI
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47344 c 43902 g 61
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/mol_type="genomic DNA"
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Submitted (13-NOV-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, Ton 7030, USA
On Nov 13, 2002 this sequence version replaced gi:23322375.
The sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequencing reads assembled using Atlas
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C., Adio-Oduola, B., Ali-osman, F.R., Allen, C., Alsbrooks, S.L., Amaratunge, H.C., Are, J.R., Ayele, M., Banks, T., Barbaria, J., Benton, J., Bimage, K., Blankenburg, K., Bonnin, D., Bouck, J., Bowie, S., Brieva, M., Brown, E., Brown, M., Bryant, N.P., Buhay, C., Burch, P., Burkett, C., Burrell, K.L., Byrd, N.C., Buhay, C., Burkett, C., Burrell, K.L., Byrd, N.C., Burkett, C., Burrell, K.L., Byrd, N.C., Burkett, C., Burrell, K.L., Byrd, N.C., Burkett, C., Burrell, K.L., Byrd, N.C., Burkett, C., Burrell, K.L., Byrd, N.C., Burkett, C., Burkett, C., Burkett, C., Burkett, C., Burkett, C., Burkett, C., Burkett, C., Burkett, C., Burkett, C., Burkett, C., Burkett, C., Burkett, C., Burkett, C., Burkett, C., Burkett, C., Burkett, C., Burkett, C., Burkett, C., Burkett, C., Burkett, C., Burkett, C., Burkett, C., Burkett, C., Burkett, C., Burkett, C., Burkett, C., Burkett, C., Burkett, C., Burkett, C., Burkett, C., Burkett, C., Burkett, C., Burkett, C., Burkett, C., Burkett, C., Burkett, C., 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Burkett, C., Burkett, C., Burk
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Baylor Plaza, Houston,
3 (bases 1 to 231485)
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Rattus norvegicus (Norway rat)
Rattus norvegicus
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Rattus norvegicus clone CH230-2I18, WORKING DRAFT SEQUENCE
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NOTE: Estimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/docs/Genbank draft data.)
NOTE: This is a 'working draft' sequence. It currently consists of 1 contigs. Gaps between the contigs are represented as runs of N. The order of the pieces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 provided by the submittor.

This sequence will be replaced
by the finished sequence as soon as it is available and
the accession number will be preserved.

1 231485; contig of 231485 bp in length.
                                              CTAACACAAGCAACAACAGCAA 768
CTAACACAAGCAACAACAGCAA 132682
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           is believed to be correct as given, however the sizes of the gaps between them are based on estimates that have
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Assembly program: Phrap; version 0.990329
Consensus quality: 21236 bases at least Q40
Consensus quality: 214916 bases at least Q30
Consensus quality: 216847 bases at least Q20
Estimated insert size: 219119; sum-of-contigs estimation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Web site: http://www.hgsc.bcm.
Contact: hgsc-help@bcm.tmc.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Quality coverage: 7x in Q20 bases; sum-of-contigs estimation
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clone end:T7"
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142856. .144354
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|mol_type="genomic DNA"
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L44405. .146054
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Simian immunodeficiency virus
Viruses; Retroid viruses; Retroviridae;
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                                                                                                                                                                                                                                       Original source text: Simian (individual_isolate Mne) DNA.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                   1 (bases 1 to 222)
Overbaugh, J. and Rudensey, L.M.
Alterations in potential sites for glycosylation predominate evolution of the simian immunodeficiency virus envelope gene
                                                                                                                                                                                                                                                                                                                                                                                                              envelope-associated protein; glycoprotein 120
                                                                                                                                                                                                                                                                                                                                                                                                                           M96201.1 GI:334607
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Patent: WO 0198334-A 44
SHIRE BIOCHEM INC. (CA)
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/mol_type=
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/db_xref="taxon:32644"
/note="HAMJ 264"
                                                                                                                                                                                                                organism="Simian immunodeficiency virus"
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'isolate="Mne"
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                  Drosophila melanogaster (fruit fly)
Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda;
Neoptera; Endopteryota; Diptera; Brachyce
Ephydroidea; Drosophilidae; Drosophila.
1 (bases 1 to 29183)
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Chen,H., Rosin,F.M. and Hannapel,D.J.
Direct Submission
Submitted (07-AUG-2001) Department of Horticulture,
University, 257 Horticulture Hall, Ames, IA 50011-1:
                                                                                                                                                    AC014153.1 GI:64
HTG; HTGS_PHASE2.
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1. (bases 1 to 2065)
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  Adams, M.
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A KNOX protein of potato interacts with several members of the TALE family of transcription factors
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GSFGSGNVLENGVSLF1GLQQEGSNLPMSIETHVSYVPLRADDMYSTAFTTMVPETA
EFNCLDSGNRQQFFWLIPSAT"
409 c 446 g 531 t
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KPMVEEMYKBEAGDAKIDSNSSSDVAPRLATKDSKVEERGELHQNAASEFEQYNSGQI
LESKSNHEADVEMEGASNAETQSQSGMENQTGEPLPAMDNCTLFQDAFVQSNDRFSEF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             translation="MATYPPSPNNORDADQTFQYFROSLPESYSEASNAPENMVFMN YSSGAYSDMLTGTSQOQHNCIDIPSIGATPFNTTSQQEILSNLGGSQMGIQDFSSWRD SRNEMLADDVFQVAQNVQGQGLSLSLGSNIPSGIGISHVQSQNENQGGGFNMSFRDDD NSQPKEQRNADYFPDNPGRDLDAMKGYNSPYGTSSIARTIPSSKYLKAAQYLLDEVV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VQNKLAKLLSMLDEIDRRYRQYYHQMQIVVSSFDVVAGEGAAKPYTALALQTISRHFR
CLRDAICDQIRASRRSLGEQDASENSKAIGISRLRFVDHHIRQQRALQQLGMMQQHAW
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/product="BEL1-related homeotic
/protein_id="AAN03627.1"
/db_xref="GI:22652127"
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/mol_type="mRNA"
/cultivar="Desiree"
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                                                                                                                                                                                                                                                                                                                                                                                                          Direct Submission

Submitted (16-MAY-2003) Wellcome Trust Sanger Institute, Hinxton, Submitted (16-MAY-2003) Wellcome Trust Sanger Institute, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: Cambridgeshire, CB10 1SA, UK. E-mail enquiries: zfish-help@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk On May 19, 2003 this sequence version replaced gi:30840166.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          For further information on this sequence e-mail to fly@ce * NOTE: This is a 'working draft' sequence.
* This sequence will be replaced
* by the finished sequence as soon as it is available and
* the accession number will be preserved.
                                                                                                                                                                    Insert size: 56408; sum-of-contigs
Insert size: 186298; 2.8% error; agarose-fp
Quality coverage: 1.39x in Q20 bases; sum-of-contigs Quality
                                                                                                                                                                                                                  Assembly program: XGAP4; version 4.5
Chemistry: Dye-terminator; 100% of reads
Consensus quality: 34830 bases at least Q40
Consensus quality: 39888 bases at least Q30
Consensus quality: 46207 bases at least Q20
                                                                                                                                                                                                                                                                                                                                Web site: http://www.sanger.ac.uk
Contact: zfish-help@sanger.ac.uk
-----Project Information
                                                                                                                                                                                                                                                                                                 Center project name: zKp69C1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi;
Cypriniformes; Cyprinidae; Danio.
1 (bases 1 to 58408)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BX510940 S8408 bp DNA linear HTG 17-MAY-2003 Danio rerio clone DKEYP-69C1, *** SEQUENCING IN PROGRESS ***, 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (16-NOV-1999) Celera Genomics, 45 West Gude Drive, Rockville, MD, USA
                                                                                                                                                          coverage: 0.90x in Q20 bases; agarose-fp
                                                                                                                                                                                                                                                                                                                                                                              Center code: SC
                                                                                                                                                                                                                                                                                                                                                                                            Center: Wellcome Trust Sanger Institute
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sims, S.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Direct Submission
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                                           NOTE: This is a 'working draft' sequence. It currently consists of 21 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence
                as soon as it is available and the accession number will be preserved.
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/mol_type="genomic DNA"
/mol_type="genomic DNA"
/db xref="taxon:7227"
/db xref= 6050 g 8602 t
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to fly@celera.com
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                /note="assembly_fragment:00221"
29463. .32085
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fragment_chain:2"
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26893. .29362
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fragment_chain:1"
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/db_xref="taxon:7955"
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 note="assembly_fragment:00292"
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fragment_chain:2"
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fragment_chain:1"
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58408: contig of 2
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AC120849.1 GI:20531830
     Zainoun,J., Zembek,L., Zimmer,A. and Łouy,m.

Direct Submitssion

Submitted (13-MAY-2002) Whitehead Institute/MIT Center for Genome
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http://ftp.genome.washington.edu/RM/RepeatMasker.html
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RS Birren, B., Linton, L., Nusbaum, C., Lander, E., Ali, A., Allen, N., Barrar, N., Barriar, N., Bastien, V., Bloom, T., Boguslavkiy, L., Anderson, S., Barrar, N., Bastien, V., Bloom, T., Boguslavkiy, L., Boukhgalter, B., Brown, A., Camarata, J., Campopiano, A., Chang, J., Chazaro, B., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S., Dodge, S., Faro, S., Ferreira, P., FitzHugh, W., Gage, D., Galagan, J., Gardyna, S., Ginde, S., Gord, S., Goyette, M., Graham, L., Grand-Pierre, N., Hagos, B., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C., Hagos, B., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C., Kamat, A., Karatas, A., Kells, C., LaRocque, K., Lamazares, R., Landers, T., Lehoczky, J., Levine, R., Lindblad-Toh, K., Liu, G., Macthews, C., McCarthy, M., McEwan, P., McKernan, K., Meldrim, J., Meneus, L., McCarthy, M., McEwan, P., McKernan, K., Meldrim, J., Meneus, L., McCarthy, M., Menga, V., Murphy, T., Naylor, J., Nguyen, C., Nicol, R., Morbu, C., Nicol, R., Norbu, C., Netta, R., Rieback, M., Riley, R., Riee, C., Rogov, P., Roman, J., Rosetti, M., Roy, A., Santos, R., Schupback, R., Seaman, S., Severy, P., Spencer, B., Stange-Thomann, N., Stojanovic, N., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W.J., Young, G., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W.J., Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.
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                                                    Submitted (13-MAY-2002) Whitehead Institute/MIT Center Research, 320 Charles Street, Cambridge, MA 02141, USA All repeats were identified using RepeatMasker: Smit, A.F.A. & Green, P. (1996-1997) http://ftp.genome.washington.edu/RM/RepeatMasker.html
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Birren, B., Linton, L., Nusbaum, C. and Lander, E.
Mus musculus, Clone RP23-342010
Unpublished
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Mus musculus (house mouse)
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* NOTE: This record contains 86 individual

* sequencing reads that have not been assembled into

* contigs. Runs of N are used to separate the reads

* and the order in which they appear is completely

* arbitrary. Low-pass sequence sampling is useful for

* identifying clones that may be gene-rich and allows

* overlap relationships among clones to be deduced.

* However, it should not be assumed that this clone

* will be sequenced to completion. In the event that

* the record is updated, the accession number will
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Contact: sequence submissions@genome.wi.mit.edu
----- Project Information
Center project name: L19545
Center clone name: 342_0_10
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This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest. The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em:, EMBL; Sw:, SWISSEROT: TT., TRAMBL; Wo:, WORMPEP: Information on the WORMPEP
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                                                                                                                                                                                                                                               SWISSPROT; Tr:, TREMBL; Wp:, WORMPEP; Information on the WORMPEP database can be found at http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence was generated from part of bacterial clone contigs of human chromosome 10, constructed by the Sanger Centre Chromosome 10 mapping Group. Further information can be found at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Draft Sequence Produced by Genome Therapeutics Corp, 100
Street, Waltham, MA 02453, USA
http://www.genomecorp.com
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (01-JUN-2002) Wellcome Trust Sanger Institute, Hinxton, Cambridgeshire, CB10 15A, UK. E-mail enquiries: hunguery@sanger.ac.uk Clone requestes clonerequest@sanger.ac.uk Con Jun 4, 2002 this sequence version replaced gi:20520536.
                                                                                                                                                                           RP11-344N10 is from the library RPCI-11.2 constructed by the group of Pieter de Jong. For further details see
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                                                                                       University, 4444 Fores 3 (bases 1 to 133237)
                                                                                                                                                                                          Direct Submission
Submitted (27-AUG-1998)
                                                                                                                                                                                                                       2 (bases 1 to 133237) Waterston, R.
                                                                                                                                                                                                                                                                Mammalia; Eutheria; Primates; Catarrhini; Homini
1 (bases 1 to 133237)
Andrews, S., Lacy, M. and Dubbelde, C.
The sequence of Homo sapiens PAC clone RP4-620P6
                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                           Homo sapiens
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AC005550
                                                                                                                                      Direct Submission
                                                                                                                                                                                                                                                  Unpublished
                                                                                                                                                                                                                                                                                                                                                      Homo sapiens (human)
                                                                                                                                                                                                                                                                                                                                                                                      AC005550.1 GI:3478668
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21; Conservative
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41513 a 25955 c 24645 g 37446 t
Web site: http://genome.wustl.edu/gsc
Contact: sapiens@watson.wustl.edu
----- Sunmary Statistics
Center project name: H_DJ0620P06
                                                          Center: Washington University Genome Sequencing Center code: WUGSC
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Pred. No.
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                                                                                                                                                                               Department of Genetics, Park Avenue, St. Louis,
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NOTICE: This sequence may not represent the entire insert of this clone. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap between neighboring data submissions.

such as compressions and repeats; all regions were covered sequence from more than one subclone; and the assembly was all regions were double stranded or sequenced with an alternate chemistry; an attempt was made to resolve all sequencing problems. confirmed by restriction digest. This sequence was finished as follows unless otherwise noted:

MAPPING INFORMATION:
The sequence of this clone was established as part of a mapping and sequencing collaboration between the NHGRI Chromosome 7 Mapping Project (Eric D. Green, Director), John D. McPherson in the Department of Genetics (Washington University), and the Washington University Genome Sequencing Center. For additional information about the map position of this sequence, see http://www.nhgri.nih.gov/DIR/GTB/CHR7, send mailto:egreen@nhgri.nih.gov, or see http://genome.wustl.edu/gsc

## SOURCE INFORMATION:

This clone was derived from human PAC library RPCI-4, prepared by Pieter de Jong and coworkers at Roswell Park Cancer Institute, method described by Ioannou et al.,

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FEATURES
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Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               6:84-9 (1994). The library is from one male donor. details, see http://bacpac.med.buffalo.edu/The clone is available from Genome Systems, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NEIGHBORING SEQUENCE INFORMATION:
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complement (2910. .387)

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KRSGGKKKDDSSDGEGNYKSEVNSKPRKERTAFTKEQIRELEAEFAHHNYLTRLRRY
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mol_type="genomic DNA"
db_xref="taxon:9606"
chromosome="7"
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RP4-620P6;
Query Match
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Matches 21; Conserv
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 0.9%; Score 21; DB nilarity 100.0%; Pred. No. 28 Conservative 0; Mismatches
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40647. .40946
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34916. .35207
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lb_xref="GI:1254905"
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| family="Alu"
|0. .75629
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                   DB 9;
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AUTHORS
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Du,H., Haakenson,W. and Dixon,R.
The sequence of Homo sapiens BAC clone RP11-568H24
Unpublished (2001)
                                                                                                                                       This sequence was finished as follows unless otherwise noted: all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by
                                                                                                                                                                                                                                                                                                   NOTICE: This sequence may not represent the entire insert of this clone. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (09-JAN-2002) Department of Genetics, Washington University, 4444 Forest Park Avenue, St. Louis, Missouri 6. On Aug 28, 2001 this sequence version replaced gi:13399437
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4 (bases 1 to 139357)
Waterston, R.H.
Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (25-SEP-1999) Genome University School of Medicine,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (Dases 1 to 119357)
Sulston, J.E. and Waterston, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (28-AUG-2001) Genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3 (bases 1 to 139357) Waterston, R.H.
                                       McPherson,
                                                        Mapping information for this clone was provided by Dr.
                                                                                 MAPPING INFORMATION:
                                                                                                                        restriction digest.
                                                                                                                                                                                                                                                                                between neighboring data submissions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Waterston, R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MO 63108,
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Homo sapiens BAC clone RP11-568H24
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (bases 1 to 139357)
                                                                                                                                                                                                                                                                                                                                                                                                                          Web site: http://genome.wustl.edu/gsc
Contact: sapiens@watson.wustl.edu
------ Summary Statistics
                                                                                                                                                                                                                                                                                                                                                                                                       Center project name: H_NH0568H24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Center: Washington University Genome Sequencing Center Center code: WUGSC
erson, Department of Genetics, Washington For additional information about the map ence, see http://genome.wustl.edu/gsc
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complete
                    ed by Dr. John D.
University, St. :
position of this
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SOURCE INFORMATION:

The RPCI-11 human BAC library was made from the blood of one male donor, as described by Osoegawa, K., Woon, P.Y., Zhao, B., Frengen, E., Tateno, M., Catanese, J.J. and de Jong, P.J. (1998) An improved approach for construction of bacterial artificial chromosome libraries. Genomics 51:1-8. The clone may be obtained either from Research Genetics, Inc. (http://www.resgen.com) or Pieter de Jong and coworkers at the Roswell Park Cancer Institute (http://bacpac.med.buffalo.edu)
VECTOR: pBACe3.6
NEIGHBORING SEQUENCE INFORMATION:
The clone sequenced to the right is RP11-178E6, 2000 bp overlap. Actual start of this clone is at base position 1 of RP11-568H24.
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The sequence between 66093 to 66578 and 104506 to 104590 is covered only by pcr products from clone DNA. he sequence contains a dinucleotide (TG) run from 65513 to 65634 in which the exact length is unknown. The sequence contains a dinucleotide (TC) run from 104386 bp to 104331 bp in which the exact length is unknown. The sequence from base position 4458 to 6187 can not be guaranted due to a tandem repeat.

Location/Qualifiers

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repeat_region
                                                                                                                                                                                                                                                   /rpt_family="Alu"
                                                                                                                                                                                                                   /note="similar to (NID:g12685340)"
                                                                                        note="CpG_island (%GC=74.6, 978. .5152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           rpt_family="AcHobo"
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/clone_lib="RPCI-11"
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                                                                                                                                                                                                                                                                                                                                          note="similar to Homo sapiens EST AI597790 (NID:g4606838)
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HTG

21-AUG-2002 15

E., Ali,A., Allen,N., lavkiy,L., Boukhgalter,B.,

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9240. .9360
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/note="similar to Homo sapiens

(NID:911259616)"

9333. .9360
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9031. .9360
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/note="match to EST BI198782
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                                                                                                                                                                                                                                                                                                                                                                                      note="match to EST BE313758"
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                                                                                                                                                                                                                                                                    Score 21; ; Pred. No.
                                                                                                                                                                                                                                    Mismatches
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28;
                                                                                                                                                                                                                                                                                                                                                                              (NID:g9134050)"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (NID:g11259763)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (NID:g11099821)"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (NID:g11265074)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (NID:g11263123)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (NID:g14653803)"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (NID:g11263123)"
                                                                                                                                                                                                                                0;
                                                                                                                                                                                                                                                                                                   Length 139357;
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VERSION
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AUTHORS
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JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE
JOURNAL
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                                                                                                                                                                                                                                                                                                                                                                                  JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Lamazares, R., Landers, T., Lehoczky, J., Levine, R., Liu, G.,
MacLean, C., Macdonald, P., Major, J., Marguis, N., Matthews, C.,
McCarthy, M., McEwan, P., McKernan, K., McPheeters, R., Meldrim, J.,
Meneus, L., Mihova, T., Mlenga, V., Murphy, T., Naylor, J., Nguyen, C.,
Norbu, C., Norman, C.H., O'Connor, T., O'Donnell, P., O'Neil, D.,
Oliver, J., Peterson, K., Phunkhang, P., Pierre, N., Pollara, V.,
Raymond, C., Retta, R., Rieback, M., Riley, R., Rise, C., Rogov, P.,
Raymond, C., Retta, R., Rieback, M., Riley, R., Rise, C., Rogov, P.,
Roman, J., Rosetti, M., Roy, A., Santos, R., Schauer, S., Schupback, R.,
Seaman, S., Severy, P., Spencer, B., Stange-Thomann, N., Stojanovic, N.,
Strauss, N., Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J.,
Topham, K., Travers, M., Travis, N., Trigillo, J., Vassiliev, H.,
Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W. J., Young, G.,
Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.,
Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Birren, B., Linton, L., Nusbaum, C., Lander, E., Ali, A., Allen, N., Anderson, S., Barna, N., Bastien, V., Boguslavkiy, L., Boukhgalter, B., Brown, A., Camarata, J., Campopiano, A., Chang, J., Chazaro, B., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cook, A., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cook, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S., Dodge, S., Faro, S., Ferreira, P., FitzHugh, W., Gage, D., Galagan, J., Gardyna, S., Ginde, S., Gord, S., Goyette, M., Graham, L., Grand-Pierre, N., Hagos, B., Heaford, A., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C., Kamat, A., Karatas, A., Kells, C., LaRocque, K., Jones, C., Kamat, A., Karatas, A., Kells, C., LaRocque, K., Janessey, D., Barassey, B., Landers T., Laborato, T., Johnson, R., Landers D., Landers D., Landers D., Landers D., Landers D., Landers D., Landers D., Landers D., Landers D., Landers D., Landers D., Landers D., Landers D., Landers D., Landers D., Landers D., Landers D., Landers D., Landers D., Landers D., Landers D., Landers D., Landers D., Landers D., Landers D., Landers D., Landers D., Landers D., Landers D., Landers D., Landers D., Landers D., Landers D., Landers D., Landers D., Landers D., Landers D., Landers D., Landers D., Landers D., Landers D., Landers D., Landers D., Landers D., Landers D., Landers D., Landers D., Landers D., Landers D., Landers D., Landers D., Landers D., Landers D., Landers D., Landers D., Landers D., Landers D., Landers D., Landers D., Landers D., Landers D., Landers D., Landers D., Landers D., Landers D., Landers D., Landers D., Landers D., Landers D., Landers D., Landers D., Landers D., Landers D., Landers D., Landers D., Landers D., Landers D., Landers D., Landers D., Landers D., Landers D., Landers D., Landers D., Landers D., Landers D., Landers D., Landers D., Landers D., Landers D., Landers D., Landers D., Landers D., Landers D., Landers D., Landers D., Landers D., Landers D., Landers D., Landers D., Landers D., Landers D., Landers D., Landers D., Landers D., Lan
                                                                                                                                                                                                                        Submitted (21-AUG-2002) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA On Aug 21, 2002 this sequence version replaced gi:17061340. All repeats were identified using RepeatMasker:

Smit, A.F.A. & Green, P. (1996-1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                 McCarthy, M., Meldrim, J., Meneus, L., Mihova, T., Mienga, V., Murphy, T., Naylor, J., Nguyen, C., Nicol, R., Norbu, C., Norman, C.H., O'Connor, T., O'Donnell, P., O'Neil, D., Oliver, J., Peterson, K., Phunkhang, P., Pierre, N., Raymond, C., Retta, R., Rise, C., Rogov, P., Roman, J., Roy, A., Schauer, S., Schupback, R., Seaman, S., Severy, P., Smith, C., Spencer, B., Stange-Thomann, N., Stojanovic, N., Talamas, J. Tesfaye, S., Theodore, J., Topham, K., Travers, M., Vassilev, H., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.
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Birren,B., Nusbaum,C., Lander,E., Ali,A., Allen,N., Anderso Barna,N., Bastien,V., Bloom,T., Boguslavkiy,L., Boukhgalten, Barna,N., Bastien,V., Bloom,T., Boguslavkiy,L., Boukhgalten, Camaratta,J., Chang,J., Chazaro,B., Choepel,Y., Collymore,A., Cook,A., Cooke,P., DeArellano,K., Dewar,K., Diaz,J.S., Dodg Faro,S., Ferreira,P., Fitzderald,M., Gage,D., Galagan,J., Gardyna,S., Gord,S., Graham,L., Grand-Pierre,N., Hagos,B., Gardyna,S., Gord,S., Graham,L., Johnson,R., Jones,C., Kamatt, Horton,L., Hulme,W., Iliev,I., Johnson,R., Jones,C., Kamatt, Kells,C., Landers,T., Levine,R., Lindblad-Toh, Liu,G., MacLean,C., Macdonald,P., Major,J., Matthews,C., MacContald,P., Major,J., Matthews,C., MacCont
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Birren, B., Nusbaum, C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AC102254.2 GI:22381162
HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_FULLTOP
Mus_musculus (house mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (23-NOV-2001) Whitehead Institute/MIT Center for Genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AC102254 146690 bp
Mus musculus clone RP24-181A10,
                                                                                                                                                                                                                                                                                                                                                                                                                      Zembek,L., Zimmer
Direct Submission
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Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mus musculus
                                                                                                                                                     http://ftp.genome.washington.edu/RM/RepeatMasker.html
----- Genome Center
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                unordered pieces
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                                       Center code: WIBR Web site: http://v
   Contact: sequence
                                                                                                                  Center: Whitehead Institute/ MIT Center
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       320 Charles Street, Cambridge, MA 02141,
http://www-seq.wi.mit.edu
sequence_submissions@genome.wi.mit.edu
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WORKING DRAFT SEQUENCE,
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RESULT

for Genome

Research

Lindblad-Toh, K.,

Talamas,J.

Kamat, A.,

Boukhgalter, B., .S., Dodge,S

Anderson, S.,

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FEATURES
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                                       misc_feature
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                                                                                                                   misc_feature
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NOTE: This is a 'working draft' sequence. It currently consists of 15 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           62868
62968
78985
79085
100398
100498
123489
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Consensus quality: 142759 bases at least Q40
Consensus quality: 144340 bases at least Q30
Consensus quality: 144347 bases at least Q20
Insert size: 151000; agarose-fp
Insert size: 14530; sum-of-contigs
Quality coverage: 7.1 in Q20 bases; agarose-fp
Quality coverage: 7.4 in Q20 bases; sum-of-contigs
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Center clone name: 181 A 10
----- Summary Statistics
Sequencing vector: Plasmid; n.
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31056
37622
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24826
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14649
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19192
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1292
2634
2734
5385
5485
                                                                                                                   /note="assembly_fragment"
9799. .14648
  /note="assembly_fragment"
24926. .30955
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14749. .19191
                                                                                                                                                              5485.
                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
                                       /note="assembly_fragment"
19292. .24825
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/mol_type="genomic DNA"
/db_xref="taxon:10090"
/clone="RP24-181A10"
                                                                                                                                                                           /note="assembly_fragment"
                                                                                                                                                                                                                  note="assembly_fragment"
                                                                                                                                                                                                                                                         note="assembly_fragment"
                                                                                                                                                                                                                                                                                                     clone
                                                                                                                                                                                                                                                                                                                                                                                                      . .146690
                                                                                                                                                                                                                                                                                                                                                                                                                                     47762: contig of 10041 bp in length
47862: gap of 100 bp
62867: contig of 15005 bp in length
62967: gap of 100 bp
78984: contig of 16017 bp in length
79084: gap of 100 bp
100397: contig of 21313 bp in length
100497: gap of 100 bp
123488: contig of 22991 bp in length
123588: gap of 100 bp
146690: contig of 23102 bp in length
                                                                                                                                                              .9698
                                                                                                                                                                                                      . 5384
                                                                                                                                                                                                                                             . 2633
                                                                                                                                                                                                                                                                                                     _lib="RPCI-24 Male Mouse
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contig of 6566
gap of 100 bp
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gap of 100 bp
contig of 6030 bp in length
gap of 100 bp
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gap of 100 bp
contig of 4443 bp in length
gap of 100 bp
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gap of 100 bp
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ACCESSION
VERSION
KEYWORDS
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* NOTE: This is a 'working draft' sequence. It currently consists of 45 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown.
                                                                                                                                                                                        Sequencing vector: M13; 0% Sequencing vector: plasmid; 100% Chemistry: Dye-primer ET; 0% of reads Chemistry: Dye-terminator Big Dye; 100% of reAssembly program: Phrap; version 0.990319 Consensus quality: 126050 bases at least Q40 Consensus quality: 130849 bases at least Q30 Consensus quality: 134078 bases at least Q30 Consensus quality: 134078 bases at least Q30 Consensus quality: 134078 bases at least Q30 Consensus quality: 134078 bases at least Q30 Consensus quality: 134078 bases at least Q30 Consensus quality: 134078 bases at least Q30 Consensus quality: 134078 bases at least Q30 Consensus quality: 134078 bases at least Q30 Consensus quality: 134078 bases at least Q30 Consensus quality: 134078 bases at least Q30 Consensus quality: 134078 bases at least Q30 Consensus quality: 134078 bases at least Q30 Consensus quality: 134078 bases at least Q30 Consensus quality: 134078 bases at least Q30 Consensus quality: 134078 bases at least Q30 Consensus quality: 134078 bases at least Q30 Consensus quality: 134078 bases at least Q30 Consensus quality: 134078 bases at least Q30 Consensus quality: 134078 bases at least Q30 Consensus quality: 134078 bases at least Q30 Consensus quality: 134078 bases at least Q30 Consensus quality: 134078 bases at least Q30 Consensus quality: 134078 bases at least Q30 Consensus quality: 134078 bases at least Q30 Consensus quality: 134078 bases at least Q30 Consensus quality: 134078 bases at least Q30 Consensus quality: 134078 bases at least Q30 Consensus quality: 134078 bases at least Q30 Consensus quality: 134078 bases at least Q30 Consensus quality: 134078 bases at least Q30 Consensus quality: 134078 bases at least Q30 Consensus quality: 134078 bases at least Q30 Consensus quality: 134078 bases at least Q30 Consensus quality: 134078 bases quality: 134078 bases quality: 144078 bases quality: 144078 bases quality: 144078 bases quality: 144078 bases quality: 144078 bases quality: 144078 bases quality: 144078 bases quality: 144078 bases quality: 144078 bases quality: 144078 bases quality: 144
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_FULLTOP
Homo sapiens (human)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Web site:http://genome.wustl.edu/gsc/index.shtmlContact: submissions@watson.wustl.edu
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Unpublished
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Waterston, R.H.
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31056. .37621
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/note="assembly
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| gap of unknown length | contig of 4404 bp in length | dan of unknown length                                       | gap of unknown length   | : gap or unknown rengrh                                    | 75: contig of 4260 bp in length | 15: gap of unknown length | 06: gap of unknown | 06: contig of 4103 bp in length                               | 03: contig of 2642 bp in length | 61: contig of 2114 bp in length<br>61: gap of unknown length | 47: gap of unknown length | 20: gap of unknown length | gap of unknown length  | 90: contig of 2185 bp in length                            | contig of 2226 bp in length | contig of 1824 bp in length | definition of 1943 bp in length for the second second length for the second length for the second second length for the second second length for the second second length for the second second length second second length second | gap of unknown length    | : gap of unknown length  | gap of unknown length                                  | de contig of 2331 bp in length | contig of 2598 bp in length | contig of 1638 bp in length | gap of unknown length                                | gap of unknown length   | gap of unknown length   | gap of unknown length | gap of unknown lengt       | gap of unknown lengt.                            | contig of 1471 h      | contig of 2171 burgin | contig of 2128 bp in length | g of 1236 )<br>unknown   | gap of unknown  | gap of unknown length                  | 88: gap of unknown length | 79: gap of unknown length | 79: contig of 2162                     | 17: gap of unknown lengtl | 62: gap of unknown length<br>17: contig of 1055 bp in<br>17: gap of unknown length | gap of unknown lengtl<br>contig of 1187 bp in<br>gap of unknown lengtl<br>contig of 1055 bp in<br>gap of unknown lengtl |
|-----------------------|-----------------------------|---|-------------------------|--|---------------------------------|---------------------------|--------------------|---|---------------------------------|--|---------------------------|---------------------------|--|--|-----------------------------|-----------------------------|--|--------------------------|--------------------------|--|--------------------------------|-----------------------------|-----------------------------|--|---|-------------------------|-----------------------|----------------------------|--|-----------------------|-----------------------|-----------------------------|--|---|--|---------------------------|---------------------------|--|---------------------------|--|---|
| •                     | /note='                     | /note="assembly_name;Contig45"<br>misc feature 40956 .42779 | misc_feature 3891340855 | ""ISC_reacure 3/01536614<br>/note="assembly name:Contiq42" | /note="a                        | misc feature 3478136914   | sc_feature 32350.  | ""ISC_reacure 29032: .32249<br>/note="assembly_name:Contig39" |                                 |  | misc_feature 2606827813   | misc_feature 2405825967   | <pre>misc_feature 22249, .23957     /note="assembly name:Contig35"</pre> | ""ISC_reacure 2003%221%0<br>/note="assembly_name:Contig34" |                             |                             | <pre>/note="assembly_name:Contig31" misc feature</pre>   | misc_feature 14965 17135 | misc_feature 12737 14864 | misc_feature 1140112636 /note="assembly name:Contid29" | 11 .                           | /note="a                    | feature                     | /note="assembly_name:Contig23" misc feature 63808088 | <pre>/note="assembly_name:Contig22" misc_feature 4118. 6279</pre> | misc_feature 2963. 4017 | sc_feature            | sc_feature 1157<br>/notes" | <pre>/chromosome="UNK" /clone="RP11-370G4"</pre> | /db_xref="taxon:9606" | /mol *:mon sapiens"   | S Location/Qualifiers .     | 67 138066: gap of unknown length<br>67 148348: contig of 10282 bp in | 38 128037: gap of unknown length<br>38 137966: contiq of 9929 bp in | 23 120722: gap of<br>23 127937: contig | 87 120622: contig of 6036 | 29 114486: contig of 4558 | 24 109828: contig<br>29 109928: gap of | ( ,                       | 07 104423: contig of 4617 bp in<br>24 104523: gap of unknown length                | bp in<br>length<br>bp in<br>length  |

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.

This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest. The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em., EMBL; Sw., SWISSPROT; Tr., TREMBL; Wp., WORMPED; Information on the WORMPED by the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the conten
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (12-MAR-2002) Wellcome Trust Sanger Institute, Hinxton, Cambridgeshire, CB10 15A, UK. E-mail enquiries: CB10 15A, UK. E-mail enquiries: humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk On Mar 21, 2002 this sequence version replaced gi:16973010. During sequence assembly data is compared from overlapping clones.
                                                                                                                                                                                                                                                                                          http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence was generated from part of bacterial clone contigs of human chromosome 6, constructed by the Sanger Centre Chromosome 6 Mapping Group. Further information can be found at http://www.sanger.ac.uk/HGP/Chr6
RP11-204E9 is from the library RPCI-11.1 constructed by the group of Pieter de Jong. For further details see
                                                                                  sections only once, except for a short overlap.
The true left end of clone RP3-322L4 is at 148973 in this sequence.
The true right end of clone RP1-135L22 is at 2000 in this sequence.
                                                                                                                                                                     IMPORTANT: This sequence is not the entire insert of clone RP11-204E9 It may be shorter because we sequence overlapping
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 150972)
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Human DNA sequence from clone RP11-204E9 on chromosome 6, complete
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                                                                                                                                                                                                                                                              nttp://www.chori.org/bacpac/home.htm
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45206. .47390
/note="assembly_name:Contig46"
47491. .50220
/note="assembly_name:Contig47"
50321. .53147
                                                    Location/Qualifiers
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53248. .55361
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55462. .58103
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                           Draft Sequence Produced by DOE Joint www.jgi.doe.gov
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/db_xref="taxon:9606"
/chromosome="6"
Completed at Stanford Human Genome Center
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Direct Submission
Submitted (06-SEP-2001) DOE Joint Genome Institute, 2800 Morive, Walnut Creek, CA 94598, USA
On Sep 6, 2001 this sequence version replaced gi:11465049.
                                                                                                                     Direct Submission
Submitted (30-NOV-2000) DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
4 (bases 1 to 156105)
DOE Joint Genome Institute and Stanford Human Genome Center.
                                                                                                                                                                                                                                                                                     Direct Submission
Submitted (12-JAN-2000) Production Sequencing Facility, DOE Submitted (12-JAN-2000) Mitchell Drive, Walnut Creek, CA 9455
Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 9455
(bases 1 to 156105)
DOE Joint Genome Institute and Stanford Human Genome Center.
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DOB Joint Genome Institute and Stanford Human Genome Center.
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short insert library derived from a single pUC clone.
Restriction digest data confirm the assembly."
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Best Local Similarity
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CE 2 (bases I to 156526)

RS Worley, K. C., Adams, C., Adio-Oduola, B., Ali-osman, F.R., Allen, C., Alsbrooks, S.L., Amaratunge, H.C., Are, J.R., Banks, T., Barbaria, J., Blabrooks, S.L., Amaratunge, H.C., Are, J.R., Bannin, D., Bouck, J., Benton, J., Bimage, K., Blankenburg, K., Bonnin, D., Bouck, J., Benton, J., Bimage, K., Brown, E., Brown, M., Bryant, N.P., Buhay, C., Bowie, S., Brieva, M., Brown, E., Brown, M., Bryant, N.P., Buhay, C., Burch, P., Burkett, C., Burrell, K.L., Byrd, N.C., Carron, T.F., Carter, M., Cavazos, S.R., Chacko, J., Chavez, D., Chen, G., Chen, R., Chen, Z., Chowdhry, I., Christopoulos, C., Cleveland, C.D., Cox, C., Coyle, M.D., Dathorne, S.R., David, R., Davila, M.L., Davis, C., Coyle, M.D., Dathorne, S.R., David, R., Davila, M.L., Davis, C., Davy-Carroll, L., Dederich, D.A., Delaney, K.R., Delgado, O., Denn, A.L., Ding, Y., Dinh, H.H., Douthwaite, K.J., Draper, H., Dugan-Rocha, S., Durbin, K.J., Earnhart, C., Edgar, D., Edwards, C., Elhaj, C., Escotto, M., Falla, T., Ferraguto, D., Flagg, N., Ford, J., Foster, P., Frantz, P., Gabisi, A., Gao, J., Garcia, A., Garner, T., Garza, N., Gill, R., Gorrell, J.H., Guevara, W., Gunaratne, P., Hale, S., Hamilton, K., Harris, C., Harris, K., Hart, M., Havlak, P., Hawes, A., Hernandez, O., Hodgson, A., Hogues, M., Holloway, C., Hollins, B., Homsi, F., Howard, S., Huber, J., Hulyk, S., Hume, J., Jackboon, L.E., Jacobson, B., Jia, Y., Johnson, R., Jolivet, S., Joudah, S., Karlsson, E., Kelly, S., Khan, U., King, L., Korvah, J., Kovah, J., Karstovic, J., Kureshi, A., Landry, N., Leal, B., Lewis, L.C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Muzny, D., Scherer, S., Adams, M.D., Holt, R.A., Evans, C.A.,
Gocayne, J.D., Tabor, P., Williamson, A., Homsi, F.H.,
Dugan-Rocha, S.D., Sodergren, E.S., Hodgson, A.H., Chen, R.C.,
Ayele, M., Scott, G.S., Worley, K.W., Amamatides, P.G., Brandon, R.C.,
Rogers, Y., An, H., Baldwin, D., Beeson, K.Y., Brown, M., Buhay, C.,
Busam, D.A., Center, A., Chen, G., Chen, Z., Clerc-Blankenburg, K.,
Davenport, L.B., Dietz, S.M., Ding, Y., Dodson, K., Doup, L.E.,
Davenport, L.B., Dietz, S.M., Ding, Y., Dodson, K., Doup, L.E.,
Draper, H., Emery-Cohen, A., Ferriera, S., Garg, N.D.S., Houck, J.,
Hostin, D., Howland, T.J., Hume, J., Dorgan, M., Murphy, B.,
Liu, W., Mattel, B., McIntosh, T.C., Morgan, M., Muy, M., Murphy, B.,
Nelson, K.A., Ndassa, Y., Nguyen, N., Perez, L., Pittman, G.S., Puri, V.,
Scheeler, F., Shen, H., Strong, R., Tector, C., Wang, Q., Williams, S.M.,
Wheeler, D., Weinstock, G., Gibbs, R. and Venter, J.C.
Direct Submission
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156526 bp DNA linear INV 01-JUJ
Drosophila melanogaster 3L BAC RP98-23H9 (Roswell Park Cancer
Institute Drosophila BAC Library) complete sequence.
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Quality: Phrap Qualit;
Estimated Total Numbe
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1 (bases 1 to 156526)
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Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Unpublished
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Location/Qualifiers
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/mol_type="genomic DNA"
/db_xref="taxon:9606"
/chromosome="5"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /clone="RP11-92M7"
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Pred. No.
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28;
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REFERENCE

Baylor Plaza, Houston, 5 (bases 1 to 156526)

TX 77030, USA

Center, Depa of Medicine,

Department

Adams, C., Adio-Oduola, B., Ali-osman, F.R., Allen, C.,

TITLE JOURNAL

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RS Worley, C. Adams, C. Adio-Oduola, B., Ali-osman, F.R., Allen, C. Alsbrooks, S.L., Amaratunge, H.C., Are, J.R., Banks, T., Barbaria, J., Blabrooks, S.L., Amaratunge, H.C., Are, J.R., Banks, T., Barbaria, J., Benton, J., Binage, K., Blankenburg, K., Bominn, D., Bouck, J., Benton, J., Binage, K., Blankenburg, K., Bominn, D., Bouck, J., Benton, J., Brown, M., Bryant, N.P., Blhay, C., Bowie, S., Brieva, M., Brown, B., Brown, M., Bryant, N.P., Blhay, C., Bowie, S., Brieva, M., Brown, B., Brown, M., Bryant, N.P., Blhay, C., Check, R., Carten, C., Cheveland, C.D., Cox, C., Chen, R., Chen, R., Chacko, J., Chavez, D., Chen, G., Chen, R., Chen, R., Chowdhry, I.S. R., Davida, M. L., Davis, C., Davis, C., Davis, C., Ding, Y., Dinh, H., Barnhatt, C., Edgar, D., Davis, C., Davy, Carroll, L., Dederich, D.A., Delaney, K.R., Delgado, O., Denn, A.L., Ding, Y., Dinh, H., Barnhatt, C., Edgar, D., Edwards, C.C., Elhaj, C., Escotto, M., Falls, T., Ferraguto, D., Flagg, N., Ford, J., Edwards, C., Elhaj, C., Escotto, M., Falls, T., Ferraguto, D., Flagg, N., Ford, J., Foster, P., Frant, P., Frant, P., Falls, T., Ferraguto, D., Flagg, N., Ford, J., Foster, P., Frant, P., Frant, P., Frant, P., Frant, P., Frant, P., Frant, P., Frant, P., Frant, P., Frant, P., Frant, P., Frant, P., Frant, P., Frant, P., Frant, P., Frant, P., Frant, P., Frant, P., Frant, P., Frant, P., Frant, P., Frant, P., Frant, P., Frant, P., Frant, P., Frant, P., Frant, P., Frant, P., Frant, P., Frant, P., Frant, P., Frant, P., Frant, P., Frant, P., Frant, P., Frant, P., Frant, P., Frant, P., Frant, P., Frant, P., Frant, P., Frant, P., Frant, P., Frant, P., Frant, P., Frant, P., Frant, P., Frant, P., Frant, P., Frant, P., Frant, P., Frant, P., Frant, P., Frant, P., Frant, P., Frant, P., Frant, P., Frant, P., Frant, P., Frant, P., Frant, P., Frant, P., Frant, P., Frant, P., Frant, P., Frant, P., Frant, P., Frant, P., Frant, P., Frant, P., Frant, P., Frant, P., Frant, P., Frant, P., Frant, P., Frant, P., Frant, P., Frant, P., Frant, P., Frant, P., Frant, P., Frant, P., 
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Loulseged,H., Lozado,R.J., Lu,X., Lucier,A., Lucier,R., Luna,R.,
Ma,J., Maheshwari,M., Mapua,P., Martin,R., Martindale,A.,
Martinez,B., Massey,E., Mawhiney,E., McLeod,M.P., Meador,M.,
Martinez,B., Massey,E., Mawhiney,E., Mitchell,T., Mohabbat,K.,
Morgan,M., Morris,S., Moser,M., Neal,D., Newtson,J., Newtson,N.,
Morgan,M., Morris,S., Moser,M., Neal,D., Newtson,J., Newtson,N.,
Morgan,M., Moyen,N., Nguyen,N., Nickerson,E., Nwokenkwo,S.,
Oguh,M., Okwuonu,G., Oragunye,N., Ovledo,R., Pace,A., Payton,B.,
Petry,J., Petra,L., Pickens,R., Primus,E., Pu,L.L.,
Quiles,M., Ren,Y., Rives,M., Rojas,A., Rojubokan,I., Rolfe,M.,
Quiles,M., Ren,Y., Rives,M., Rojas,A., Rojubokan,I., Rolfe,M.,
Ruiz,S., Savery,G., Scherer,S., Scott,G., Shen,H., Shooshtari,N.,
Stone,H., Sutton,A., Svatek,A., Tabor,P., Tamerisa,A., Tamerisa,K.,
Tang,H., Tansey,J., Taylor,C., Taylor,T., Telfrod,B., Thomas,N.,
Thomas,S., Usmani,K., Vasquez,L., Vera,V., Villalon,D., Vinson,R.,
Wall,R., Wang,S., Ward-Moore,S., Warren,R., Washington,C.,
Watlington,S., Williams,G., Williamson,A., Waespington,C.,
Wu,Y., Wu,Y.F., Zhou,J., Zorrilla,S., Nelson,D.,
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Direct Submission
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Submitted (31-AUG-2001) Human Genome Sequencing
                                                                                                                                                     Weinstock, G. and Gibbs, R.
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Burch, P., Burkett, C., Burrell, K.L., Byrd, N.C., Carron, T.F., Carter, M., Cavazos, S.R., Chacko, J., Chavez, D., Chen, G., Coxer, C., Coyle, M.D., Dathorne, S.R., David, R., Davida, M.L., Davis, C., Coyle, M.D., Dathorne, S.R., David, R., Davida, M.L., Davis, C., Coyle, M.D., Dathorne, S.R., David, R., Davida, M.L., Davis, C., Davy, Carroll, L., Dederich, D.A., Delaney, K.R., Delgado, O., Denn, A.L., Ding, Y., Dinh, H.H., Douthwaite, K.J., Draper, H., Davis, C., Edgar, D., Edwards, C.C., Elhaj, C., Escotto, M., Falls, T., Ferragutto, D., Flagg, N., Ford, J., Foster, P., Frantz, P., Gabisi, A., Gao, J., Garcia, A., Garner, T., Garza, N., Gill, R., Gorrell, J.H., Guevara, W., Gunaratne, P., Hale, S., Hamilton, K., Harris, C., Harris, K., Hart, M., Haylak, P., Hawes, A., Hernandez, J., Hernandez, O., Hodgson, A., Hogues, M., Holloway, C., Hollins, B., Homsi, F., Howard, S., Huber, J., Hulyk, S., Hume, J., Jackson, E., Jacobson, B., Jia, Y., Johnson, R., Jolivet, S., Joudah, S., Karlsson, E., Kelly, S., Khan, U., King, L., Korvah, J., Kovar, C., Kratovic, J., Kureshi, A., Landry, N., Leal, B., Lewis, L. C., Lewis, L., Li, J., Li, Z., Lichtarge, O., Lieu, C., Liu, J., Liu, W., Loulseged, H., Lozado, R.J., Lu, X., Martin, R., Martindale, A., Martinez, E., Massey, E., Mawiney, E., McLeod, M., P., Meador, M., Mei, G., Metker, M., Negua, P., Martin, R., Martindale, A., Mogran, M., Okwuonu, G., Oragunye, N., Nickerson, E., Nwokenkwo, S., Oragunye, N., Oviedo, R., Pace, A., Payton, B., Peery, J., Peters, L., Pickens, R., Primus, E., Pul, L., Sisson, I., Sodergren, E., Sonaike, T., Sparks, A., Stanley, H., Shooshtari, N., Stenney, H., Shooshtari, N., Stenney, H., Shooshtari, N., Stenney, H., Shooshtari, N., Stenney, H., Shooshtari, N., Walliamson, A., Washington, C., Wu, Y., Wu, Y., Wu, Y., Wu, Y., Wu, Y., Zorrilla, S., Nelson, D., Weitston, D., Vinson, R., Washington, C., Wu, Y., Wu, Y., F., Zhou, J., Zorrilla, S., Nelson, D., Direct, Submission
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Benton, J., Bimage, K., Blankenburg, K., Bonnin, D., Bouck, J.,
Bowie, S., Brieva, M., Brown, E., Brown, M., Bryant, N.P., Buhay, C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Barbaria, J.,
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REFERENCE AUTHORS REFERENCE AUTHORS COMMENT JOURNAL JOURNAL TITLE JOURNAL Submitted (01-JUN-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA On Apr 6, 2002 this sequence version replaced gi:15383763. INFORMATION: http://www.hgsc.bcm.tmc.edu/ or email Submitted (06-APR-2002) Human Genome Sequencing Center, Depai of Molecular and Human Genetics, Baylor College of Medicine, Baylor Plaza, Houston, TX 77030, USA 7 (Dases 1 to 156526) Direct Submission
Submitted (03-FEB-2002) Human Genome Sequencing Center, Depa of Molecular and Human Genetics, Baylor College of Medicine, Baylor Plaza, Houston, TX 77030, USA Direct BCM-HGSC Direct Submission BCM-HGSC (bases 1 to 156526) Submission Department Department One

CLONE LENGTH: This sequence does not necessarily represent the entire insert of this clone. Overlapping regions of clones are only sequenced and submitted once, so the sequence for the remainder of the insert may be found in the record for the adjacent clones. Overlapping clones are noted at the beginning and end of the Features listing.

ANNOTATION OF FEATURES:

STSs are identified using ePCR (Genome of a local database that includes entries local mapping efforts. Res. 7:541-550) searches from dbSTS, GDB, and

source

/organism="Homo sapiens'
/mol\_type="genomic DNA"
/db\_xref="taxon:9606"

Location/Qualifiers

15851

Repeats are identified using RepeatMasker (A. Smit and P. Green, unpublished.) for Human and Mouse sequences.

Genes and Region of sequence similarity are identified by BLAST (Nuc. Acids Res. 25:3389-3402) similarity (expect < 1e-34) to the

EST and cDNA sequences. Genes demonstrate at least two exons flanked by consensus splice sites that maintained sequence continuity across the splice junctions. Sequences that are not identical matches are annotated as similar.

Matches Query Match Best Local Local Similarity 21; Conservative 0.9%; Score 21; 100.0%; Pred. No. 0; Mismatches DB 3; 28; 0 Length 156526; 0,

0

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1508

100271 AAACCAAATTCTCAAATTGAG 100251

AAACCAAATTCTCAAATTGAG 1528

REFERENCE AUTHORS SOURCE ORGANISM ACCESSION VERSION RESULT 84 AL135926 LOCUS DEFINITION COMMENT KEYWORDS JOURNAL requests: clonerequest@sanger.ac.uk

On Aug 14, 2000 this sequence version replaced gi:9621473.

During sequence assembly data is compared from overlapping clones.

Where differences are found these are annotated as variations
together with a note of the overlapping clone name. Note that the
variation annotation may not be found in the sequence submission
corresponding to the overlapping clone, as we submit sequences with
only a small overlap as described above.

This sequence has been finished according to sequence map criteria
as follows. An attempt is made to resolve all sequencing problems,
such as compressions and repeats, but not necessarily within known
annotated human repeat sequence elements (e.g. Alu). Where the
sequence is ambiguous, there is an annotation using the 'unsure' IMPORTANT: This sequence is not the entire insert of clone RP11-375F2 It may be shorter because we sequence overlapping sections only once, except for a 100 base overlap. The true right end of clone RP11-375F2 is at 158519 in this sequence. The true right end of clone RP1-10C16 is at 100 in this http://www.sanger.ac.uk/HGP/Chr1
RP11-375F2 is from the library RPCI-11.2 constructed a Park Cancer Institute by the group of Pieter de Jong. details see http://bacpac.med.buffalo.edu/
VECTOR: pBACe3 6 http://www.sanger.ac.uk/Projects/C elegans/wormpep This sequence was generated from part of bacterial clone contigs of human chromosome 1, constructed by the Sanger Centre Chromosome 1 Mapp. The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em., EMBL; Swr., SWISSPROT; Tr., TREMBL; Wp., WORMPEP; Information on the WORMPEP database can be found at Direct Submission Submitted (03-OCT-2000) Sanger Centre, Hinxton, Cambri CB10 1SA, UK. B-mail enquiries: humquery@sanger.ac.uk Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1. (bases 1 to 158519) AL135926 DNA linear PRI 30-Human DNA sequence from clone RPI-375F2 on chromosome 1 Cc pseudogene similar to UBLI (ubiquitin-like 1 (sentrin)), a pseudogene similar to ribosomal protein L29, ESTs, STSs and Chapman,J AL135926.12 complete sequence. feature key. Homo sapiens Homo sapiens (human) Further information can be found GI:9801286 at Chromosome 1 Mapping Cambridgeshire, STSs and GSSs, PRI 30-NOV-2000 at the Roswell . For further Contains

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/clone_lib="RPCI-11.2"
460. .675
   /note="L1M4 repeat: matches 3093, .3194 of consensus"
16339, .17215
                                                                                                                                   note="MLT1E repeat: matches 385.complement(14529. .15003)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ;061. .6158
/note="AluY repeat: matches 214. .311 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1775. .1824
/note="MIR repeat: matches 85.
                                                                    note="match: GSS: 15371. .15463
                                                                                                                                                                                                       .3267. .13410
note="24 copies 6 mer tatata 78% conserved"
.3654. .13742
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                note="AluSx repeat: matches 1.
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                                                  note="MIR repeat: matches 60. .153 of consensus"
                                                                                                                                                                                  note="MLT1E repeat: matches
                                                                                                                                                                                                                                            3254. .13403
note="75 copies 2 mer at 76% conserved"
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                                                                                                                                                                                                                                                                                                         3164. .13253
                                                                                                                                                                                                                                                                                                                                                                                                                                                             note="unidirectional dGTP only"
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                                                                                                                                                                        4045. .14226
                                                                                                                                                                                                                                                                                        note="L2 repeat: matches 2576. .2669 of
                                                                                                                                                                                                                                                                                                                                                       2419. .13151
note="L2 repeat: matches 1683.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              note="AluY repeat: matches 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             note="MLT1D repeat: matches 13. .381 of consensus"
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2419. .13151
                                                                                                                                                                                                                                                                                                                         91. .13572
:e="match: GSS:
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                                                                                                  e="match: GSS: Em:AQ798857"
1. .15366
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                                                                  .15463
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                                                                                  Em: AQ221861"
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17225. .17961
/note="L1PA3 repeat: matches 5410.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          17962. .19671
/note="L1PA7 repeat:
19672. .20271
                                                                  note="match: GSS: 3174. .33222
                                                                                                   complement (32404.
                                                                                                                                                    note="match: GSS: Em:AQ747371"
                                                                                                                                                                                                                                   latch: EST8: Em:AI191222 Em:AI248769
satch: proteins: Tr:Q9PT08 Tr:O23759 Sw:P55853 Tr:Q9Z172
w:Q93068 Sw:P55845 Sw:P55855 Sw:O13351 Sw:Q12306
r:O97102 Tr:O57686"
                                                                                                                                                                                                                                                                                                                                gene="bA375F2.1"
note="bA375F2.1 (similar to UBL1 (ubiquitin-like
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    note="AluY repeat: matches 1. .282 7110. .27647
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:1083. .22136
                                                                                                                   note="match: GSS: Em:AQ093192"
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                                                                                                                                                                                                                                                                                                                                                                                                                           note="L2 repeat: matches
1722. .32025
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            note="MIR repeat: matches 71.
0761. .30877
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7233. .27346
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1253. .31494
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   note="LIMC4 repeat: matches 6621. .7006 of consensus"
7982. .28315
Tote="LIMC4 repeat: matches 7094. .7422 of consensus"
3256. .28552
TOTE="LIMC5 repeat: matches 7262. .7589 of consensus"
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7. .27437
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3. .26184
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                                   .33725
                                                    repeat: matches 2624.
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 Score
 21;
                                                                                  Em: AQ195587"
                                                                                                     32630)
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Length 158519;
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This sequence was finished as follows unless otherwise noted: all the particular to the overlap as described with a national sequence was finished as follows unless otherwise noted: all the particular to the overlap as described where the particular to the overlap as described above.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest. The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em; EMBL; Sw; SWISSPROT; Tr; TREMBL; Wp; WORMPEP; Information on the WORMPEP database can be found at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (19-OCT-2001) Sanger Centre, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Group. Further information can be found at http://www.sanger.ac.uk/HGP/Chrl
RP11-239E12 is from the library RPCI-11.1 constructed of Pieter de Jong. For further details see
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             http://www.sanger.ac.uk/Projects/C elegans/wormpep This sequence was generated from part of bacterial clone contigs of human chromosome 1, constructed by the Sanger Centre Chromosome 1 Mapp.
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                                                                                                                                                                                                                                                                                                                                                                                                                                           http://www.chori.org/bacpac/home.htm
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ilarity 100.0%;
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/note="Sequence from uni-directional terminator reads only."
1711 c 32256 g 53507 t
                                                                                                                                                                                                                                                                                             organism="Homo sapiens'
/mol_type="genomic DNA"
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Homo sapiens BAC clone RP11-368K23
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On Feb 10, 2
                                                                                                                                                       Submitted (07-NOV-2001) Department of Genetics, Washington University, 4444 Forest Park Avenue, St. Louis, Missouri 6
                                                                                                                                                                                                                                   Submitted (09-AUG-2001)
University, 4444 Forest
7 (bases 1 to 177385)
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Submitted (11-FEB-2001) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St.
                                                                                                                                                                                                                                                                                                                                                                                                                                   5 (bases 1 to 177385) Waterston, R.H.
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Submitted (25-SEP-1999) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St.
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                                                                                                                                                                                                                Waterston,
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Direct Submission
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Mammalia; Eutheria; Primates;
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Center project name: H_NH0368K23
                    Contact: sapiens@watson.wustl.edu
                                                                           Center: Washington University Genome Sequencing Center code: WUGSC
                                                           Web site: http://genome.wustl
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sapiens BAC clone RP11-368K23
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                                                                                                                                                                                                                                                               USA
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NOTICE: This sequence may not represent the entire insert of this clone. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap between neighboring data submissions.

This sequence was finished as follows unless otherwise noted.

This sequence was finished as follows unless otherwise noted: all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >=

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30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by restriction digest.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The clone sequenced to the right is RP11-328L5, 200 bp overlap. Actual start of this clone is at base position 1 of RP11-368K23; actual end is at base position 24222 of RP11-328L5.

Location/Qualifiers
1. .177385
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mapping information for this clone was provided by Dr. John D. McPherson, Department of Genetics, Washington University, St. Louis MO. For additional information about the map position of this sequence, see http://genome.wustl.edu/gsc
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NEIGHBORING SEQUENCE INFORMATION:
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clone_lib="RPCI-11"
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Homo sapiens chromosome UNK clone
SEQUENCE, 44 unordered pieces.
AC104075
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Waterston,R.H.
Direct Submission
Submitted (03-DEC-2001) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Center: Washington University Genome Sequencing Center Center code: WUGSC
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HTG; HTGS_PHASE1; HTGS_I
Homo sapiens (human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Center project name: H_NH0371N22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: submissions@watson.wustl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Web
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Waterston, R.H.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                NOTE: This is a "working draft' sequence. It currently consists of 44 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     npublished
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24198
                 /note="assembly_name:Contig10"
1308. .3233
                                                                            /mol_type="genomic DN
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/chromosome="UNK"
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/mol_type="genomic DNA"
 note="assembly_name:Contig13"
                                                              clone="RP11-371N22"
                                                                                                                                                      ocation/Qualifiers
                                                                                                                                                                 152581: gap of unknown length
161842: contig of 9261 bp in length
161942: gap of unknown length
176479: contig of 14537 bp in length
176579: gap of unknown length
17961: contig of 1382 bp in length
179861: gap of unknown length
179258: contig of 1197 bp in length
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179358: gap of unknown length
180629: contig of 1271 bp in length
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of unknown length
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RESULT 88
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VERSION
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Best Local Similarity
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                                                                       AC117257 180643 bp DNA line Mus musculus chromosome UNK clone RP24-484F21,
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51045. .54856
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/note="assembly_name:Contig33"
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/note="assembly_name:Contig14"
4907. .6495
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78085. .83855
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24198. .26002
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                                   misc_feature
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequencing vector: M13; 0%
Sequencing vector: plasmid; 100%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (09-MAY-2002) Genome Sequencing Center, 4444 Forest Parkway, St. Louis, MO 63108, USA
On May 9, 2002 this sequence version replaced gi:20069845.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Insert size: 193000; agarose-fp
Insert size: 180243; sum-of-contigs
Quality coverage: 9.47 in Q20 bases; agarose-fp
Quality coverage: 10.41 in Q20 bases; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Center project name: M_BB0484F21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Web site:http://genome.wustl.edu/gsc/index.shtml
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Center: Washington University Genome Center code: WUGSC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              McPherson, J.D. and Waterston, R.H. Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: submissions@watson.wust]
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NOTE: This is a 'working draft' sequence. It currently consists of 5 contigs. The true order of the pieces is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                                                                                                                                                   be preserved
                                                                                                                                                                                                                                                                                                                                                                                                                                                           as soon as it is available and the accession number
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                                                                           /note="assembly_name:Contig10" 63733. .160534
                                     /note="assembly_name:Contig11"
160635. .162109
   /note="assembly_name:Contig7"
|62210. .171033
                                                                                                                                                                      'mol_type="genomic DNA"
'db_xref="taxon:10090"
                                                                                                                                                                                                         organism="Mus musculus"
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                                                                                                                                  clone="RP24-484F21"
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                                                                                                                                                                                                                                                               2: contig of 63632 bp in length
2: gap of unknown length
4: contig of 96802 bp in length
4: gap of unknown length
9: contig of 1475 bp in length
9: gap of unknown length
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3: contig of 9510 bp in length.
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O'Chemitred (11.IN-2002) Whitehead Inctitute (MIT Center for Cormonal Colory of the Colory of the Colory of the Colory of the Colory of the Colory of the Colory of the Colory of the Colory of the Colory of the Colory of the Colory of the Colory of the Colory of the Colory of the Colory of the Colory of the Colory of the Colory of the Colory of the Colory of the Colory of the Colory of the Colory of the Colory of the Colory of the Colory of the Colory of the Colory of the Colory of the Colory of the Colory of the Colory of the Colory of the Colory of the Colory of the Colory of the Colory of the Colory of the Colory of the Colory of the Colory of the Colory of the Colory of the Colory of the Colory of the Colory of the Colory of the Colory of the Colory of the Colory of the Colory of the Colory of the Colory of the Colory o
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                       Anderson, S., Arachchi, H.M., Barna, N., Bastien, V., Bloom, T.,
Boguslavkiy, L., Boukhgalter, B., Camarata, J., Chang, J., Choepel, Y.,
Collymore, A., Cook, A., Cooke, P., Corum, B., DeArellano, K.,
Diaz, J.S., Dodge, S., Dooley, K., Dorris, L., Erickson, J., Faro, S.,
Ferreira, P., FitzGerald, M., Gage, D., Galagan, J., Gardyna, S.,
Graham, L., Grand-Pierre, N., Hafez, N., Hagopian, D., Hagos, B.,
Hall, J., Horton, L., Hulme, W., Illev, I., Johnson, R., Jones, C.,
Kamat, A., Karatas, A., Kells, C., Landers, T., Levine, R.,
Lindblad-Toh, K., Liu, G., Lui, A., Mabbitt, R., MacLean, C.,
Macdonald, P., Major, J., Manning, J., Matthews, C., McCarthy, M.,
Meldrim, J., Meneus, L., Mihova, T., Mlenga, V., Murphy, T., Naylor, J.,
Nguyen, C., Nicol, R., Norbu, C., O'Connor, T., O'Donnell, P.,
O'Neil, D., Oliver, J., Peterson, K., Phukhang, P., Pierre, N.,
Pachunka R., Damesew, H., Paylor, J.,
Pachunka R., Damesew, H., Paylor, J., Pierre, N.,
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Mus musculus clone RP23-239013,
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Birren, B., Nusbaum, C.
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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       Raymond, C.,
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Rise, C., Rogov, P.,
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Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
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On Mar 8, 2003 this sequence version replaced gi:28195423.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NOTE: This is a 'working draft' sequence. It currently consists of 5 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    as soon as it is available be preserved.
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Insert size: 181147; sum-of-contigs
Quality coverage: 8.0 in Q20 bases; agarose-fp
Quality coverage: 7.6 in Q20 bases; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequencing vector: Plasmid; n/a; 100% of reads Chemistry: Dye-terminator Big Dye; 100% of reads Assembly program: Phrap; version 0.960731 (Consensus quality: 18074) bases at least Q30 (Consensus quality: 18094) bases at least Q30 (Consensus quality: 181059 bases at least Q30)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: sequence submissions@genome.wi.mit.edu
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15698: gap of 100 bp
17443: contig of 1745 bp in length
17543: gap of 100 bp
39808: contig of 22265 bp in length
39908: gap of 100 bp
76850: contig of 36942 bp in length
76950: gap of 100 bp
181547: contig of 104597 bp in length.
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REFERENCE
AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                              Chemistry: Dye-terminator-amersham: 47% of reads Chemistry: Dye-primer-amersham: 8% of reads Assembly program: Phrap; version 0.990319 Consensus quality: 0 bases at least Q40 Consensus quality: 0 bases at least Q30 Consensus quality: 0 bases at least Q30 Consensus quality: 0 bases at least Q30 Estimated insert size: ##; agarose-fp estimation Estimated insert size: ##; agarose-fp estimation
Base score cutoff: 0.2; Minimal exon length: 3 bp > 'Repeats': BLASTN 2.0.14 (Altschul et al.)
Database(s): * RepBase: ALU (human), released 22-DEC-1995 .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequencing vector: ###;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (09-SBP-2000) GBF, Dept. of Genome Analysis, Mascheroder Weg 1, D-38124 Braunschweig, Germany, E-mail: info.genome@gbf.de On Feb 17, 2003 this sequence version replaced gi:15384820.
All annotations in this database entry are developed by computational tools. It is therefore not explicitly noted in the feature lines that evidence is not experimental.

Mapping was performed at The Sanger Centre
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AL513424.3 GI:28
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Contact: info.genome@gbf.de
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Center: GBF, Braunschweig
Center code: GBF
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1 (bases 1 to 184365)
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Mapping information is available via
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
                                                                   & Skolnick)
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                                                                                                                                                       Grail (Xu et al.), Vers.
                                                                                                                                                                                                                                                                   GeneFinder (Green), Vers. 084
Organism: human
GenScan (Burge & Karlin), Vers. 1.0
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                                                                                                                                                                                                                                                                                                                                     Analysis and annotation were performed with the automatic + first-pass' annotation and submission tool +
                                                                                                                                  Organism: human
                                                                                                                                                          Used matrix: vertebrate; cail (Xu et al.), Vers. 1
                                                                                      Prior probability: 0.04; Overlapping
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Project Information
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noMitter' (Hornischer & Bloecker).
Programs used by 'AnnoMitter';
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Pred. No.
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                       exon
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STS database: 'dbSTS markers'
> 'tRNA Scan': tRNAscan-SE (Lowe & Eddy), Vers. 1.11.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Minimum identity: 70 %;
> 'ESTs': BLASTN 2.0.14
Database(s): * embl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         e-PCR (Schuler)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RepBase: MER (primate), released 22-DEC-1995 .
RepBase: MIR2 (primate), released 22-DEC-1995 .
RepBase: THE (primate), released 22-DEC-1995 .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Using sequence with masked repeats

Minimum score: 60; Minimum identity: 70 %;

'Tandem Repeats': GDE 2.2 option 'tandem'

Minimum length 2 bp; Maximum length 20 bp; Score threshold 2

Treat N's as mismatches? YES; Allow uniform consensi? NO >

'Inverted Repeats': GDE 2.2 option 'inverted'

'Micro Satellites': GDE 2.2 option 'sputnik' (Abajian) > 'CpG

Islands': GDE 2.2 option 'cpg'

CGG island region size 100 bp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              * RepBase: L1 (primate), released 22-DEC-1995 RepBase: MIR (primate), released 22-DEC-1995 .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            embl (EST, other), released -DEC-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Minimum GC contents 50 %; Observed/Expected 0.6 > 'STS Scan':
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Margin: 50; Number of mismatches allowed: 0; Word
                                                                                                                        /note="XPOUND prediction, score : complement (3150 . .3200) /note="92% identity: matches 61. /rpt family="THE" 5882 . .5901
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="91% identity: matches 62.
/rpt_family="THE"
114. .224
/note="XPOUND prediction, complement(8738. .8890)
/note="GENSCAN prediction,
                                                                                                                                                                                                                                                                                                                                                                                                            complement (2475. .2583)
/note="88% identity: matches 334. .442 of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 complement (2323. .2378)
/note="91% identity: matches 369. .424 of consensus"
                                                                                                                                                                                                                                                /rpt_family="L1"
complement(2696.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          complement (2371. .2457)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="XPOUND prediction,
complement(1943. 1981)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="assembly_fragment~clone_end:T7~vector_side:left
assembly_fragment~clone_end:SP6~vector_side:right"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/chromosome="9"
                                                                                                                                                                                                                                                                                                                                               2479. .2666
/note="MZEF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  complement (2006.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="94% identity: matches 85.
/rpt_family="THE"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="86% identity: matches 57.
/rpt_family="ALU"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    note="XPOUND prediction,
                                                                                                 'note="GA repeat"
                                                                                                                                                                                                                                                                                              note="85% identity: matches 829. .924 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                          rpt_family="ALU"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         note="XPOUND prediction,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      clone="RP11-109M15"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  clone_lib="RPCI-11.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               * RepBase: THR ((human), released 22-DEC-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .184365
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    family="ALU"
                                                                                                                                                                                                                                                                                                                                               prediction, score = 0.982"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (Altschul et al.)
(EST, human), rel
                                                                                                                                                                                                                                                   .2752)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                .2017)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       score = 0.240"
                                                score = 0.334"
                                                                                                                                                                                                                      score = 0.274"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          score = 0.375"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           score = 0.212"
     score = 6.37"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               released -DEC-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .143 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .141 of consensus"
                                                                                                                                                                           .111 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  .195 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; Score threshold 20 consensi? NO >
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LOCUS

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Best Local Similarity
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131311 CCTCATGGAGATCATTACCAT 131291
                                                          21;
                  CCTCATGGAGATCATTACCAT 580
                                            u.9%; Score 21;
ilarity 100.0%; Pred. No.
Conservative 0: wire
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            complement(13176. .13440)
/note="84% identity: matches 162.
/rpt_family="L1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 complement(12722. .12984)
/note="88% identity: matches 154.
/rpt_family="ALU"
                                                                                                                                                                                                                          /note="CA repeat"
complement(20400..20508)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     complement (15894. .15983)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="XPOUND prediction, score = 0.227"
14887. .14942
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /rpt_type=INVERTED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /rpt_
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /rpt_type=INVERTED
12721. .13003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="TCTT repeat"
10724. .10894
                                                                                                                                                                                                                                                                                      note="XPOUND prediction, score = 0.325"
19806. 19835
| note="homology = 93.3%, counts = 15"
| rpt_family="ac repeat"
                                                                                                                                                                                                                                                                                                                                                    /note="XPOUND prediction,
18859. .18883
                                                                                                                                                                                                                                                                                                                                                                                                                                              complement (16156. .16224)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="84% identity: matches 71. .160 of
/rpt_family="THE"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="XPOUND prediction,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /rpt_
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           12709. .13002
/note="IR1, 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="MZEF prediction,
l1716. .11793
                                                                                                                                                 note="87% identity: matches 175.
                                                                                                                                                                                                            note="88% identity: matches 494.
                                                                                                                                                                                                                                                                                                                                                                                note="XPOUND prediction, 18420. .18547
                                                                                                                                                                                                                                                                                                                                                                                                                        note="GENSCAN prediction,
                                                                                                                                                                                                                                                                                                                                                                                                                                                           note="XPOUND prediction,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      note="XPOUND prediction,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       note="90% identity: matches 8.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="IR1',
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            note="82% identity: matches 312. .597 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      note="TTTA repeat"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      note="XPOUND prediction,
12705. .12719
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      note="XPOUND prediction, 
12302. .12394
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         note="XPOUND prediction,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           note="XPOUND
                                                                                                                                                                                                                                                                      _type=TANDEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            family="ALU"
                                                                                                                                                                                                  family="ALU"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 tamily="L1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .14694
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .16146
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .13453
                                                                                                                   prediction,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        79% complementary to IR1' (13162. .13453)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     79% complementary to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         prediction,
                                                          Mismatches
                                                                        DB 9;
27;
                                                                                                                     score = 0.739
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 score = 0.808"
                                                                                                                                                                                                                                                                                                                                                                  score = 0.422"
                                                                                                                                                                                                                                                                                                                                                                                                score = 0.382"
                                                                                                                                                                                                                                                                                                                                                                                                                                                           score = 0.244"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         score = 0.319"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   score = 0.640"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        score = 0.626"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             score = 0.203"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         score = 0.273"
                                                                                                                                                                                                                                                                                                                                                                                                                             score = 0.90"
                                                          0
                                                                                       Length 184365;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            . 424
                                                            Indels
                                                                                                                                                                   . 259
                                                                                                                                                                                                               .602
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .416
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TITLE
JOURNAL
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AC120080
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                                                             JOURNAL
                                                                                                                                                                                                                                  Allen, C., Allen, H., Alsbrooks, S., Adams, C., Alder, J., Allen, C., Allen, H., Alsbrooks, S., Amin, A., Anguiano, D., Allen, H., Alsbrooks, S., Amin, A., Anguiano, D., Allen, H., Alsbrooks, S., Amin, A., Anguiano, D., Allen, H., Alsbrooks, S., Amin, A., Anguiano, D., Allen, H., Alsbrooks, S., Amin, A., Anguiano, D., Allen, H., Alsbrooks, S., Amin, A., Anguiano, D., Allen, H., Alsbrooks, S., Amin, A., Anguiano, D., Allen, H., Alsbrooks, S., Alsbrooks, S., Baden, H., Baddon, H., Baddon, H., Baddon, H., Baddon, D., Baddon, D., Baddon, D., Baddon, D., Baddon, D., Baddon, D., Barber, M., Barrstead, M., Benahmed, F., Biswalo, K., Blair, J., Blankenburg, K., Blyth, P., Brown, M., Chen, C., Chen, Z., Chu, J., Chacko, J., Chavez, D., Chen, B., Chen, K., Chen, C., Coyle, M., Cree, A., D. Souza, L., Davila, M., Baroctto, M., Bugene, C., Coyle, M., Cree, A., D. Souza, L., Davila, M., Baroctto, M., Bugene, C., Evans, C.A., Falls, T., Fan, G., Delgado, O., Denson, S., Deramo, C., Ding, Y., Dinh, H., Divya, K., Draper, H., Davya, K., Dunn, A., Durbin, K., Duval, B., Eaves, K., Egan, A., Escotto, M., Bugene, C., Evans, C.A., Falls, T., Fan, G., Falls, T., Fan, G., Praser, C.M., Gabisi, A., Ganta, R., Garcia, A., Garrier, T., Garza, M., Gunaratne, P., Havlak, P., Hawes, A., Henderson, N., Herndandez, J., Herndandez, S., Finls, S., Hulyk, S., Hulyk, S., Hulyk, S., Hulyk, S., Hulyk, S., Hulyk, S., Hulyk, S., Hulyk, S., Hulyk, S., Hulyk, S., Hulyk, S., Hulyk, S., Kally, S., Kally, S., Kally, S., Kally, S., Kally, S., Kally, S., Kally, S., Kally, S., Kally, S., Kally, S., Kally, S., Kally, S., Kally, S., Kally, S., Kally, S., Kally, S., Kally, S., Kally, S., Kally, S., Kally, S., Kally, S., Kally, S., Kally, S., Kally, S., Kally, S., Kally, S., Kally, S., Kally, S., Kally, S., Kally, S., Kally, S., Kally, S., Kally, S., Kally, S., Kally, S., Kally, S., Kally, S., Kally, S., Kally, S., Kally, S., Kally, S., Kally, S., Kally, S., Kally, S., Kally, S., Kally, S., Kally, S., Kally, S., Kally, S., Kally, S., Kally, S., Kally, S., Kall
Submitted (03-MAY-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
                                                                                             Direct Submission
                                                                                                                       Worley, K.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Rattus norvegicus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_ENRICHED RALLUS norvegicus (Norway rat)
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PROGRESS
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BASE COUNT
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TITLE
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On Nov 19, 2002 this sequence version replaced gi:23194715.
The sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequencing reads assembled using Atlas (http://www.hgsc.bcm.tmc.edu/projects/rat/). Each contig described in the feature table below represents a scaffold in the Atlas assembly (a 'contig-scaffold'). Within each contig-scaffold, individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence only contigs will be indicated in the feature
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Rat Genome Sequencing Consortium.
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(see http://www.hgsc.bcm.tmc.edu/docs/Genbank draft data.html).

NOTE: This is a "working draft" sequence. It currently
consists of 2 contigs. The true order of the pieces
is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will
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Consensus quality: 176123 bases at least Q40
Consensus quality: 178360 bases at least Q30
Consensus quality: 179208 bases at least Q20
Estimated insert size: 182713; sum-of-contigs estimation
Quality coverage: 6x in Q20 bases; sum-of-contigs estimation
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Center code: BCM
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                                                                                               end sequence:BZ241333"
185598. .186478
/note="clone_boundary
clone_end:Sp6
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clone_end:T7"
6257._.7382
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clone_end:T7
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/mol_type="genomic DNA"
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/clone="CH230-373P11"
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                          8245 others
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Danio rerio (zebrafish)
Danio rerio
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (09-JUN-2003) Wellcome Trust Sanger Institute, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: zfish-help@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Insert size: 191350; sum-of-contigs
Insert size: 180369; 6.9% error; agarose-fp
Quality coverage: 6.99x in Q20 bases; sum-of-contigs Quality
coverage: 7.42x in Q20 bases; agarose-fp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Assembly program: XGAP4; version 4.5 Chemistry: Dye-terminator; 100% of reads Consensus quality: 190069 bases at least Consensus quality: 190312 bases at least Consensus quality: 190418 bases at least consensus quality: 190418 bases at least
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Web site: http://www.sanger.ac.uk
Contact: zfish-help@sanger.ac.uk
------ Project Information
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1 (bases 1 to 191750)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NOTE: This is a 'working draft' sequence. It currently consists of 5 contigs. The true order of the pieces is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                                                                                                                                           be preserved.
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/note="assembly_fragment:00083
fragment_chain:1"
                                                                                     /db_xref="taxon:7955"
/clone="DKEY-148L4"
                                              /clone_lib="DanioKey"
1. .57919
                                                                                                                                   /organism="Danio rerio"
/mol_type="genomic DNA"
                                                                                                                                                                                                  ocation/Qualifiers
                                                                                                                                                                                                                    57919: contig of 57919 bp in length 58019: gap of 100 bp 64419: contig of 6400 bp in length 64519: gap of 100 bp 79865: contig of 15346 bp in length 79965: gap of 100 bp 138076: contig of 58111 bp in length 138176: gap of 100 bp 191750: contig of 53574 bp in length.
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7-148L4, *** SEQUENCING IN PROGRESS ***,
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27;
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are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be

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NOTE: This is a 'working draft' sequence. It currently consists of 27 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs N, but the exact sizes of the gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hattori, M., Ishii, K., Toyoda, A., Taylor, T.D., Hong-Seog, P., Fujiyama, A., Yada, T., Totoki, Y., Watanabe, H. and Sakaki, Y. Direct Submission
Submitted (22-MAR-2000) Masahira Hattori, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC), and Chemical Research (RIKEN), Genomic Sciences Center (GSC), The Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control 
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On May 30, 2000 this sequence version replaced gi:7328537.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Kitasato Univ., 1-15-1 Kitasato, Sagamihara, Kanagaw
Japan (E-mail:hattori@gsc.riken.go.jp,
URL:http://hgp.gsc.riken.go.jp/, Tel:81-42-778-9923,
Fax:81-42-778-9924)
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                Sequencing vector: PCR products; 100% of reads Sequencing vector: PCR products; 100% of reads Chemistry: Dye-terminator ET-amersham; 100% of reads Assembly program: Phrap; version 0.990329
Consensus quality: 177276 bases at least Q40
Consensus quality: 185320 bases at least Q30
Consensus quality: 188340 bases at least Q20
Consensus quality: 188040 bases at least Q20
Consensus quality: 188070 bases at least Q20
Consensus quality: 1988070 bases at least Q20
Consensus quality: 1988070 bases; sum-of-contigs
Quality coverage: 4.92x in Q20 bases; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: hattori@gsc.riken.go.jr
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60959: gap of 100 bp
72673: contig of 11714 bp in length
72773: gap of 100 bp
85821: contig of 13048 bp in length
85921: gap of 100 bp
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182015: gap of 100 bp
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19127: gap of 100 bp
191605: contig of 1378 bp in 16
191705: gap of 1728 bp in 16
193433: contig of 1728 bp in 16
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170735: gap of 100 bp
175232: contig of 4497 bp
175332: gap of 100 bp
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Submitted (12-DEC-2001) DOE Joint Genome Institute, 2800 Mitchell
Drive, Walnut Creek, CA 94598, USA
On Dec 12, 2001 this sequence version replaced gi:16328262.
Draft Sequence Produced by DOE Joint Genome Institute
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Direct Submission
Submitted (23-OCT-2001) DOE Joint Genome Institute,
Drive, Walnut Creek, CA 94598, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (29-FEB-2000) Production Sequencing Facility, DOE Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 9459 (Dases 1 to 193547)

DOE Joint Genome Institute and Stanford Human Genome Center.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ACU24569 193547 bp DNA linear PRI 12-DEC.
Homo sapiens chromosome 5 clone CTD-2188H20, complete sequence.
ACU24569
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DOE Joint Genome Institute and Stanford Human Genome Center.
                                                                                                                                                                                                                                                                                 Finishing Completed at Stanford Human Genome Center www-shgc.stanford.edu Quality: Phrap Quality >=40 99.6% of Sequence; Estimated Total Number of Errors is 0.4.
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DOB Joint Genome Institute and Stanford Human Genome Center
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DOE Joint Genome Institute.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Direct Submission
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RESULT 95

|   | TITLE<br>JOURNAL<br>COMMENT   | TITLE JOURNAL REFERENCE AUTHORS TITLE JOURNAL REFERENCE AUTHORS   | AC114491 LOCUS DEFINITION ACCESSION VERSION VERSION KEYWORDS SOURCE ORGANISM REFERENCE AUTHORS   |
|---|---|---|--|
| Center: University of Washington Genome Center Center Code: UMGC  Web site: http://www.genome.washington.edu Contact: uwgchtgs@u.washington.edu Drafting Center: SC  Center Clone name: RP11-770C12 (sc0661)  Center project name: chr-1  Center project name: chr-1  Center project name: chr-1  Center project name: chr-1  Center clone name: RP11-770C12 (sc0661)  Sequencing vector: plasmid; 43% of reads Sequencing vector: plasmid; 108752; 57% of reads Chemistry: Dye-terminator ET; 80% of reads Chemistry: Dye-terminator ET; 80% of reads Chemistry: Dye-terminator ET; 80% of reads Consensus quality: 207698 bases at least Q40 Consensus quality: 207698 bases at least Q30 Consensus quality: 207698 bases at least Q30 Consensus quality: 207698 bases at least Q30 Consensus quality: 207698 bases at least Q20  Insert size: 207698; sum-of-contigs  Ouality coverage: 9.9x in Q20 bases; sum-of-contigs  Ouality coverage: 9.9x in Q20 bases; sum-of-contigs  Ouality coverage: 9.9x in Q20 bases; sum-of-contigs  Overlapping Sequences:  S: Mapping in progress 3': RP11-436H6 AL513187, 2000-bp overlap  Sequence Quality abseen annotated with sequence quality estimates computed by the Phrap assembly program.  All manually edited bases have been reduced to quality zero.  Quality levels above 40 are expected to have less than  1 error in 10,000 bp.  Base-by-base quality values are not generally visible from the Gensank flat file format but are available as part  of this entry's ASN.1 file.  This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., Phred granity years) and the assembly was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by the assembly were covered by the resolve all sequencing problems.  Sequence validation: | ission 30-APR-2002) Genome Center, Univ Seattle, WA 98195, USA 002 this sequence version replac | Direct Submission Unpublished 2 (bases 1 to 207698) 2 (bases 1 to 207698) 2 (bases 1 to 207698) 3 (bases 1 to 207698) 3 (bases 1 to 207698) 3 (bases 1 to 207698) 3 (bases 1 to 207698) 3 (bases 1 to 207698) 3 (bases 1 to 207698) 3 (bases 1 to 207698) 3 (bases 1 to 207698) 3 (bases 1 to 207698) 3 (bases 1 to 207698) 3 (bases 1 to 207698) 4 (bases 1 to 207698) 5 (bases 1 to | AC114491 207698 bp DNA linear PRI 30-APR-2002 Homo sapiens chromosome 1 clone RP11-270C12, complete sequence. AC114491.1 GI:19310310 HTG. HOMO sapiens (human) Homo sapiens Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Bukaryota; Metazoa; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 207698) 1 (bases 1 to 207698) Kaul, R.K., Olson, M.V., Zhou, Y., James, R.A., Rouse, G., Wu, Z., Saenphimmachak, C., Phelps, K.A., Buckley, D., Raymond, C. and Haugen, E. D. |

This sequence has been validated by Multiple Complete Digest fingerprinting. Comparison of the experimentally derived digest fragments with sequence-predicted fragments is given below. The electronically-digested sequence consists of both insert and vector, in order to accurately represent the entire circular BAC. Small fragments below a variable cutoff (approximately 400-800 bp) are not resolved in the fingerprint and hence do not appear in the table. There are no significant remaining discrepancies between the experimental and predicted values. Uniquely ordered fragments are separated by dashed lines.

ECORI

| 6250 | 1 44 1 | 638  | 317  | 4371 | 5992 | 2080  | ۱ :   | : :  |      |      | 1934 | 5801 |        | : :  | 1164 |      | 2860  | 5780 |      | 2266 | 295  |       | 744  | 4201 |      | 588   |      | 69   | 1                                       | Мар       |     |
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| 248  | 5423   | 63   | 131  | 52   | 320  |       |       |      | 1275 | :    | :    |      |        | : !  | 8593 |      |       | . :  |      | 6658 |      | :     |      |      |      | 19478 | 206  | ω    |   | qDerM     | Bg1 |
| <800 | 5497   | 6410 | 1249 | 5497 | 3215 | 14529 | 1692  | 1249 | 1249 | 1556 | 6410 | 3018 | 9578   | 2554 | 8565 | 1249 | 4892  | 5843 | 2720 | 8565 | <800 | 24165 | 7854 | 1836 | 7270 | 19218 | 2058 | 3787 |   |           | II  |
| 2527 | :      | 238  | 520  | 5845 | 3127 | 2683  | 7440  |      | 3213 |      |      |      | !<br>! |      |      | ,    | 5942  |      |      | 9462 | : :  | :     | 505  |      | 449  | 512   | :    |      | 1 | SeqDerMap | 1   |
| 2491 | 1620   | <800 | <800 | 5812 | 3064 | 2693  | 7392  | 2693 | 3434 | 4448 | 3591 | 2491 | 9221   | 6382 | 3591 | 8677 | 60,03 | 731  | <800 | 9221 | 1501 | 4963  | <800 | 2129 | <800 | <800  | 6382 | 3784 |   | 18        | :   |

| VERSION<br>VERSION<br>KEYWORDS                                     |  |      | Qy , 1219          | Query Match<br>Best Local S |      |   |      |      |      |      |      |      |                 |                      |         |       |      |      |      |      |   |       |       |      |       |       |         |         |                      |      |                    |
|--|--|------|--------------------|-----------------------------|------|---|------|------|------|------|------|------|-----------------|----------------------|---------|-------|------|------|------|------|---|-------|-------|------|-------|-------|---------|---------|----------------------|------|--------------------|
| AC119573<br>AC119573.3 GI:30017949<br>HTG; HTGS_PHASE2; HTGS_DRAFT | AC119573<br>Mus musculus clone<br>pieces |      | .9 AACTGTTAAAAATCT | a i                         | 6476 | -   | 1    | 3346 | 678  |      | 1476 | 2447 | 2499            | 5752                 | 1552    | 3734  | 2127 | 7431 | 2134 | 5483 | 1519  |       | 1642  | 684  | 1153  | 845   | 8253    |         | 4453                 | 3000 | 557                |
| GI:3001794<br>HASE2; HTGS  | s clone RP2                              |      | AATCTTGAAAG        | .04                         | 6358 | 2381  | <800 | 3365 | <800 | 1511 | 1511 | 2506 | 2506            | 5747                 | 1511    | 3660  | 2087 | 7350 | 2087 | 5369 | 1511  | 2878  | 1578  | <800 | 1111  | 839   | 8138    | 22765   | 4397                 | 3024 | <b>&lt;</b> 800    |
| DRAFT.   | , <sup>b</sup>                           | 9934 | ; MIBMACCHES       | core 21;<br>Pred. No.       |      |   |      |      |      |      |      |      |                 |                      | •       |       |      |      |      | 2375 | 4505  | 2551  | 3438  | 2535 | _ :   | 3005  | 6907    | 9793    | : :                  | 2673 | 1318               |
|  | DNA 1<br>WORKING DRAFT                   |      | ·                  | , <sub>9</sub>              | •    |   |      |      |      |      |      |      |                 |                      |         |       | -    |      |      | 2554 | 4535  | 2554  | 3410  | 2554 | 10774 | 3018  | 6913    | 9578    | 4535                 | 2720 | 1249               |
|  | linear HTG<br>DRAFT SEQUENCE,            |      | inders o;          | 7698                        | 6215 | 2246  |      | 336  | 3632 | 1    | 2097 | 716  | 632             | 1537                 | 3208    | 3846  | 250  |      | 3900 | 179  | 5094  | 10650 | 11091 | 2704 |       | 11097 | 331     | 16194   | 553                  | 4827 | 11716              |
|  | 23-APR-2003<br>5 ordered                 |      | Gaps 0;            |                             | 6382 | 2232  | <800 | <800 | 3784 | <800 | 2048 | <800 | <b>&lt;8</b> 00 | 1501                 | 3194    | 3784  | <800 | 954  | 3784 | <800 | 4963  | 10274 | 10703 | 2827 | 731   | 10703 | <800    | 16511   | <800                 | 4714 | 11413              |
|  |  |      | •                  |                             |      |   |      |      |      |      |      |      |                 |                      |         |       |      |      |      |      |   |       |       |      |       |       | •       |         |                      |      |                    |
|  |  |      |                    |                             |      |   |      |      |      |      |      |      |                 |                      |         |       |      |      |      |      |   |       |       |      |       |       |         |         |                      |      |                    |
|  |  |      | COMMEN             | JOURNAL                     |      | Spencer, B., Stange-Thomann, N., Stojanovic, N., Stubbs, N., Talamas, J., Tesfaye, S., Theodore, J., Topham, K., Travers, M., |      |      |      |      |      |      |                 | REFERENCE<br>AUTHORS | JOURNAL | TITLE |      |      |      |      | McCarthy, M., McEwan, P., McKernan, K., Meldrim, J., Meneus, L., Mihova, T., Mlenga, V., Murphy, T., Naylor, J., Nguyen, C., Nicol, R., |       |       |      |       |       | AUTHORS | JOURNAL | REFERENCE<br>AUTHORS |      | SOURCE<br>ORGANISM |

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1 44490: contig of 44490 bp in length

44491 44590: gap of 100 bp

* 44591 112691: contig of 68101 bp in length

* 112692 112791: gap of 100 bp

* 112792 149514: contig of 36723 bp in length

* 1149515 149614: gap of 100 bp

* 149615 206355: contig of 56741 bp in length

* 206356 206455: gap of 100 bp

206456 219687: contig of 13232 bp in length
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21; Conserv
Muzny, D.Marie., Metzker, M.Lee., Abramzon, S., Adams, C., Alder, J., Allen, C., Allen, H., Alsbrooks, S., Amin, A., Anguiano, D., Anyalebechi, V., Aoyagi, A., Ayodeji, M., Baca, E., Baden, H., Baldwin, D., Bandaranaike, D., Barber, M., Barnstead, M., Benahmed, F., Biswalo, K., Blair, J., Blankenburg, K., Blyth, P., Brown, M., Bryant, N., Buhay, C., Burch, P., Burrell, K., Calderon, E., Cardenas, V., Carter, K., Cavazos, I., Ceasar, H., Center, A., Chacko, J., Chavez, D., Chen, G., Chen, R., Chen, Y., Chen, Z., Chu, J., Cleveland, C., Cockrell, R., Cox, C., Coyle, M., Cree, A., D'Souza, L., Davila, M.L., Davis, C., Davy-Carroll, L., De Anda, C., Dederich, D.,
                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                          HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_FULLTOP Rattus norvegicus (Norway rat)
                                                                                                                                                                                                                                                                               Rattus.
                                                                                                                                                                                                                                                                                                                                                        Rattus norvegicus
                                                                                                                                                                                                                                                                                                                                                                                                                          AC098602
AC098602.7 GI:30581472
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Rattus norvegicus clone CH230-138H1, WORKING DRAFT SEQUENCE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AC098602
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         is believed to be correct as given, however the sizes of the gaps between them are based on estimates that have provided by the submittor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TTACCATCTGAAACTGTTAAA 190507
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This sequence will be replaced by the finished sequence as soon as it is available and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   are represented as runs of N. The order of the pieces
                                                                                                                                                                                                                                              (bases 1 to 223266)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0.9%; Score 21; DB clarity 100.0%; Pred. No. 27 Conservative 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="assembly_fragment
clone_end:T7
vector_side:right"
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206456. .219687
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="assembly_fragment"
149615. 206355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="assembly_fragment"
112792. .149514
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Location/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="assembly_fragment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           clone_lib="RPCI-23 Female Mouse BAC"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /db_xref="taxon:10090"
/clone="RP23-75H23"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  type="genomic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         side:right"
0 c 40411 g
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27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             linear
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REFERENCE AUTHORS TITLE

JOURNAL

COMMENT

Web site: http://www.hgsc.bcm.tmc.edu/Contact: hgsc-help@bcm.tmc.edu

Center: Baylor Co

College

of Medicine

REFERENCE AUTHORS

JOURNAL

JOURNAL TITLE

ocus

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Delgado, O., Denson, S., Deramo, C., Ding, Y., Dinh, H., Divya, K., Draper, H., Dugan-Rocha, S., Dunn, A., Durbin, K., Duval, B., Eaves, K., Egan, A., Escottco, M., Eugene, C., Evans, C.A., Falls, T., Fan, G., Fernandez, S., Finley, M., Flagg, N., Forbes, L., Foster, M., Foster, P., Fraser, C.M., Gabhsi, A., Ganta, R., Garcia, A., Garner, T., Garza, M., Gebregeorgis, E., Geer, K., Gill, R., Gracia, A., Garner, T., Garza, M., Gebregeorgis, E., Geer, K., Gill, R., Gracy, M., Guerra, W., Guerra, W., Guerra, W., Guerra, W., Guerra, W., Guerra, W., Guerra, W., Guerra, W., Guerra, W., Guerra, W., Guerra, W., Guerra, W., Guerra, W., Guerra, W., Guevara, W., Gunzathe, P., Hadlah, S.L., Henderson, N., Hernandez, J., Hernandez, R., Halak, P., Hawes, A., Henderson, N., Hernandez, J., Hernandez, R., Hull, Y., Johnson, B., Johnson, R., Jolivet, A., Jockson, L., Jacob, L., Jiang, H., Johnson, B., Johnson, R., Jolivet, A., Jockson, L., Jacob, L., Liu, J., Liu, J., Liu, J., Liu, J., Liu, J., Lu, M., Johnson, B., Johnson, R., Jolivet, A., Jockson, L., Jacob, L., Lebow, H., Levan, J., Lewis, L., Li, Z., Liu, J., Liu, J., Liu, J., Liu, J., London, P., Longacre, S., Lopez, J., Lorandon, R., Johnson, R., Jolivet, A., Martin, K., Martin, R., Martinez, E., Mangum, B., Mapua, P., Martin, K., Martin, R., Martinez, E., Mangum, B., Mapua, P., Martin, K., Martin, R., Martinez, E., Mangum, B., Mapua, P., Martin, K., Martin, R., Martinez, E., Mangum, A., Milosa, Jevis, A., Miner, G., Minja, E., Montemayor, J., Moore, S., Morgan, M., McLeod, M.P., McNeill, T. Z., Meenen, E., Milosa, M., Morris, S., Munidasa, M., Murphy, M., Nair, L., Mankeryis, C., Neal, D., Newton, N., Nguyen, N., Norris, S., Parks, K., Palster, G., Minja, E., Montemayor, J., Moore, S., Markeryis, C., Neal, D., Newton, N., Nguyen, N., Norris, S., Parks, K., Palster, M., Richards, S., Reigh, R., Riggs, F., Rives, C., Rodkey, T., Rojas, A., Popovic, D., Pfannkoch, C., Pala, S., Parks, K., Palster, M., Richards, S., Raigs, D., Marten, J., Walter, R., Welz, S., Mither, R., Walt
                                                                     of Molecular and Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
On May 13, 2003 this sequence version replaced gi:23617936.
The sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequencing reads assembled using Atlas (http://www.hgsc.bcm.tmc.edu/projects/rat/). Each contig described in the feature table below represents a scaffold in the Atlas assembly (a 'contig-scaffold'). Within each contig-scaffold, individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence reads. Both end sequences and whole genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Worley, K.C.
Direct Submission
Submitted (26-OCT-2001) Human Genome Sequencing Center, Department Of Molecular and Human Genetics, Baylor College of Medicine, One of Molecular and Human Genetics, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Rat Genome Sequencing Consortium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (bases
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Genome Center
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RESULT 98
AC106341
                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE
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ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VERSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
Matches 21; Conserv
                                                                                                                                                                                                                                                                                                                                                                  AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     source
Nuzny, D. Marie . Metzker, M.Lee., Abramzon, S., Adams, C., Alder, J., Allen, C., Allen, H., Alabrooke, S., Amin, A., Anguiano, D., Anyalebechi, V., Aoyagi, A., Ayodeji, M., Baca, E., Baden, H., Baldwin, D., Bandaranaike, D., Barber, M., Barnstead, M., Benahmed, F., Biswalo, K., Blair, J., Blankenburg, K., Blyth, P., Brown, M., Bryant, N., Buhay, C., Burch, P., Burrell, K., Calderon, E., Cardenas, V., Carter, K., Cavazos, I., Ceasar, H., Center, A., Checko, J., Chacko, J., Chen, G., Chen, R., Chen, Y., Chen, Z., Chen, Z., Chen, A., Davila, M. L., Davis, C., Davy-Carroll, L., De Anda, C., Dederich, D., Delgado, O., Denson, S., Denamo, C., Ding, Y., Dinh, H., Divya, K., Egan, A., Escotto, M., Eugene, C., Evans, C.A., Falls, T., Fan, G., Fernandez, S., Finley, M., Flagg, N., Forbes, L., Foster, M., Foster, P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2127 CAGTAGAGGAAACACCTGCTG 2147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AC106341
AC106341.5 GI:30581326
HTG; HTGS PHASE1; HTGS DRAFT; HTGS ENRICHED.
Rattus norvegicus (Norway rat)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Rattus norvegicus clone CH230-154023, ***, 2 unordered pieces.
                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Rattus norvegicus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AC106341
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           65373
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           be preserved.
                                                                                                                                                                                                                                                                                                                                                                                         (bases 1 to 226427)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Assembly program: Atlas 3.0;
Consensus quality: 207235 bases at least Q40
Consensus quality: 209483 bases at least Q30
Consensus quality: 211150 bases at least Q20
Estimated insert size: 228805; sum-of-contigs estimation
Quality coverage: 7x in Q20 bases; sum-of-contigs estimat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           221314
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="clone_boundary
clone_end:T7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 site:EcoRI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /clone="CH230-138H1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /mol_type="genomic DNA"
/db_xref="taxon:10116"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        organism="Rattus norvegicus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     nd_sequence:RWAWW37TJB"
44898 c 44784 g 57395 t 10816 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     221213: contig of 221213 bp in length 221313: gap of unknown length 223266: contig of 1953 bp in length.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 21; DB 2; Pred. No. 27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               226427 bp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCING
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F IN PROGRESS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0
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REFERENCE AUTHORS TITLE JOURNAL

TITLE JOURNAL

REFERENCE TITLE JOURNAL

AUTHORS

COMMENT

Center: Baylor Co Center code: BCM Web site: http://

-- Genome Center College

of Medicine

Web site: http://www.hgsc.bcm.tmc.edu/ Contact: hgsc-help@bcm.tmc.edu ------ Project Information

Assembly program: Atlas 3.0;
Consensus quality: 211153 bases at least Q40

Center clone name: CH230-154023 Center project name: GKSI 밁 Ś

Cocus

SOURCE

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AL Submitted (13-MAY-2003) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

On May 13, 2003 this sequence version replaced gi:25007771.

The sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequencing reads assembled using Atlas (http://www.hgsc.bcm.tmc.edu/projects/rat/). Each contig described in the feature table below represents a scaffold in the Atlas assembly (a 'contig-scaffold'). Within each contig-scaffold, individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence may extend beyond the ends of the clone and there may be sequence contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence contigs will be indicated in the feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hernandez R., Hines, S., Hladdun, S.L., Hodgson, A., Hogues, M.,
Hollins, B., Howells, S., Hladdun, S.L., Hodgson, A., Hogues, M.,
Jackson, L., Jacob, L., Jiang, H., Johnson, R., Hogues, M.,
Karpathy, S., Kelly, S., Kelly, S., Khan, Z., King, L., Kovar, C.,
Karpathy, S., Kelly, S., Kelly, S., Khan, Z., King, L., Kovar, C.,
Liu, J., Liu, W., Liu, Y., London, P., Longacre, S., Lopez, J.,
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Maheshwari, M., Mahindartne, M., Mahmoud, M., Malloy, K., Mangum, A.,
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Mawhiney, S., Wcleod, M.P., McNeill, T.Z., Menen, E.,
Martinez, S., Munidasa, M., Murphy, M., Nair, L.,
Nankervis, C., Neal, D., Newton, N., Nguyen, N., Norris, S.,
Naokelemeth, O., Okwuonu, G., Olarnpunsagoon, A., Pal, S., Parks, K.,
Pasternak, S., Paul, H., Perez, A., Perez, L., Pfannkoch, C.,
Plopper, F., Poindexter, A., Popovic, D., Primus, E., Pu, L.-L.,
Plazor, M., Quiroz, J., Rachlin, E., Reeves, K., Regier, M.A., Reigh, R.,
Reilly, B., Reilly, M., Ren, Y., Reuter, M., Richards, S., Shen, H.,
Sanders, W., Savery, G., Scherer, S., Scott, G., Shatsman, S., Shen, H.,
Sneed, A., Sodergren, E., Song, X.-Z., Sorelle, R., Sosa, J.,
Shetty, J., Shvartsbeyn, A., Sisson, I., Sitter, C.D., Smajs, D.,
Shetty, J., Shvartsbeyn, A., Sisson, I., Sitter, C.D., Smajs, D.,
Steinle, M., Strong, R., Sutton, A., Vatek, A., Trejos, Z., Usmani, K.,
Valas, R., Wu, J., Yakub, S., Yen, J., Waite, F.,
Wang, Q., Wang, S., Warren, J., Water, R., Wooden, H., Worley, K.,
Williams, G., Willson, R., Wu, J., Yakub, S., Yen, J., Yoon, L., Yoon, V.,
Yu, F., Zhang, J., Zhou, J., Zhou, J., Zhou, S., Dunn, D., von
Niederhausern, A., Weiss, R., Smith, D.R., Holt, R.A., Smith, H.O.,
Weinstock, G. and Gibbs, R.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (12-JAN-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA 3 (bases 1 to 226427)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Rat Genome Sequencing Consortium.
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VERSION
KEYWORDS
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AC112436
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AUTHORS
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Best Local Similarity
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                   Muzny, D. Marie, Metzker, M. Lee., Abramzon, S., Adams, C., Alder, J.,
Allen, C., Allen, H., Alsbrooks, S., Anin, A., Angulano, D.,
Anyalebechi, V., Aoyagi, A., Ayodeji, M., Baca, E., Baden, H.,
Baldwin, D., Bandaranaike, D., Barber, M., Barnstead, M., Benahmed, F.,
Baldwin, D., Bandaranaike, D., Barber, M., Barnstead, M., Benahmed, F.,
Bliswalo, K., Blair, J., Blankenburg, K., Blyth, P., Brown, M.,
Bryant, N., Buhay, C., Burch, P., Burrell, K., Calderon, E.,
Cardenas, V., Carter, K., Cavazos, I., Ceasar, H., Center, A.,
Chen, Z., Chen, Z., Chen, Z., Chen, Z., Chu, J.,
Chacko, J., Chavez, D., Chen, G., Chen, R., Chen, Y., Chen, Z., Chu, J.,
Cleveland, C., Cockreil, R., Cox, C., Coyle, M., Cree, A., D'Souza, L.,
Davila, M. L., Davis, C., Davy, Carroll, L., De Anda, C., Dederich, D.,
Delgado, O., Denson, S., Dunn, A., Durbin, K., Duval, B., Baves, K.,
Eggan, A., Escotto, M., Eugene, C., Evans, C.A., Falls, T., Fan, G.,
Fernandez, S., Finley, M., Flagg, N., Forbes, L., Foster, M., Foster, P.,
Fraser, C.M., Gabisi, A., Ganta, R., Garcia, A., Garrer, T., Garza, M.,
Gebregeorgis, B., Geer, K., Gill, R., Garddy, M., Guerra, W., Guevaa, M.,
Gunaratne, P., Haaland, W., Hamilton, C., Hamilton, K.,
Henderson, N., Hernandez, J.,
Hander, J., Hamilton, C., Hamilton, K.,
Harley, Y., Havlak, P., Hawes, A., Henderson, N., Hernandez, J.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AC112436 236764 bp DNA linear HTG 15-NOV-2002
Rattus norvegicus clone CH230-153L4, *** SEQUENCING IN PROGRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Rattus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa;
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(see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).

NOTE: This is a 'working draft' sequence. It currently
consists of 2 contigs. The true order of the pieces
is not known and their order in this sequence record is
arbitrary. Gaps between the contigs are represented as
runs of N, but the exact sizes of the gare unknown.
This record will be updated with the finished sequence
as soon as it is available and the accession number will
be preserved.
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225387
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223249. .225286
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48875 c 48593 g
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/mol_type="genomic DNA"
/db_xref="taxon:10116"
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Rodentia;
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Henderson, N., Hernandez, J., S.L., Hodgson, A., Hogues, M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 2;
27;
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REFERENCE AUTHORS

JOURNAL

COMMENT

Web site: http://www.hgsc.bcm.tmc.edu/Contact: hgsc-help@bcm.tmc.edu

Center: Baylor College of Medicine Center code: BCM

JOURNAL REFERENCE

AUTHORS TITLE

JOURNAL

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SOURCE

ORIGIN

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Submitted (15-NOV-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
On Nov 15, 2002 this sequence version replaced gi:22856698.
The sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequencing reads assembled using Atlas (http://www.hgsc.bcm.tmc.edu/projects/rat/). Each contig described in the feature table below represents a scaffold in the Atlas assembly (a 'contig-scaffold'). Within each contig-scaffold, individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Norgan, M., Norris, K., Morris, S., Munidasa, M., Murphy, M., Nair, L., Nankervis, C., Neal, D., Newton, N., Nguyen, N., Norris, S., Nwaokelemeh, O., Okwuonu, G., Olarnpunsagoon, A., Pal, S., Parks, K., Pasternak, S., Paul, H., Perez, A., Perez, L., Pfannkoch, C., Plopper, F., Poindexter, A., Popovic, D., Primus, E., Pu, L.-L., Plopper, M., Quiroz, J., Rachlin, E., Reeves, K., Regier, M.A., Reigh, R., Reilly, B., Reilly, M., Ren, Y., Reuter, M., Richards, S., Riggs, F., Rives, C., Rodkey, T., Rojas, A., Rose, M., Rose, R., Ruiz, S.J., Sanders, W., Savery, G., Scherer, S., Scott, G., Shatsman, S., Shen, H., Shetty, J., Shvartsbeyn, A., Sisson, I., Sitter, C.D., Smajs, D., Shetty, J., Shvartsbeyn, A., Sisson, I., Sitter, C.D., Smajs, D., Shetty, J., Strong, R., Song, X.-Z., Sorelle, R., Sosa, J., Sneed, A., Sodergren, E., Song, X.-Z., Sorelle, R., Sosa, J., Steinle, M., Strong, R., Sutton, A., Svatek, A., Tabor, P., Taylor, C., Taylor, T., Thomas, N., Thomas, S., Tingey, A., Trejos, Z., Usmani, K., Valas, R., Vera, V., Villasana, D., Waldron, L., Walker, B., Wang, J., Warren, J., Warren, R., Wei, X., White, F., Waright, D., Wright, R., Wu, J., Yakub, S., Yen, J., Yoon, L., Yoon, V., Yu, F., Zhang, J., Zhou, X., Zhou, S., Dunn, D., von, V., Weinstock, G., and Gibbs, R.A.
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Mahindartne, M., Mahhmoud, M., Malloy, K., Mangum, A., Martin, R., Martinez, E., Mangum, B., Martin, R., Martinez, E., Mahiney, S., McLeod, M.P., McNeill, T.Z., Meenen, E., Milosavljevic, A., Miner, G., Minja, E., Montemayor, J., Moore, S., Mair, L., Montemayor, J., Moore, S., Mair, L., Montemayor, J., Mair, L., Mair, L., Martinez, B., Mair, L., Mair, L., Mair, L., Mair, L., Mair, L., Mair, L., Mair, L., Mair, L., Mair, L., Mair, L., Mair, L., Mair, L., Mair, L., Mair, L., Mair, L., Mair, L., Mair, L., Mair, L., Mair, L., Mair, L., Mair, L., Mair, L., Mair, L., Mair, L., Mair, L., Mair, L., Mair, L., Mair, L., Mair, L., Mair, L., Mair, L., Mair, L., Mair, L., Mair, L., Mair, L., Mair, L., Mair, L., Mair, L., Mair, L., Mair, L., Mair, L., Mair, L., Mair, L., Mair, L., Mair, L., Mair, L., Mair, L., Mair, L., Mair, L., Mair, L., Mair, L., Mair, L., Mair, L., Mair, L., Mair, L., Mair, L., Mair, L., Mair, L., Mair, L., Mair, L., Mair, L., Mair, L., Mair, L., Mair, L., Mair, L., Mair, L., Mair, L., Mair, L., Mair, L., Mair, L., Mair, L., Mair, L., Mair, L., Mair, L., Mair, L., Mair, L., Mair, L., Mair, L., Mair, L., Mair, L., Mair, L., Mair, L., Mair, L., Mair, L., Mair, L., Mair, L., Mair, L., Mair, L., Mair, L., Mair, L., Mair, L., Mair, L., Mair, L., Mair, L., Mair, L., Mair, L., Mair, L., Mair, L., Mair, L., Mair, L., Mair, L., Mair, L., Mair, L., Mair, L., Mair, L., Mair, L., Mair, L., Mair, L., Mair, L., Mair, L., Mair, L., Mair, L., Mair, L., Ma
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Rat Genome Sequencing Consortium.
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-- Genome Center
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RESULT 100
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Best Local
                                                                                                                                                                                                                                                                                AUTHORS
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2127 CAGTAGAGGAAACACCTGCTG 2147
                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                               Rattus norvegicus
                                                                                                                                                                                                                                                                                                                                                                             HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_ENRICHED RATTUS norvegicus (Norway rat)
                                                                                                                                                                                                                                                                                                                                                                                                                    AC130777.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                     4 unordered
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Rattus norvegicus clone CH230-24M8,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NOTE: Estimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/docs/Genbank draft/data.h NOTE: This is a 'working draft' sequence. It currently consists of 4 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    be preserved.
                                                                                                                                                                                                                                                                                              (bases 1 to 240929)
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233807
233907
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4988. .6368
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48477 c 48404 g
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="wgs_contig"
231874. .233806
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /mol_type="genomic DNA
/db_xref="taxon:10116"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             organism="Rattus norvegicus"
                                                                                                                                                                                                                                                                                                                                                                                                                  GI:23267876
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4887: contig of 4887 bp in length
4987: gap of unknown length
233806: contig of 228819 bp in length
233906: gap of unknown length
235915: contig of 1109 bp in length
235115: gap of unknown length
235115: gap of unknown length
235764: contig of 1649 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 21;
; Pred. No.
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, *** SEQUENCING IN PROGRESS ***,
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                                                    Foster, P.,
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В ş

Focus

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Hollins, B., Howells, S., Hulk, S., Hume, J., Idebird, D., Jackson, A., Jackson, L., Jackson, L., Jang, H., Johnson, B., Johnson, R., Jolivet, A., Karpathy, S., Kelly, S., Kelly, S., Khan, Z., King, L., Kovar, C., Karpathy, S., Kelly, S., Kelly, S., Khan, Z., King, L., Kovar, C., Kowls, C., Kraft, C.L., Lebbw, H., Levan, J., Lewis, L., Li, Z., Liu, J., Liu, J., Liu, J., Liu, J., Liu, J., Liu, J., Liu, J., Loused, H., Lozado, R.J., Lu, X., Ma, J., Liu, J., Lorensuhewa, L., Loulseged, H., Lozado, R.J., Lu, X., Ma, J., Lovez, J., Loue, J., Loue, J., Loue, J., Loue, J., Loue, J., Loue, J., Loue, J., Loue, J., Loue, J., Loue, J., Loue, J., Loue, J., Loue, J., Loue, J., Loue, J., Loue, J., Loue, J., Loue, J., Loue, J., Loue, J., Loue, J., Loue, J., Loue, J., Loue, J., Loue, J., Loue, J., Loue, J., Loue, J., Loue, J., Loue, J., Loue, J., Loue, J., Loue, J., Loue, J., Loue, J., Loue, J., Loue, J., Loue, J., Loue, J., Loue, J., Loue, J., Loue, J., Loue, J., Loue, J., Loue, J., Loue, J., Loue, J., Loue, J., Loue, J., Loue, J., Loue, J., Loue, J., Loue, J., Loue, J., Loue, J., Loue, J., Loue, J., Loue, J., Loue, J., Loue, J., Loue, J., Loue, J., Loue, J., Loue, J., Loue, J., Loue, J., Loue, J., Loue, J., Loue, J., Loue, J., Loue, J., Loue, J., Loue, J., Loue, J., Loue, J., Loue, J., Loue, J., Loue, J., Loue, J., Loue, J., Loue, J., Loue, J., Loue, J., Loue, J., Loue, J., Loue, J., Loue, J., Loue, J., Loue, J., Loue, J., Loue, J., Loue, J., Loue, J., Loue, J., Loue, J., Loue, J., Loue, J., Loue, J., Loue, J., Loue, J., Loue, J., Loue, J., Loue, J., Loue, J., Loue, J., Loue, J., Loue, J., Loue, J., Loue, J., Loue, J., Loue, J., Loue, J., Loue, J., Loue, J., Loue, J., Loue, J., Loue, J., Loue, J., Loue, J., Loue, J., Loue, J., Loue, J., Loue, J., Loue, J., Loue, J., Loue, J., Loue, J., Loue, J., Loue, J., Loue, J., Loue, J., Loue, J., Loue, J., Loue, J., Loue, J., Loue, J., Loue, J., Loue, J., Loue, J., Loue, J., Loue, J., Loue, J., Loue, J., Loue, J., Loue, J., Loue, J., Loue, J., Loue, J., Loue, J., Loue, J., Loue, J., Lou
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (22-SEP-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA. On Sep 22, 2002 this sequence version replaced gi:22218436. The sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequening reads assembled using Atlas and whole sequence time sequence years assembled using Atlas (http://www.hgsc.bcm.tmc.edu/projects/rat/). As a result, the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (14-AUG-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA 3 (bases 1 to 240929)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2 (bases 1 to 240929)
Rat Genome Sequencing Consortium
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                                               Center project name: GNZE
Center clone name: CH230-24M8
Center clone name: CH230-24M8
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Centersus quality: 220582 bases at least Q30
Centersus quality: 222697 bases at least Q20
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Centersus quality: 222697 bases at least Q20
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Quality coverage: 4x in Q20 bases; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: hgsc-help@bcm.tmc.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Web site: http://www.hgsc.bcm.tmc.edu/
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TITLE JOURNAL REFERENCE AUTHORS

TITLE JOURNAL

COMMENT

NOTE: Estimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/docs/Genbank\_draft\_data.html).
NOTE: This is a "working draft' sequence. It currently consists of 4 contigs. The true order of the pieces

REFERENCE AUTHORS TITLE JOURNAL

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Search completed: November 14, 2003, 06:25:58 Job time: 8795 secs
                                                                                                                                                                                                                                                    BASE COUNT
ORIGIN
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                                                                                                                                                               Query Match 0.9%; Score 21; DB 2; Length 240929; Best Local Similarity 100.0%; Pred. No. 27; Matches 21; Conservative 0; Mismatches 0; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                      misc_feature
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                                                                                                          1919 ATTAAATTTGCTTGGTTTGAT 1939
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120442
120542
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1120542, 1121801
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Rattus norvegicus"
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|/db xref="reaxon:10116"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     10759: contig of 10759 bp in length 10859: gap of unknown length 120441: contig of 10582 bp in length 120541: gap of unknown length 239388: contig of 118847 bp in length 239488: gap of unknown length 239488: gap of unknown length 240929: contig of 1441 bp in length.
                                                                                                                                                                                                                                                                       16895 others
                                                                                                                                                                 0
                                                                                                                                                                 Gaps
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В